

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 3, 2003, 08:09:29 ; Search time 19.5358 Seconds

(Without alignments)
531.460 Million cell updates/sec

Title: US-09-644-668a-9

Perfect score: 561
Sequence: 1 EIVLTQSPGTLSTLSPGERAT.....CQOYSSPWTFGQTKVEIK 108

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database: PIR 73:*

1: PIR1:.*
2: PIR2:.*
3: PIR3:.*
4: PIR4:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	555	98.9	108	2	C30608 Ig kappa chain V-I
2	552	98.4	129	1	K3HUI1 Ig kappa chain pre
3	546	97.3	109	2	H30601 Ig kappa chain V-I
4	545	97.1	109	2	B30601 Ig kappa chain V-I
5	544	97.0	109	2	D30601 Ig kappa chain V-I
6	542	96.6	109	2	C30601 Ig kappa chain V-I
7	541	96.4	129	1	K3HUIA Ig kappa chain pre
8	538	95.9	109	2	PH0963 Ig kappa chain V-I
9	538	95.9	109	2	F30607 Ig kappa chain V-I
10	537	95.7	109	2	A30608 Ig kappa chain V-I
11	537	95.7	129	2	S49532 Ig kappa chain V-I
12	536	95.5	109	2	G30601 Ig kappa chain V-I
13	536	95.5	129	2	S46369 Ig kappa chain var
14	536	95.5	134	2	S38643 Ig kappa chain V-I
15	535	95.4	109	1	K3HUI1 Ig kappa chain V-I
16	534.5	95.3	114	2	S46375 Ig kappa chain V-I
17	533	95.0	109	1	K3HUI1 Ig kappa chain V-I
18	531	94.7	107	2	PH0965 Ig kappa chain V-I
19	531	94.5	109	2	G30607 Ig kappa chain V-I
20	530	94.5	109	2	F30601 Ig kappa chain V-I
21	530	94.5	128	2	S20636 Ig kappa chain V-I
22	521	92.9	109	1	K3HUI1 Ig kappa chain V-I
23	520	92.7	110	2	S20635 Ig kappa chain V-I
24	519	92.5	108	2	B30608 Ig kappa chain V-I
25	519	92.5	121	2	S40327 Ig kappa chain V-I
26	516.5	92.1	110	2	E30607 Ig kappa chain V-I
27	515	91.8	124	2	S20633 Ig kappa chain - h
28	515	91.8	129	2	A32274 Ig kappa chain pre
29	514.5	91.7	108	2	H44151 Ig kappa chain V-I

30	513	91.4	109	2	F44151 Ig kappa chain V-I
31	509	90.7	108	1	K3HUI1 Ig kappa chain V-I
32	509	90.7	215	2	J50242 Ig kappa chain V-I
33	507.5	90.5	110	2	S44120 Ig kappa chain V-I
34	507	90.4	130	2	S20637 Ig kappa chain V-I
35	506	90.2	109	1	K3HUI1 Ig kappa chain V-I
36	505.5	90.1	108	2	E30609 Ig kappa chain V-I
37	505	90.0	114	2	T03036 Ig kappa chain - h
38	501.5	89.4	104	2	PH0964 Ig kappa chain V-I
39	501.5	89.4	129	2	S40325 Ig kappa chain - h
40	500	89.1	109	2	S47181 Ig kappa chain V-I
41	492	87.7	108	2	S33988 Ig kappa chain V-I
42	491	87.5	96	2	A30601 Ig kappa chain V-I
43	491	87.5	116	2	B27594 Ig kappa chain pre
44	491	87.5	215	2	A23746 Ig kappa chain V-I
45	488.5	87.1	111	2	S23628 Ig kappa chain V-I

ALIGNMENTS

RESULT 1
C30608
Ig kappa chain V-III region (Pie) - human (fragment)
C/Species: Homo sapiens (man)
C/Date: 29-Jun-1989 #sequence_revision 29-Jun-1989 #text_change 21-Jan-2000
C/Accession: C30608
R/Goni, F.R.; Chen, P.P.; McGinnis, D.; Arjonilla, M.L.; Fernandez, J.; Carson, D.; So
J. Immunol. 142, 3158-3163, 1989
A/Title: Structural and idiotypic characterization of the L chains of human IgM autoan
A/Reference number: A30601; MUID:89215279; PMID:2496160
A/Accession: C30608
A/Status: preliminary
A/Molecule type: protein
A/Residues: 1-108 <CON>
C/Superfamily: Immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin
F.16-91/Domain: immunoglobulin homology <IMM>

Query Match 98.9%; Score 555; DB 2; Length 108;
Best Local Similarity 98.1%; Pred. No. 1.9e-39;
Matches 106; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 EIVLTQSPGTLSTLSPGERATLSCRASQSVSSFFLAWYQOKPGAPRLIYAGSSRRANGIP 60
DB 1 EIVLTQSPGTLSTLSPGERATLSCRASQSVSSFFLAWYQOKPGAPRLIYAGSSRRANGIP 60
OY 61 DRFGSGSGTDFTLTISRLEPEDPAVYYCOQYSSPWTFGQTKVEIK 108
DB 61 DRFGSGSGTDFTLTISRLEPEDPAVYYCOQYSSPWTFGQTKVEIK 108

RESULT 2

K3HUI1
Ig kappa chain precursor V-III region (Hic) - human
C/Species: Homo sapiens (man)
C/Date: 30-Jun-1990 #sequence_revision 30-Jun-1990 #text_change 21-Jan-2000
C/Accession: P00021
R/Klips, T.J.; Tomhave, E.; Chen, P.P.; Carson, D.A.
J. Exp. Med. 167, 840-852, 1988
A/Title: Autoantibody-associated kappa light chain variable region gene expressed in cl
A/Reference number: P00021; MUID:8817307; PMID:3127527
A/Accession: P00021
A/Molecule type: mRNA
A/Residues: 1-129 <KTP>
C/Comment: The protein is one of the surface immunoglobulin M autoantibodies expressed
C/Genetics:
A/Gene: GDB:IGKV3
A/Cross-references: GDB:136266
A/Map position: 2p12-2p11
C/Complex: An immunoglobulin heterotetramer subunit consists of two identical light (k
chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into]
C/Superfamily: immunoglobulin V region; immunoglobulin homology

Qy 61 DRFGSGSGTDFLTITSLRLEPEDFAVYVCCQYGSPPWTFGGTVEIK 108
 |||||
 Db 61 DRFGSGSGTDFLTITSLRLEPEDFAVYVCCQYGSPPWTFGGTVEIK 108

RESULT 7

K3H9HA
 Ig kappa chain precursor V-III region (Hab) - human

C/Species: Homo sapiens (man)
 C/Date: 30-Jun-1990 #sequence_revision 30-Jun-1990 #text_change 21-Jan-2000
 C/Accession: P10022

R/Kipps, T.J.; Tomhave, E.; Chen, P.P.; Carson, D.A.

J. Exp. Med. 167, 840-852, 1988

A/Title: Autoantibody-associated kappa light chain variable region gene expressed in chr

A/Reference number: P10021; MUID:88171307; PMID:3127527

A/Accession: P10022

A/Molecule type: mRNA

A/Residues: 1-129 <KIP>

C/Comment: The protein is one of the surface immunoglobulin M autoantibodies expressed i

C/Genetics:

A/Gene: GDB:IGKV3

A/Cross-references: GDB:136266

A/Map position: 2p12-2p11

C/Complex: An immunoglobulin heterotetramer subunit consists of two identical light (ka

hain disulfide bonds. In some cases, such as Iga and Igm, the subunits associate into 1a

C/Superfamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: autoantibody; chronic lymphocytic leukemia; heterotetramer; immunoglobulin

F/1-20/Domain: signal sequence #status predicted <SIG>

F/21-129/Product: Ig kappa chain V-III region (Hab) #status predicted <MAT>

F/21-117/Region: V segment

F/36-111/Domain: immunoglobulin homology <IMM>

F/44-55/Region: complementarity-determining 1

F/71-77/Region: complementarity-determining 2

F/110-117/Region: complementarity-determining 3

F/118-129/Region: J segment (JTK)

F/43-109/Disulfide bonds: #status predicted

Query Match 96.4%; Score 541; DB 1; Length 129;
 Best Local Similarity 97.2%; Pred. No. 3,2e-38;
 Matches 105; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 EIVLTQSPGTLISLSPGERATLSCAASQSVSSFLAWYQOKPGQAPRLITYGASSRATGIP 60
 |||||
 Db 21 EIVLTQSPGTLISLSPGERATLSCAASQSVSSSYLAWYQOKPGQAPRLITYGASSRATGIP 80

Qy 61 DRFGSGSGTDFLTITSLRLEPEDFAVYVCCQYGSPPWTFGGTVEIK 108
 |||||
 Db 81 DRFGSGSGTDFLTITSLRLEPEDFAVYVCCQYGSPPWTFGGTVEIK 128

RESULT 8

PH0963
 Ig kappa chain V region (G6+ CUL-SMI) - human (fragment)

C/Species: Homo sapiens (man)
 C/Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 21-Jan-2000
 C/Accession: PH0963

R/Martin, T.; Duffy, S.F.; Carson, D.A.; Kipps, T.J.

J. Exp. Med. 175, 983-991, 1992

A/Title: Evidence for somatic selection of natural autoantibodies.

A/Reference number: PH0952; MUID:92202880; PMID:1552291

A/Accession: PH0963

A/Status: nucleic acid sequence not shown

A/Molecule type: DNA

A/Residues: 1-109 <MAR>

C/Superfamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: heterotetramer; immunoglobulin

F/1-23/Region: framework 1

F/16-91/Domain: immunoglobulin homology <IMM>

F/24-34/Region: complementarity-determining 1

F/35-50/Region: complementarity-determining 2

F/51-56/Region: complementarity-determining 3

F/57-89/Region: framework 3

F/90-97/Region: complementarity-determining 3
 Query Match 95.9%; Score 538; DB 2; Length 109;
 Best Local Similarity 97.2%; Pred. No. 4.8e-38;
 Matches 105; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 EIVLTQSPGTLISLSPGERATLSCAASQSVSSFLAWYQOKPGQAPRLITYGASSRATGIP 60
 |||||
 Db 1 EIVLTQSPGTLISLSPGERATLSCAASQSVSSSYLAWYQOKPGQAPRLITYGASSRATGIP 60

Qy 61 DRFGSGSGTDFLTITSLRLEPEDFAVYVCCQYGSPPWTFGGTVEIK 108
 |||||
 Db 61 DRFGSGSGTDFLTITSLRLEPEDFAVYVCCQYGSPPWTFGGTVEIK 108

RESULT 9

F30607
 Ig kappa chain V-III region (Bor) - human (fragment)

C/Species: Homo sapiens (man)

C/Date: 29-Jun-1989 #sequence_revision 29-Jun-1989 #text_change 21-Jan-2000

C/Accession: F30607

R/Goni, F.R.; Chen, P.P.; McGinnis, D.; Arjonilla, M.L.; Fernandez, J.; Carson, D.; Sol

J. Immunol. 142, 3158-3163, 1989

A/Title: Structural and idiotypic characterization of the L chains of human Igm autoant

A/Reference number: A30601; MUID:89215279; PMID:2496160

A/Accession: F30607

A/Status: preliminary

A/Molecule type: protein

A/Residues: 1-109 <GON>

C/Superfamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: heterotetramer; immunoglobulin

F/16-91/Domain: immunoglobulin homology <IMM>

Query Match 95.9%; Score 538; DB 2; Length 109;
 Best Local Similarity 96.3%; Pred. No. 4.8e-38;
 Matches 104; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 EIVLTQSPGTLISLSPGERATLSCAASQSVSSFLAWYQOKPGQAPRLITYGASSRATGIP 60
 |||||
 Db 1 EIVLTQSPGTLISLSPGERATLSCAASQSVSSSYLAWYQOKPGQAPRLITYGASSRATGIP 60

Qy 61 DRFGSGSGTDFLTITSLRLEPEDFAVYVCCQYGSPPWTFGGTVEIK 108
 |||||
 Db 61 DRFGSGSGTDFLTITSLRLEPEDFAVYVCCQYGSPPWTFGGTVEIK 108

RESULT 10

A30608
 Ig kappa chain V-III region (Son) - human (fragment)

C/Species: Homo sapiens (man)
 C/Date: 29-Jun-1989 #sequence_revision 29-Jun-1989 #text_change 21-Jan-2000
 C/Accession: A30608

R/Goni, F.R.; Chen, P.P.; McGinnis, D.; Arjonilla, M.L.; Fernandez, J.; Carson, D.; Sol

J. Immunol. 142, 3158-3163, 1989

A/Title: Structural and idiotypic characterization of the L chains of human Igm autoant

A/Reference number: A30601; MUID:89215279; PMID:2496160

A/Accession: A30608

A/Status: preliminary

A/Molecule type: protein

A/Residues: 1-109 <GON>

C/Superfamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: heterotetramer; immunoglobulin

F/16-91/Domain: immunoglobulin homology <IMM>

Query Match 95.7%; Score 537; DB 2; Length 109;
 Best Local Similarity 96.3%; Pred. No. 5.9e-38;
 Matches 104; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 EIVLTQSPGTLISLSPGERATLSCAASQSVSSFLAWYQOKPGQAPRLITYGASSRATGIP 60
 |||||
 Db 1 EIVLTQSPGTLISLSPGERATLSCAASQSVSSSYLAWYQOKPGQAPRLITYGASSRATGIP 60

Qy 61 DRFGSGSGTDFLTITSLRLEPEDFAVYVCCQYGSPPWTFGGTVEIK 108
 |||||

Db 61 NRFGSGSGTDFLTITLSRLEPEDFAVYCCQYGSPPFGGTRLEIK 108

RESULT 11

S49532
anti-Sm antibody VL chain (V kappa 3/J kappa 2) - human
C/Species: Homo sapiens (man)
C/Date: 01-Feb-1995 #sequence_revision 12-May-1995 #text_change 21-Jan-2000
C/Accession: S49532
R/Mahmoudi, M.; Edwards, J.; Cairns, E.; Bell, D.
submitted to the EMBL Data Library, October 1994
A/Description: Molecular characterization of natural human anti-Sm autoantibodies.
A/Reference number: S48797
A/Accession: S49532
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-129 <MAN>
A/Cross-references: EMBL:Z46345; NID:G560843; PID:CAA86464.1; PID:G560844
C/Superfamily: immunoglobulin V region; immunoglobulin homology
F/36-111/Domain: immunoglobulin homology <IMM>

Query Match 95.7%; Score 537; DB 2; Length 129;
Best Local Similarity 96.3%; Pred. No. 6.6e-38;
Matches 104; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 EIVLTQSPGTLISPGERATLSCRASQSVSSFLAWYQKPGQAPRLIYGASSRATGIP 60
Db 21 EIVLTQSPGTLISPGERATLSCRASQSVSSFLAWYQKPGQAPRLIYGASSRATGIP 80
Qy 61 DRFGSGSGTDFLTITLSRLEPEDFAVYCCQYGSPPFGGTRLEIK 108
Db 81 DRFGSGSGTDFLTITLSRLEPEDFAVYCCQYGSPPFGGTRLEIK 128

RESULT 12

G30601
Ig kappa chain V-III region (Goc) - human (fragment)
C/Species: Homo sapiens (man)
C/Date: 29-Jun-1989 #sequence_revision 29-Jun-1989 #text_change 21-Jan-2000
C/Accession: G30601
R/Goni, F.R.; Chen, P.P.; McGinnis, D.; Arjona, M.L.; Fernandez, J.; Carson, D.; Sold
J. Immunol. 142, 3158-3163, 1989
A/Title: Structural and idiotypic characterization of the L chains of human Igm autoanti
A/Reference number: A30601; MUID:89215279; PMID:2496160
A/Accession: G30601
A/Status: preliminary
A/Molecule type: protein
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotrimer; immunoglobulin
F/16-91/Domain: immunoglobulin homology <IMM>

Query Match 95.5%; Score 536; DB 2; Length 109;
Best Local Similarity 96.3%; Pred. No. 7.1e-38;
Matches 104; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 EIVLTQSPGTLISPGERATLSCRASQSVSSFLAWYQKPGQAPRLIYGASSRATGIP 60
Db 1 EIVLTQSPGTLISPGERATLSCRASQSVSSFLAWYQKPGQAPRLIYGASSRATGIP 60
Qy 61 DRFGSGSGTDFLTITLSRLEPEDFAVYCCQYGSPPFGGTRLEIK 108
Db 61 DRFGSGSGTDFLTITLSRLEPEDFAVYCCQYGSPPFGGTRLEIK 108

RESULT 13

S46369
IG light chain variable region (VJ) - human
C/Species: Homo sapiens (man)
C/Date: 07-May-1995 #sequence_revision 21-Jul-1995 #text_change 21-Jan-2000
C/Accession: S46369
R/Bensimon, C.; Chaetagner, P.; Zouali, M.

EMBO J. 13, 2951-2962, 1994
A/Title: Human lupus anti-DNA autoantibodies undergo essentially primary V(chi) gen
A/Reference number: S46369; MUID:94313975; PMID:8039491

A/Accession: S46369
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-129 <BEN>
A/Cross-references: EMBL:Z27170
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: immunoglobulin
F/36-111/Domain: immunoglobulin homology <IMM>

Query Match 95.5%; Score 536; DB 2; Length 129;
Best Local Similarity 95.4%; Pred. No. 8.3e-38;
Matches 103; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy 1 EIVLTQSPGTLISPGERATLSCRASQSVSSFLAWYQKPGQAPRLIYGASSRATGIP 60
Db 21 EIVLTQSPGTLISPGERATLSCRASQSVSSFLAWYQKPGQAPRLIYGASSRATGIP 80
Qy 61 DRFGSGSGTDFLTITLSRLEPEDFAVYCCQYGSPPFGGTRLEIK 108
Db 81 DRFGSGSGTDFLTITLSRLEPEDFAVYCCQYGSPPFGGTRLEIK 128

RESULT 14

S38643
Ig kappa chain V region - human (fragment)
C/Species: Homo sapiens (man)
C/Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 21-Jan-2000
C/Accession: S38643
R/Bensimon, C.; Chaetagner, P.; Zouali, M.
submitted to the EMBL Data Library, November 1993
A/Description: Low rate of receptor-editing in human lupus anti-DNA autoantibodies.
A/Reference number: S38643
A/Accession: S38643
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-134 <BEN>
A/Cross-references: EMBL:Z27170; NID:G415955; PID:CAA81694.1; PID:G415956
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotrimer; immunoglobulin
F/41-116/Domain: immunoglobulin homology <IMM>

Query Match 95.5%; Score 536; DB 2; Length 134;
Best Local Similarity 95.4%; Pred. No. 8.6e-38;
Matches 103; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy 1 EIVLTQSPGTLISPGERATLSCRASQSVSSFLAWYQKPGQAPRLIYGASSRATGIP 60
Db 26 EIVLTQSPGTLISPGERATLSCRASQSVSSFLAWYQKPGQAPRLIYGASSRATGIP 85
Qy 61 DRFGSGSGTDFLTITLSRLEPEDFAVYCCQYGSPPFGGTRLEIK 108
Db 86 DRFGSGSGTDFLTITLSRLEPEDFAVYCCQYGSPPFGGTRLEIK 133

RESULT 15

K3HUS1
Ig kappa chain V-III region (Sie) - human (tentative sequence)
C/Species: Homo sapiens (man)
C/Date: 06-Jul-1982 #sequence_revision 06-Jul-1982 #text_change 31-Mar-2000
C/Accession: A01892
R/Andrews, D.W.; Capra, J.D.
Biochemistry 20, 5816-5822, 1981
A/Title: Amino acid sequence of the variable regions of light chains from two idiot
A/Reference number: A90450; MUID:82046598; PMID:6794615
A/Accession: A01892
A/Molecule type: protein
A/Residues: 1-109 <AND>
C/Comment: This chain was isolated from an Igm with anti-gamma globulin activity.
C/Genetics:

A/Gene: GDB:IGKV3

A:Cross-references: GDB:136266
A:Map position: 2p12-2p11
C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kappa) chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into 16
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer
F:16-91/Domain: immunoglobulin homology <IMM>
F:23-89/Disulfide bonds: #status predicted

Query Match 95.4%; Score 535; DB 1; Length 109;
Best Local Similarity 95.4%; Pred.No. 8.6e-38;
Matches 103; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 EIVLTQSPGTLSLSPGERATLSCRASQSYSSFLAWYQQKPGQAPRLIYGASSRATGIP 60
DB 1 EIVLTQSPGTLSLSPGERATLSCRASQSYSSFLAWYQQKPGQAPRLIYGASSRATGIP 60
QY 61 DRFGSGSGGTDFTLTISRLEPDPFAVYYCOQYSSPFTFGGTVEIK 108
DB 61 DRFGSGSGGTDFTLTISRLEPDPFAVYYCOQYSSPFTFGGTVEIK 108

Search completed: June 3, 2003, 08:22:38
Job time : 20.5358 secs

GenCore version 5.1.6
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OM protein - protein search, using SW model

Run on: June 3, 2003, 08:02:44 ; Search time 9.95222 Seconds

(without alignment)
450.095 Million cell updates/sec

Title: US-09-644-668a-9

Perfect score: 561

Sequence: 1 EIVLTQSGPTLSLSPGERAT.....COQYSSPWTFCQGTKEIK 108

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	552	98.4	129	1	KV3M_HUMAN
2	541	96.4	129	1	KV3L_HUMAN
3	535	95.4	109	1	KV3B_HUMAN
4	533	95.0	109	1	KV3D_HUMAN
5	521	92.9	109	1	KV3E_HUMAN
6	509	90.7	108	1	KV3A_HUMAN
7	506	90.2	109	1	KV3G_HUMAN
8	475.5	84.8	128	1	KV3K_HUMAN
9	472	84.1	100	1	KV3C_HUMAN
10	469	83.6	129	1	KV3H_HUMAN
11	458	81.6	109	1	KV3F_HUMAN
12	421.5	75.1	115	1	KV3I_HUMAN
13	420.5	75.0	134	1	KV4C_HUMAN
14	420	74.9	116	1	KV3J_HUMAN
15	414.5	73.9	114	1	KV4A_HUMAN
16	395.5	70.5	108	1	KV4R_HUMAN
17	395	70.4	133	1	KV4B_HUMAN
18	394.5	70.3	108	1	KV4M_HUMAN
19	392.5	70.0	108	1	KV4H_HUMAN
20	385.5	68.7	108	1	KV4F_HUMAN
21	385.5	68.7	108	1	KV4V_HUMAN
22	382.5	68.2	108	1	KV4I_HUMAN
23	379.5	67.6	108	1	KV4O_HUMAN
24	379.5	67.6	111	1	KV3O_MOUSE
25	377.5	67.3	108	1	KV4L_HUMAN
26	377	67.2	107	1	KV4D_HUMAN
27	376.5	67.1	108	1	KV4Y_HUMAN
28	374.5	66.8	111	1	KV3Q_MOUSE
29	374.5	66.8	131	1	KV3I_MOUSE
30	372.5	66.4	111	1	KV3H_MOUSE
31	371.5	66.2	108	1	KV4O_HUMAN
32	371.5	66.2	111	1	KV3M_MOUSE
33	370.5	66.0	129	1	KV4W_HUMAN

34	369.5	65.9	108	1	KV4E_HUMAN	P01597	homo sapien
35	369.5	65.9	108	1	KV4N_HUMAN	P01606	homo sapien
36	369.5	65.9	111	1	KV3A_MOUSE	P01654	mus musculus
37	369.5	65.9	111	1	KV3C_MOUSE	P01656	mus musculus
38	367.5	65.5	111	1	KV3L_MOUSE	P01658	mus musculus
39	367.5	65.5	111	1	KV3M_MOUSE	P01662	mus musculus
40	365.5	65.2	111	1	KV3B_MOUSE	P01663	mus musculus
41	365.5	65.2	110	1	KV3N_MOUSE	P01666	mus musculus
42	365	65.1	110	1	KV3P_MOUSE	P01668	mus musculus
43	365	65.1	113	1	KV3D_HUMAN	P01617	homo sapien
44	364.5	65.0	112	1	KV3G_HUMAN	P01659	mus musculus
45	363.5	64.8	108	1	KV4O_HUMAN	P01607	homo sapien

ALIGNMENTS

RESULT 1

KV3M_HUMAN STANDARD; PRT; 129 AA.

AC P18136; 01-NOV-1990 (Rel. 16, Created)

DT 01-NOV-1990 (Rel. 16, Last sequence update)

DT 15-JUL-1999 (Rel. 38, Last annotation update)

DE Ig kappa chain V-II region HIC precursor.

OS Homo sapiens (Human)

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

OX NCBI_TaxID=9606;

RN (1)

RP SEQUENCE FROM N.A.

RX MEDLINE=88171307; PubMed=3127527;

RA Kips T.J., Tomhave B., Chen P.P., Carson D.A.;

RT "Autoantibody-associated kappa light chain variable region gene expressed in chronic lymphocytic leukemia with little or no somatic mutation. Implications for etiology and immunotherapy."

RL J. Exp. Med. 167:840-852(1988).

CC -I- DISEASE: THE PROTEIN IS ONE OF THE SURFACE IMMUNOGLOBULIN M

CC AUTOANTIBODIES EXPRESSED IN PATIENTS WITH CHRONIC LYMPHOCYTIC

CC LEUKEMIA.

DR PIR: P10021; K3HHT.

DR HSSP; P80362; 1WTL.

DR InterPro; IPR003006; IG_MHC.

DR InterPro; IPR003596; IG_V.

DR Pfam: PF00047; Ig; 1.

DR SMART; SMO0406; IGV.1.

KM Immunoglobulin V region; signal.

FT SIGNAL 1 20

FT CHAIN 1 129

FT DOMAIN 21 43

FT DOMAIN 44 55

FT DOMAIN 56 70

FT DOMAIN 71 77

FT DOMAIN 78 109

FT DOMAIN 110 118

FT DOMAIN 119 129

FT DISULFD 43 109

FT NON TER 129 129

SO SEQUENCE 129 AA; 14070 MW; 7395528EA2B74D6 CRC64;

Query Match 98.4%; Score 552; DB 1; Length 129;

Best Local Similarity 98.1%; Pred. No. 2,6e-50;

Matches 106; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY	1	EIVLTQSGPTLSLSPGERATLSGRASQSVSSFLAWYQQRPGAPRLITIGASSRATGIP	60
DB	21	EIVLTQSGPTLSLSPGERATLSGRASQSVSSFLAWYQQRPGAPRLITIGASSRATGIP	80
QY	61	DRSGSSGSDPFLITSLRLEPDAFYVYCOQYSSPWTFCQGTKEIK	108
DB	81	DRSGSSGSDPFLITSLRLEPDAFYVYCOQYSSPWTFCQGTKEIK	128

FT NON TER 129 129
 SQ SEQUENCE 129 AA; 14275 MW; 5C13B411B860CC14 CRC64;

Query Match
 Best Local Similarity 83.6%; Score 469; DB 1; Length 129;
 Matches 92; Conservative 9; Mismatches 6; Indels 2; Gaps 2;

QY 1 EIVLTQSPGTSLSRGERATLSCRASQSVSSFLAWYQKQKQAPRLITYGASSRATGIP 60
 21 EIVMTQSPATLSVSPGERATLSCRASQSVSN-LAWYQKQKQAPRLITYGASTRATGIP 79
 QY 61 DRFGSGSGTDFLTITSLRLEPEDPAVYVYCOOYGSSPFTFGGCTKYEIK 108
 80 ARFGSGSGTDFLTITSLRLOSEDPFAVYVYCOQYNNPMTFGGCTKYEIK 128

RESULT 11
 KV3F HUMAN
 ID KV3F HUMAN STANDARD; PRT; 109 AA.
 AC P01624;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Ig kappa chain V-III region FCM.
 OS Homo sapiens (Human).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 NC NCB1_TaxID=9606;
 RN [1]
 RP MEDLINE=76276460; PubMed=60899;
 RA Klapper D.G., Capra J.D.;
 RT "The amino acid sequence of the variable regions of the light chains
 from two idiotypically cross reactive IGM anti-gamma globulins.",
 RL Ann. Immunol. (Paris) 127C:261-271(1976)
 CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGM WITH ANTI-GAMMA
 CC GLOBULIN ACTIVITY.
 CC PIR: A01897; K3HUPM.
 DR HSSP; P80362; 1MTL.
 DR InterPro; IPR003006; IG_MHC.
 DR InterPro; IPR003596; IG_V.
 DR Pfam; PF00047; Ig_1.
 DR SMART; SM00406; IGV_1.
 KW Immunoglobulin V region.
 FT DISULFID 23 89
 FT NON TER 109 109
 SQ SEQUENCE 109 AA; 11922 MW; 62821DDC6A8ABA86 CRC64;

Query Match
 Best Local Similarity 81.6%; Score 458; DB 1; Length 109;
 Matches 88; Conservative 11; Mismatches 9; Indels 0; Gaps 0;

QY 1 EIVLTQSPGTSLSRGERATLSCRASQSVSSFLAWYQKQKQAPRLITYGASSRATGIP 60
 21 EIVMTQSPATLSVSPGERATLSCRASQSVSN-LAWYQKQKQAPRLITYGASTRATGIP 79
 QY 61 DRFGSGSGTDFLTITSLRLEPEDPAVYVYCOOYGSSPFTFGGCTKYEIK 108
 80 ARFGSGSGTDFLTITSLRLOSEDPFAVYVYCOQYNNPMTFGGCTKYEIK 108

RESULT 12
 KV3I HUMAN
 ID KV3I HUMAN STANDARD; PRT; 115 AA.
 AC P04433;
 DT 13-AUG-1987 (Rel. 05, Created)
 DT 13-AUG-1987 (Rel. 05, Last sequence update)
 DT 15-JUN-1999 (Rel. 38, Last annotation update)
 DE Ig kappa chain V-III region VG precursor (Fragment).
 OS Homo sapiens (Human).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 NC NCB1_TaxID=9606;

RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=85087932; PubMed=6440122;
 RA Pech M., Zachau H.G.;
 RT "Immunoglobulin genes of different subgroups are interdigitated
 within the VK locus.",
 RL Nucleic Acids Res. 12:9229-9236(1984).
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 CC -----
 DR EMBL; X01668; -; NOT_ANNOTATED_CDS.
 DR PIR; A01900; K3HUVG.
 DR HSSP; P80362; 1MTL.
 DR InterPro; IPR003006; IG_MHC.
 DR InterPro; IPR003596; IG_V.
 DR Pfam; PF00047; Ig_1.
 DR SMART; SM00406; IGV_1.
 KW Immunoglobulin V region; Signal.
 FT SIGNAL 1 20
 FT CHAIN 21 >115 IG KAPPA CHAIN V-III REGION VG.
 FT DOMAIN 21 43 FRAMEWORK-1.
 FT DOMAIN 44 54 COMPLEMENTARITY-DETERMINING-1.
 FT DOMAIN 55 69 FRAMEWORK-2.
 FT DOMAIN 70 76 COMPLEMENTARITY-DETERMINING-2.
 FT DOMAIN 77 108 FRAMEWORK-3.
 FT DOMAIN 109 115 COMPLEMENTARITY-DETERMINING-3.
 FT DISULFID 43 108 BY SIMILARITY.
 FT NON TER 115 115
 SQ SEQUENCE 115 AA; 12575 MW; 2DB47CDA3A11D555 CRC64;

Query Match
 Best Local Similarity 75.1%; Score 421.5; DB 1; Length 115;
 Matches 85; Conservative 3; Mismatches 7; Indels 1; Gaps 1;

QY 1 EIVLTQSPGTSLSRGERATLSCRASQSVSSFLAWYQKQKQAPRLITYGASSRATGIP 60
 21 EIVMTQSPATLSVSPGERATLSCRASQSV-SYLAWYQKQKQAPRLITYASNRATGIP 79
 QY 61 DRFGSGSGTDFLTITSLRLEPEDPAVYVYCOOYGSSP 96
 80 ARFGSGSGTDFLTITSLRLEPEDPAVYVYCOQYNNPMTFGGCTKYEIK 115

RESULT 13
 KV4C HUMAN
 ID KV4C HUMAN STANDARD; PRT; 134 AA.
 AC P06314;
 DT 01-JAN-1988 (Rel. 06, Created)
 DT 01-APR-1988 (Rel. 07, Last sequence update)
 DT 15-JUN-1999 (Rel. 38, Last annotation update)
 DE Ig kappa chain V-IV region B17 precursor.
 OS Homo sapiens (Human).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 NC NCB1_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=86041854; PubMed=2997713;
 RA Marsh P., Mills P., Gould H.;
 RT "Detection of a unique human V kappa IV germline gene by a cloned
 RT cDNA probe.",
 RL Nucleic Acids Res. 13:6531-6544(1985).
 RN [2]
 RP REVISION TO 76.
 RA Marsh P.;
 RL Submitted (OCT-1986) to the EMBL/Genbank/DBJ databases.

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DR EMBL: X02990; CAA26733.1; -
 DR PIR: A01905; KAHU17.
 DR HSSP: P80362; 1WTL.
 DR InterPro: IPR003006; IG_MHC.
 DR InterPro: IPR003596; IG_V.
 DR Pfam: PF00047; IG; 1.
 DR SMART: SM00406; IG; 1.
 DR Immunoglobulin V region; signal.
 FT CHAIN 1 20
 FT DOMAIN 21 134 IG KAPPA CHAIN V-IV REGION B17.
 FT DOMAIN 21 43 FRAMEWORK-1.
 FT DOMAIN 44 60 COMPLEMENTARITY-DETERMINING-1.
 FT DOMAIN 61 75 FRAMEWORK-2.
 FT DOMAIN 76 82 COMPLEMENTARITY-DETERMINING-2.
 FT DOMAIN 83 114 FRAMEWORK-3.
 FT DOMAIN 115 121 COMPLEMENTARITY-DETERMINING-3.
 FT DOMAIN 122 133 FRAMEWORK-4.
 FT DISULFID 43 114 BY SIMILARITY.
 FT NON TER 134 134
 SQ SEQUENCE 134 AA; 14966 MW; 6413A22FD0738632 CRC64;

Query Match 75.0%; Score 420.5; DB 1; Length 134;
 Best Local Similarity 69.0%; Pred. No. 1.1e-36;
 Matches 78; Conservative 19; Mismatches 11; Indels 5; Gaps 1;

QY 1 EIVLTQSPGTLISLSPGERATLSCRASQSV-----SSFLAWYQKQKQAPRLIYGASSR 55
 DB 21 DIWMTQSPDLAVLSERATINCKSSQSVLLYSNDKNRYLAWYQKQKQAPRLIYGASTR 80
 QY 56 ATGIDPRFGSGSGSDTFTLTISRLEPEDFAVYVYCGQYSGSPFTFGGTQYKIK 108
 DB 81 ESGVPRFGSGSGSDTFTLTISRLEPEDFAVYVYCGQYVLPFTFGGTQYKIK 133

RESULT 14
 KV4J HUMAN STANDARD; PRT; 116 AA.
 ID KV4J HUMAN STANDARD; PRT; 116 AA.
 AC P04434;
 DT 13-AUG-1987 (Rel. 05, Created)
 DT 13-AUG-1987 (Rel. 05, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE IG kappa chain V-III region VH precursor (Fragment).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxId=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=85087932; PubMed=6440122;
 RA Pech M., Zachau H.G.;
 RT "Immunoglobulin genes of different subgroups are interdigitated
 RT within the VK locus".
 RL Nucleic Acids Res. 12:9229-9236(1984).

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DR EMBL: X02725; -; NOT_ANNOTATED_CDS.
 DR PIR: A01901; KAHUYH.
 DR HSSP: P80362; 1WTL.

DR InterPro: IPR003006; IG_MHC.
 DR InterPro: IPR003596; IG_V.
 DR Pfam: PF00047; IG; 1.
 DR SMART: SM00406; IG; 1.
 DR Immunoglobulin V region; signal.
 FT CHAIN 1 20
 FT DOMAIN 21 116 IG KAPPA CHAIN V-III REGION VH.
 FT DOMAIN 21 43 FRAMEWORK-1.
 FT DOMAIN 44 55 COMPLEMENTARITY-DETERMINING-1.
 FT DOMAIN 56 70 FRAMEWORK-2.
 FT DOMAIN 71 77 COMPLEMENTARITY-DETERMINING-2.
 FT DOMAIN 78 109 FRAMEWORK-3.
 FT DOMAIN 110 116 COMPLEMENTARITY-DETERMINING-3.
 FT DISULFID 43 109 BY SIMILARITY.
 FT NON TER 116 116
 SQ SEQUENCE 116 AA; 12757 MW; 51CD5BA53B21929 CRC64;

Query Match 74.9%; Score 420; DB 1; Length 116;
 Best Local Similarity 85.4%; Pred. No. 1e-36;
 Matches 82; Conservative 5; Mismatches 9; Indels 0; Gaps 0;

QY 1 EIVLTQSPGTLISLSPGERATLSCRASQSVSSFLAWYQKQKQAPRLIYGASSRATGIP 60
 DB 21 EIVMTQSPDLAVLSERATINCKSSQSVLLYSNDKNRYLAWYQKQKQAPRLIYGASTRATISIP 80
 QY 61 DRFGSGSGSDTFTLTISRLEPEDFAVYVYCGQYSGSP 96
 DB 81 ARFGSGSGSDTFTLTISRLEPEDFAVYVYCGQYSGSP 116

RESULT 15
 KV4A HUMAN STANDARD; PRT; 114 AA.
 ID KV4A HUMAN STANDARD; PRT; 114 AA.
 AC P01625;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE IG kappa chain V-IV region Len.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxId=9606;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=76004342; PubMed=50995;
 RA Schneider M., Hilschmann N.;
 RT "The primary structure of a monoclonic immunoglobulin-L-chain of
 RT subgroup IV of the kappa type (Bence-Jones protein Len)".
 RL Hoppe-Seyler's Z. Physiol. Chem. 356:507-557(1975).
 RN [2]
 RP REVISION TO 9.
 RA Salomon A.;
 RL Submitted (AUG-1996) to the SWISS-PROT data bank.
 CC -I- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
 CC -I- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.
 DR PIR: A01903; KAHULN.
 DR HSSP: P01607; IREI.
 DR InterPro: IPR003006; IG_MHC.
 DR InterPro: IPR003596; IG_V.
 DR Pfam: PF00047; IG; 1.
 DR SMART: SM00406; IG; 1.
 DR Immunoglobulin V region; Bence-Jones protein.
 FT CHAIN 1 23
 FT DOMAIN 24 40 FRAMEWORK-1.
 FT DOMAIN 41 55 COMPLEMENTARITY-DETERMINING-1.
 FT DOMAIN 56 62 FRAMEWORK-2.
 FT DOMAIN 63 94 COMPLEMENTARITY-DETERMINING-2.
 FT DOMAIN 95 101 FRAMEWORK-3.
 FT DOMAIN 102 113 COMPLEMENTARITY-DETERMINING-3.
 FT DISULFID 23 94 BY SIMILARITY.
 FT NON TER 114 114
 SQ SEQUENCE 114 AA; 12640 MW; 0647F1D17F236485 CRC64;

[illegible]

Search completed: June 3, 2003, 08:15:43
Job time : 10.9522 secs

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OM protein - protein search, using sw model

Run on: June 3, 2003, 08:07:54 ; Search time 53.8157 Seconds

(without alignments)
413.506 Million cell updates/sec

Title: US-09-644-668a-9

Sequence: 1 EIVLTQSGTSLSPGERAT.....CQGVSSFWTGGTKVRIK 108

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 671580 segs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

SPTREMBL 21:*

- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mhc:*
- 8: sp_organelle:*
- 9: sp_plant:*
- 10: sp_rodent:*
- 11: sp_virus:*
- 12: sp_vertebrate:*
- 13: sp_vertebrate:*
- 14: sp_unclassified:*
- 15: sp_virus:*
- 16: sp_bacteriap:*
- 17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	530	94.5	109	4 Q9UL78	Q9UL78 homo sapien
2	511	91.1	109	4 Q9UL86	Q9UL86 homo sapien
3	446.5	79.6	108	4 Q9UL83	Q9UL83 homo sapien
4	442	78.8	109	4 Q9UL85	Q9UL85 homo sapien
5	406.5	72.5	108	4 Q9UL77	Q9UL77 homo sapien
6	400.5	71.4	108	4 Q9UL79	Q9UL79 homo sapien
7	383.5	68.4	108	4 Q9UL70	Q9UL70 homo sapien
8	383	68.3	107	4 Q96SA9	Q96SA9 homo sapien
9	364	64.3	107	4 Q9UL81	Q9UL81 homo sapien
10	360.5	64.3	111	11 Q920B9	Q920B9 mus musculu
11	355	63.3	238	11 Q99M37	Q99M37 mus musculu
12	354	63.3	106	5 Q9U410	Q9U410 schistosoma
13	350.5	62.5	109	11 Q920B6	Q920B6 mus musculu
14	349	62.2	134	11 Q9VD06	Q9VD06 mus musculu
15	348.5	62.1	107	11 Q9ER29	Q9ER29 mus musculu
16	347.5	61.9	108	11 Q8VIJ0	Q8VIJ0 mus musculu

17	344.5	61.4	114	4 Q9UL80	Q9UL80 homo sapien
18	343.5	61.2	116	4 Q96PF6	Q96PF6 homo sapien
19	342.5	61.1	99	11 Q9JL74	Q9JL74 mus musculu
20	342	61.0	238	11 Q8VCI6	Q8VCI6 mus musculu
21	341.5	60.9	233	11 Q9IM69	Q9IM69 mus musculu
22	340.5	60.7	298	11 Q9OYF0	Q9OYF0 mus musculu
23	339.5	60.5	234	11 Q8VCP0	Q8VCP0 mus musculu
24	338	60.2	239	11 Q8VC55	Q8VC55 mus musculu
25	337.5	60.2	214	11 Q9RI45	Q9RI45 mus musculu
26	337.5	60.2	234	11 Q8R062	Q8R062 mus musculu
27	335	59.7	239	4 Q8TCD0	Q8TCD0 homo sapien
28	331	59.0	235	11 Q9IWI2	Q9IWI2 mus musculu
29	330.5	58.9	107	11 Q9UL84	Q9UL84 mus musculu
30	329.5	58.7	103	11 Q9UL80	Q9UL80 mus musculu
31	326.5	58.2	101	11 Q9JL78	Q9JL78 mus musculu
32	323	57.6	104	11 Q9JL82	Q9JL82 mus musculu
33	322.5	57.5	234	11 Q9IMF8	Q9IMF8 mus musculu
34	315.5	56.2	127	11 Q92SE9	Q92SE9 mus musculu
35	313.5	55.9	97	11 Q9UL76	Q9UL76 mus musculu
36	283.5	50.5	109	6 Q9N0W5	Q9N0W5 oryctolagus
37	280	49.9	241	11 Q92IA6	Q92IA6 mus musculu
38	268.5	47.9	234	11 Q8R028	Q8R028 mus musculu
39	266	47.4	233	4 Q8TBC9	Q8TBC9 homo sapien
40	266	47.4	237	4 Q8WTU4	Q8WTU4 homo sapien
41	266	47.4	237	4 Q8WTU6	Q8WTU6 homo sapien
42	248.5	44.3	112	4 Q96JDI	Q96JDI homo sapien
43	245.5	43.6	218	11 Q92SE1	Q92SE1 mus musculu
44	244.5	43.6	236	4 Q96E61	Q96E61 homo sapien
45	242	43.1	110	4 Q8TE63	Q8TE63 homo sapien

ALIGNMENTS

RESULT 1

Q9UL78 PRELIMINARY; PRT; 109 AA.

AC Q9UL78;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE Myosin-reactive immunoglobulin light chain variable region (Fragment).
DE Homo sapiens (Human).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalle N.N., Berney S.M., Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal fetus";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035036; AAD56272.1; -.
DR HSSP; P80362; IWTL.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF00047; IG; 1.
DR SMART; SM00406; IGV; 1.
FT NON_TER
FT NON_TER
SQ SEQUENCE 109 AA; 11646 MW; 5F675C528C7BE197 CRC64;

Query Match 94.5%; Score 530; DB 4; Length 109;
Best Local Similarity 96.3%; Pred. No. 3.6e-49;
Matches 104; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Q9 1 EIVLTQSGTSLSPGERATISCRASQSVSSFLAWYQKPGQAPRLIYQASSRRANGIP 60
DB 1 EIVLTQSGTSLSPGERATISCRASQSVSSFLAWYQKPGQAPRLIYQASSRRANGIP 60

QY 61 DRFGSGSGTDFLTITSLRLEPEDFAVYVCOQYSSPWTFCGTVEIK 108
 DB 61 DRFGSGSGTDFLTITSLRLEPEDFAVYVCOQYSSPWTFCGTVEIK 108

RESULT 2

Q9UL86 PRELIMINARY; PRT; 109 AA.

AC Q9UL86; 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE Myosin-reactive immunoglobulin kappa chain variable region (Fragment).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID=9606;
 RN 1)
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98277139; PubMed=9614934;
 RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M., Young D.C.;
 RT "Myosin-reactive autoantibodies in rheumatic carditis and normal fetus."
 RL Clin. Immunol. Immunopathol. 87:184-192(1998).
 DR EMBL; AF035028; AAD56264.1; -
 DR HSSP; P80362; 1MTL.
 DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR003596; Ig_v.
 DR Pfam; PF00047; Ig_1.
 DR SMART; SM00406; IGV; 1.
 FT NON_TER 1
 FT NON_TER 109
 SQ SEQUENCE 109 AA; 11928 MW; 243325F72C7DAC83 CRC64;

Query Match 91.1%; Score 511; DB 4; Length 109;
 Best Local Similarity 92.6%; Pred. No. 3.9e-47;
 Matches 100; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 1 EIVLTQSGTISLSPGERATLSCRASQSVSSFLAWYQKPGQAPRLIYGASTRATGIP 60
 DB 1 EIVLTQSGTISLSPGERATLSCRASQSVSSFLAWYQKPGQAPRLIYGASTRATGIP 60
 QY 61 DRFGSGSGTDFLTITSLRLEPEDFAVYVCOQYSSPWTFCGTVEIK 108
 DB 61 DRFGSGSGTDFLTITSLRLEPEDFAVYVCOQYSSPWTFCGTVEIK 108

RESULT 3

Q9UL83 PRELIMINARY; PRT; 108 AA.

AC Q9UL83; 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE Myosin-reactive immunoglobulin light chain variable region (Fragment).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID=9606;
 RN 1)
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98277139; PubMed=9614934;
 RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M., Young D.C.;
 RT "Myosin-reactive autoantibodies in rheumatic carditis and normal fetus."
 RL Clin. Immunol. Immunopathol. 87:184-192(1998).
 DR EMBL; AF035031; AAD56267.1; -
 DR HSSP; P80362; 1MTL.
 DR InterPro; IPR003006; Ig_MHC.

DR InterPro; IPR003596; Ig_v.
 DR Pfam; PF00047; Ig_1.
 DR SMART; SM00406; IGV; 1.
 FT NON_TER 1
 FT NON_TER 108
 SQ SEQUENCE 108 AA; 11834 MW; 9F9C5A92EBA96BEA CRC64;

Query Match 79.6%; Score 446.5; DB 4; Length 108;
 Best Local Similarity 82.4%; Pred. No. 3e-40;
 Matches 89; Conservative 9; Mismatches 9; Indels 1; Gaps 1;

QY 1 EIVLTQSGTISLSPGERATLSCRASQSVSSFLAWYQKPGQAPRLIYGASTRATGIP 60
 DB 1 EIVLTQSGTISLSPGERATLSCRASQSVSSFLAWYQKPGQAPRLIYGASTRATGIP 59
 QY 61 DRFGSGSGTDFLTITSLRLEPEDFAVYVCOQYSSPWTFCGTVEIK 108
 DB 60 DRFGSGSGTDFLTITSLRLEPEDFAVYVCOQYSSPWTFCGTVEIK 107

RESULT 4

Q9UL85 PRELIMINARY; PRT; 109 AA.

AC Q9UL85; 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE Myosin-reactive immunoglobulin kappa chain variable region (Fragment).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID=9606;
 RN 1)
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98277139; PubMed=9614934;
 RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M., Young D.C.;
 RT "Myosin-reactive autoantibodies in rheumatic carditis and normal fetus."
 RL Clin. Immunol. Immunopathol. 87:184-192(1998).
 DR EMBL; AF035029; AAD56265.1; -
 DR HSSP; P80362; 1MTL.
 DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR003596; Ig_v.
 DR Pfam; PF00047; Ig_1.
 DR SMART; SM00406; IGV; 1.
 FT NON_TER 1
 FT NON_TER 109
 SQ SEQUENCE 109 AA; 11761 MW; FB1E43E7C7AFACCC CRC64;

Query Match 78.8%; Score 442; DB 4; Length 109;
 Best Local Similarity 81.7%; Pred. No. 9.2e-40;
 Matches 89; Conservative 9; Mismatches 9; Indels 2; Gaps 2;

QY 1 EIVLTQSGTISLSPGERATLSCRASQSVSSFLAWYQKPGQAPRLIYGASTRATGIP 60
 DB 1 EIVLTQSGTISLSPGERATLSCRASQSVSSFLAWYQKPGQAPRLIYGASTRATGIP 59
 QY 61 DRFGSGSGTDFLTITSLRLEPEDFAVYVCOQYSSPWTFCGTVEIK 108
 DB 60 DRFGSGSGTDFLTITSLRLEPEDFAVYVCOQYSSPWTFCGTVEIK 108

RESULT 5

Q9UL77 PRELIMINARY; PRT; 108 AA.

AC Q9UL77; 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE Myosin-reactive immunoglobulin light chain variable region (Fragment).

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OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OC NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035037; AAD56273.1; -.
DR HSSP; P01607; IREI.
DR InterPro; IPR003006; IG_MHC.
DR Myosin-reactive immunoglobulin light chain variable region
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
FT NON_TER 1
FT NON_TER 108
SQ SEQUENCE 108 AA; 11738 MW; C06681716C4D16F3 CRC64;

Query Match 72.5%; Score 406.5; DB 4; Length 108;
Best Local Similarity 71.3%; Pred. No. 5.7e-36;
Matches 77; Conservative 14; Mismatches 16; Indels 1; Gaps 1;

QY 1 EIVLTSPGTLISLSPGERATLSCRASQSVSSFLAWYQKPGQAPRLIYGASSRATGIP 60
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
1 DIQMTQSPSSLSASVGDRVTITCRASQSI-SNYLAWYQKPGKPKANLLIYAASLQSGVP 59
Db 60 SRFSGSGSGTDFTLTISLSIQPEDFATYYCOQSYSTSTGEGTKEIK 107

QY 61 DRFGSGSGGTDFTLTISLRLPEDPFAVYYCOQYSSPMTFGGTKEIK 108
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
60 SRFSGSGSGTDFTLTISLSIQPEDFATYYCOQSYSTSTGEGTKEIK 107

Db 60 SRFSGSGSGTDFTLTISLSIQPEDFATYYCOQSYSTSTGEGTKEIK 107

RESULT 6
Q9UL79 PRELIMINARY; PRT; 108 AA.
ID Q9UL79
AC Q9UL79;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE Myosin-reactive immunoglobulin light chain variable region
DE (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OC NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035035; AAD56271.1; -.
DR HSSP; P01607; IREI.
DR InterPro; IPR003006; IG_MHC.
DR Myosin-reactive immunoglobulin light chain variable region
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
FT NON_TER 1
FT NON_TER 108
SQ SEQUENCE 108 AA; 11787 MW; DB5845F19724FB4E CRC64;

Query Match 71.4%; Score 400.5; DB 4; Length 108;
Best Local Similarity 72.2%; Pred. No. 2.5e-35;
Matches 78; Conservative 11; Mismatches 18; Indels 1; Gaps 1;

QY 1 EIVLTSPGTLISLSPGERATLSCRASQSVSSFLAWYQKPGQAPRLIYGASSRATGIP 60
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
1 DIQMTQSPSSLSASVGDRVTITCRASQSI-SNYLAWYQKPGKPKANLLIYAASLQSGVP 59
Db 1 DIVMTQSPSSLSASVGDRVTITCRASQSI-SNYLAWYQKPGKPKANLLIYAASLQSGVP 59

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QY 61 DRFGSGSGGTDFTLTISLRLPEDPFAVYYCOQYSSPMTFGGTKEIK 108
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
60 SRFSGSGSGTDFTLTISLSIQPEDFATYYCOQYSPFPFGGTKEIK 107

Db 60 SRFSGSGSGTDFTLTISLSIQPEDFATYYCOQYSPFPFGGTKEIK 107

RESULT 7
Q9UL70 PRELIMINARY; PRT; 108 AA.
ID Q9UL70
AC Q9UL70;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE Myosin-reactive immunoglobulin light chain variable region
DE (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OC NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035044; AAD56280.1; -.
DR HSSP; P01607; IREI.
DR InterPro; IPR003006; IG_MHC.
DR Myosin-reactive immunoglobulin light chain variable region
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
FT NON_TER 1
FT NON_TER 108
SQ SEQUENCE 108 AA; 11633 MW; B7BEDC3E41FCC437 CRC64;

Query Match 68.4%; Score 383.5; DB 4; Length 108;
Best Local Similarity 65.7%; Pred. No. 1.6e-33;
Matches 71; Conservative 18; Mismatches 18; Indels 1; Gaps 1;

QY 1 EIVLTSPGTLISLSPGERATLSCRASQSVSSFLAWYQKPGQAPRLIYGASSRATGIP 60
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
1 DIQMTQSPSSLSASVGDRVTITCRASQSI-SNYLAWYQKPGKPKANLLIYAASLQSGVP 59
Db 1 DIQMTQSPSSLSASVGDRVTITCRASQSI-SNYLAWYQKPGKPKANLLIYAASLQSGVP 59

QY 61 DRFGSGSGGTDFTLTISLRLPEDPFAVYYCOQYSSPMTFGGTKEIK 108
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
60 SRFSGSGSGTDFTLTISLSIQPEDFATYYCOQYSPFPFGGTKEIK 107

Db 60 SRFSGSGSGTDFTLTISLSIQPEDFATYYCOQYSPFPFGGTKEIK 107

RESULT 8
Q96SA9 PRELIMINARY; PRT; 107 AA.
ID Q96SA9
AC Q96SA9;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE Anti-streptococcal/anti-myosin immunoglobulin kappa light chain
DE variable region (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OC NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98375893; PubMed=9712075;
RA Adderson B.E., Shikman A.R., Ward K.B., Cunningham M.W.;
RA "Molecular analysis of polyclonal monoclonal antibodies from
RT rheumatic carditis: human anti-N-acetylglucosamine/anti-myosin
RT antibody V region genes";
RL J. Immunol. 161:2020-2031(1998).
DR EMBL; U96396; AAB68785.1; -.
DR InterPro; IPR003006; IG_MHC.

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DR Pfam, PF00047; 1g; 1.
FT NON TER 1
SQ SEQUENCE 107 AA; 11520 MW; 4BB439C5B577F16 CRC64;
Query Match
Best Local Similarity 70.4%; Pred. No. 1.8e-33;
Matches 76; Conservative 13; Mismatches 17; Indels 2; Gaps 2;

QY 1 EIVLTOSPGTSLSPGERATLSCRASQSVSSFLAWYQKPGAPRLIYGASSRATGIP 60
DB 1 DIQMTQSPSSLSASVGRVITTCASQSI-SNYLNMWQKPGKAPKLLIYAASLSQSGVP 59

QY 61 DRESGSGSGTDFLTITISRLPEPDAVYVYCOQYSSPWTFCGKVEIK 108
DB 60 SRFSGSGSGTDFLTITISRLPEPDAVYVYCOQ-SYSTITFCGKVEIK 106

RESULT 9
QY 09UL81 PRELIMINARY; PRT; 107 AA.
AC 09UL81;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DE 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Myosin-reactive immunoglobulin light chain variable region
DE (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN 1
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berny S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus."
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035033; AAD56269.1; -.
DR HSSP; P01607; 1REI.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF00047; 1g; 1.
DR SMART; SM00406; IGV; 1.
FT NON TER 1
FT NON TER 107
SQ SEQUENCE 107 AA; 11501 MW; 070549FDE0754748 CRC64;

Query Match
Best Local Similarity 64.9%; Score 364; DB 4; Length 107;
Matches 72; Conservative 15; Mismatches 19; Indels 2; Gaps 2;

QY 1 EIVLTOSPGTSLSPGERATLSCRASQSVSSFLAWYQKPGAPRLIYGASSRATGIP 60
DB 1 DIQMTQSPSSLSASVGRVITTCASQSI-SNYLNMWQKPGKAPKLLIYAASLSQSGVP 59

QY 61 DRESGSGSGTDFLTITISRLPEPDAVYVYCOQYSSPWTFCGKVEIK 108
DB 60 SRFSGSGSGTDFLTITISRLPEPDAVYVYCOQ-SYSTITFCGKVEIK 106

RESULT 10
QY 0920B9 PRELIMINARY; PRT; 111 AA.
AC 0920B9;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAY-2002 (TrEMBLrel. 19, Last annotation update)
DE Pterin-mimicking anti-idiotypic kappa chain variable region
DE (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

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OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN 1
RP SEQUENCE FROM N.A.
RA Aikin J.D., Iape A., Jennings I.G., Horatis O., Cotton R.G.H.;
RT "Definition of the idiotope of Pterin-Mimicking Antibodies Expressed
RT in Mammalian Cells."
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB307935; AAL09419.1; -.
DR InterPro; IPR003006; IG_MHC.
DR Pfam; PF00047; 1g; 1.
FT NON TER 1
FT NON TER 111
SQ SEQUENCE 111 AA; 12046 MW; 1E46988A6858526 CRC64;

Query Match
Best Local Similarity 64.3%; Score 360.5; DB 11; Length 111;
Matches 71; Conservative 17; Mismatches 20; Indels 3; Gaps 1;

QY 1 EIVLTOSPGTSLSPGERATLSCRASQSVSS--SFLAWYQKPGAPRLIYGASSRAT 57
DB 1 DIVLTQSPASLSAVSGORATISCRASKSVSTGYSMWYQKPGAPRLIYLASNLSS 60

QY 58 GIPDRFSGSGSGTDFLTITISRLPEPDAVYVYCOQYSSPWTFCGKVEIK 108
DB 61 GVPAPFSGSGSGTDFLTITISRLPEPDAVYVYCOQHSRELPYTGKVEIK 111

RESULT 11
QY 099M37 PRELIMINARY; PRT; 238 AA.
AC 099M37;
DT 01-UN-2001 (TrEMBLrel. 17, Created)
DT 01-UN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Hypothetical 26.3 kDa protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN 1
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC002035; AAH02035.1; -.
DR HSSP; P01679; 2FBJ.
DR InterPro; IPR003599; IG.
DR InterPro; IPR003597; IG_CL.
DR InterPro; IPR003600; IG_Like.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF00047; 1g; 2.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGV; 1.
DR SMART; SM00406; IGV; 1.
DR SMART; SM00410; IG_Like; 1.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 238 AA; 26344 MW; FB2B06A0B801330A CRC64;

Query Match
Best Local Similarity 63.3%; Score 355; DB 11; Length 238;
Matches 66; Conservative 23; Mismatches 19; Indels 4; Gaps 1;

QY 1 EIVLTOSPGTSLSPGERATLSCRASQSVSS--SFLAWYQKPGAPRLIYGASSRA 56
DB 20 DVMTQTPPLSLPVSLGQASISCSQSIYHNSNTYLTLEWLRPGQSPKLLIYKSNRF 79

QY 57 TGIIDRFSGSGSGTDFLTITISRLPEPDAVYVYCOQYSSPWTFCGKVEIK 108
DB 80 SGVDRFSGSGSGTDFLTITISRLPEPDAVYVYCOQHSRELPYTGKVEIK 131

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RESULT 12

Q9U410 PRELIMINARY; PRT; 106 AA.

AC Q9U410; 01-MAY-2000 (TRENBLrel. 13, Created)

DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)

DT 01-DEC-2001 (TRENBLrel. 19, Last annotation update)

DE Monoclonal anti-idiotypic antibody NP30 immunoglobulin light chain variable region (Fragment).

OS Schistosoma japonicum (Blood fluke).

OC Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea; Strigeidae; Schistosomatoidea; Schistosomidae; Schistosoma.

OX NCBI_TaxID=6182;

RN [1]

RP SEQUENCE FROM N.A.

RA Song X.T., Feng Z.Q., Qiu Z.N., Li Y.Q., Huang H.L., Guan X.H.;

RT "Amplification, cloning and sequence analysis of the light chain variable region gene of monoclonal anti-idiotypic antibody NP30 of Schistosoma japonicum";

RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.

DR EMBL; AF207620; AAF19434.1; -

DR HSSP; P01679; 2FBJ.

DR InterPro; IPR003006; IG_MHC.

DR InterPro; IPR003596; IG_v.

DR Pfam; PF00047; IG_1.

DR SMART; SM00406; IGv; 1.

DR NON_TER 1

FT NON_TER 106

SO SEQUENCE 106 AA; 11478 MW; F20F544426BAE63E CRC64;

Query Match

Best Local Similarity 63.1%; Score 354; DB 5; Length 106;

Matches 67; Conservative 18; Mismatches 21; Indels 2; Gaps 1;

QY 1 EIVLTQSPGTLISLSPGERATISCRASQSVSSFLAWYQKPGAPRLITYGASRRATGIP 60

DB 1 ENLITQSPALMSASGKVTWTCSSSV--SYVWYLOKPSRLLITYDTSNLASGVP 58

QY 61 DRFGSSGSGTDFLTITSLRLEPEDFAVYVCOQYGSPPMTFGGTVEIK 108

DB 59 VRFSGSGGTSTYLTISRMEADATYYCQWTSYPTFGSGTKLEK 106

RESULT 13

Q920B6 PRELIMINARY; PRT; 109 AA.

AC Q920B6; 01-DEC-2001 (TRENBLrel. 19, Created)

DT 01-DEC-2001 (TRENBLrel. 19, Last sequence update)

DT 01-MAR-2002 (TRENBLrel. 20, Last annotation update)

DE Pterin-mimicking anti-idiotypic kappa chain variable region (Fragment).

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RA Atkin J.D., Tape A., Jennings I.G., Horaltis O., Cotton R.G.H.;

RT "Definition of the idiotope of Pterin-Mimicking Antibodies Expressed in Mammalian Cells";

RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.

DR EMBL; AF307938; AAL09422.1; -

DR InterPro; IPR003006; IG_MHC.

DR Pfam; PF00047; IG_1.

DR NON_TER 1

FT NON_TER 109

SO SEQUENCE 109 AA; 11943 MW; DAD3F98E05DD1501 CRC64;

Query Match

Best Local Similarity 62.5%; Score 350.5; DB 11; Length 109;

Matches 63; Conservative 22; Mismatches 22; Indels 1; Gaps 1;

QY 1 EIVLTQSPGTLISLSPGERATISCRASQSVSSFLAWYQKPGAPRLITYGASRRATGIP 60

DB 1 DIQWTQSPALSASVGETVITTCRASGNI-HNYLAWYQKQKSPQLLVNAKTLADGVP 59

QY 61 DRFGSSGSGTDFLTITSLRLEPEDFAVYVCOQYGSPPMTFGGTVEIK 108

DB 60 SRFSGSGGTQYSLKINLQEDFGSYICQHFMTPTFGGTLEIK 107

RESULT 14

Q8VD0 PRELIMINARY; PRT; 134 AA.

AC Q8VD0; 01-MAR-2002 (TRENBLrel. 20, Created)

DT 01-MAR-2002 (TRENBLrel. 16, Last sequence update)

DT 01-JUN-2002 (TRENBLrel. 21, Last annotation update)

DE Anti-MOG 212 variable light chain (Fragment).

GN ANTI-MOG KAPPA.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RA Chernaiova Y.I.

RC STRAIN-BALB/C;

RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.

RP STRAIN-BALB/C;

RC Sambi P.I.

RT "Targeting T cells to the CNS";

RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.

DR EMBL; AJ416311; CAC94866.1; -

DR InterPro; IPR003599; IG_v.

DR InterPro; IPR003006; IG_MHC.

DR InterPro; IPR003596; IG_v.

DR Pfam; PF00047; IG_1.

DR SMART; SM00409; IG; 1.

DR SMART; SM00406; IGv; 1.

DR NON_TER 134

FT NON_TER 134

SO SEQUENCE 134 AA; 14525 MW; CDF8E2236E2D0CE CRC64;

Query Match

Best Local Similarity 62.2%; Score 349; DB 11; Length 134;

Matches 65; Conservative 16; Mismatches 25; Indels 2; Gaps 1;

QY 1 EIVLTQSPGTLISLSPGERATISCRASQSVSSFLAWYQKPGAPRLITYGASRRATGIP 60

DB 23 QIVLTQSPALMSASGKVTWTCSSSI--SYHWYQKQKGTSPKWIYDTSNLASGVP 80

QY 61 DRFGSSGSGTDFLTITSLRLEPEDFAVYVCOQYGSPPMTFGGTVEIK 108

DB 81 ARFSGSGGTSTYLTISRMEADATYYCQWTSYPTFGSGTKLEK 128

RESULT 15

Q9ER29 PRELIMINARY; PRT; 107 AA.

AC Q9ER29; 01-MAR-2001 (TRENBLrel. 16, Created)

DT 01-MAR-2001 (TRENBLrel. 16, Last sequence update)

DT 01-DEC-2001 (TRENBLrel. 19, Last annotation update)

DE Anti human TNF-alpha light chain variable region (Fragment).

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RA Chen P., Deng J.B., Wang Z.L., Han H., Su C.Z.;

RT "Cloning and sequencing of the light chain fragment of variable region genes of an anti-hTNF-a monoclonal antibody";

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 3, 2003, 08:02:14 ; Search time 48.6553 Seconds

(without alignments)
295.776 Million cell updates/sec

Title: US-09-644-668A-9

Perfect score: 561
Sequence: 1 EIVLTQSPGRLSLSPGERAT.....CQVGSSEPTWGQGRKVEIK 108

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database :

A Geneseq 101002:*

1: /SID2/gcgdata/geneseq/geneseq-emb1/AA1980.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	554	98.8	235	21 AAY93702
2	554	98.8	235	21 AAY93729
3	547.5	97.6	109	23 AAB07233
4	546	97.3	129	14 AAR38672
5	545	97.1	108	22 AAB62770
6	544	97.0	384	22 AAM24101
8	543.5	96.9	109	23 AAG39666
9	542	96.6	384	22 AAB07231
10	542	96.6	384	22 AAU14461
				Human novel protei

11	542	96.6	384	22 AAU14463	Human novel protei
12	542	96.6	384	22 AAU14464	Human novel protei
13	538	95.9	109	22 AAB62773	Human HIV-1 monoc
14	535.5	95.5	226	22 AAB99374	Human interleukin
15	535.5	95.5	226	22 AAB99397	Human interleukin
16	535.5	95.5	226	22 AAB75007	Human interleukin
17	535.5	95.5	226	22 AAB75030	Human interleukin
18	534.5	95.3	109	23 AAB84096	Human V kappa subg
19	533.5	95.1	107	20 AAB80729	Human IL-4 receptor
20	529	94.3	108	23 AAO21549	Antibody screening
21	528.5	94.2	226	22 AAB93394	Human interleukin
22	528.5	94.2	226	22 AAB75027	Anti-IL8 monoclon
23	526.5	93.9	226	22 AAB93378	Human interleukin
24	526.5	93.9	226	22 AAB75011	Anti-IL8 monoclon
25	523.5	93.3	226	22 AAB99391	Human interleukin
26	523.5	93.3	226	22 AAB75024	Anti-IL8 monoclon
27	523	93.2	307	22 AAU14225	Human novel protei
28	523	93.2	312	22 AAU14227	Human novel protei
29	522.5	93.1	226	22 AAB99390	Human interleukin
30	522.5	93.1	226	22 AAB75023	Human interleukin
31	521	92.9	108	22 AAB69689	Humanised CMV5 ant
32	521	92.9	108	23 AAB30492	Human anti-CD40 m
33	521	92.9	108	23 AAB30495	Human anti-CD40 m
34	520.5	92.8	226	22 AAB99376	Human interleukin
35	520.5	92.8	226	22 AAB75009	Anti-IL8 monoclon
36	520.5	92.8	246	23 AAB45253	Human BlyS binding
37	520	92.7	106	18 AAW31722	Human BlyS binding
38	520	92.7	109	22 AAB62768	Human BlyS binding
39	520	92.7	253	23 AAB45488	Human BlyS binding
40	517.5	92.2	107	14 AAR38592	Human BlyS binding
41	517.5	92.2	107	19 AAB58493	Human BlyS binding
42	517	92.2	108	15 AAB54307	Human BlyS binding
43	517	92.2	108	17 AAW1265	Human BlyS binding
44	517	92.2	108	21 AAY95117	Anti-HIV gp120 imm
45	517	92.2	108	21 AAY98226	Anti-gp120 antibod

ALIGNMENTS

RESULT 1	AA93702	standard; Protein; 235 AA.
ID	AA93702	
XX	AA93702	
AC	AA93702	
XX	AA93702	
DT	03-OCT-2000	(first entry)
XX	03-OCT-2000	
DE	The kappa chain of immunoglobulin clone 4.1.1.	
XX	Cytotoxic T-lymphocyte antigen-4; CTLA-4; antibody; immune system;	
KW	hyperimmunity disorder; autoimmune disease; diabetes; graft rejection;	
KW	proliferative disorder; cancer; immunodeficient disorder.	
XX		
OS	Homo sapiens.	
XX		
XX	MO200037504-A2.	
XX		
PD	29-JUN-2000.	
XX		
PF	23-DEC-1999;	99MO-US30895.
XX		
PR	23-DEC-1998;	98US-0113647.
XX		
PA	(PRIZ) PRIZER INC.	
PA	(ABGE-) ABGENIX INC.	
XX		
PI	Hanson DC, Neveu MJ, Mueller EE, Hanke JH, Gilman SC, Davis CG;	
XX	Corvalan JR;	
XX	WPI: 2000-442647/38.	
DR		
DR	N-PSDB; AAA46865.	
XX		

PT Novel antibodies capable of binding cytotoxic T-lymphocyte antigen
 PT (CTLA)-4 containing specified heavy and light chain sequences, useful
 PT for treating, e.g. immune disorders -

PS Claim 3; Fig 1A; 157bp; English.

CC The present sequence represents a kappa chain of an antibody of the
 CC invention. The antibody is directed cytotoxic T-lymphocyte antigen
 CC (CTLA)-4. Antibodies of the invention are composed of a heavy chain
 CC variable region, comprising a modified contiguous sequence from a
 CC FRI-FR3 sequence encoded by a human VH3-33 family gene. The
 CC modifications are contained in CDR1, CDR2 and/or framework regions.
 CC The antibodies may be used to inhibit CTLA-4 and down-regulate the
 CC immune system to treat hyperimmunity disorders (e.g. autoimmune
 CC disease, diabetes and graft rejection) and proliferative disorders
 CC (e.g. cancer). CTLA-4 stimulatory agents may be used to up-regulate
 CC immune system to up-regulate immunodeficient disorders.

XX Sequence 235 AA;

Query Match 98.8%; Score 554; DB 21; Length 235;
 Best Local Similarity 97.2%; Pred. No. 2.5e-34;

Matches 105; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 EIVLTQSPGTLISLSPGERATLSCRASQSVSSFLAWYQQRGQAPRLIYGASRRATGIP 60
 DB 21 EIVLTQSPGTLISLSPGERATLSCRASQSVSSFLAWYQQRGQAPRLIYGASRRATGIP 80
 QY 61 DRFGSGSGGTDFTLTISRLEPEDPAVYYCCQYSSSPWTFGGTKVEIK 108
 DB 81 DRFGSGSGGTDFTLTISRLEPEDPAVYYCCQYSSSPWTFGGTKVEIK 128

RESULT 2

AAV93729 standard; Protein; 235 AA.

AC AAV93729;

DT 03-OCT-2000 (first entry)

XX The kappa chain of immunoglobulin clone 4.1.1.

KW Cytotoxic T-lymphocyte antigen-4; CTLA-4; antibody; immune system;
 KW hyperimmunity disorder; autoimmune disease; diabetes; graft rejection;
 KW proliferative disorder; cancer; immunodeficient disorder.

OS Homo sapiens.

XX Key Location/Qualifiers
 FT Peptide 1..20
 FT /note= "signal peptide"

PN WO200037504-A2.

PD 23-JUN-2000.

PP 23-DEC-1999; 99WO-US30895.

PR 23-DEC-1998; 98US-0113647.

PA (PF12) PFIZER INC.
 PA (ABGE-) ABGENIX INC.

PI Hansen DC, Neveu MJ, Mueller EE, Hanke JH, Gilman SC, Davis CG,
 PI Corvahan JR;

DR WPI; 2000-442647/38.
 DR N-PSDB; AAA46893.

PT Novel antibodies capable of binding cytotoxic T-lymphocyte antigen
 PT (CTLA)-4 containing specified heavy and light chain sequences, useful
 PT for treating, e.g. immune disorders -

XX Claim 3; Fig 22g; 157bp; English.

CC The present sequence represents a kappa chain of an antibody of the
 CC invention. The antibody is directed cytotoxic T-lymphocyte antigen
 CC (CTLA)-4. Antibodies of the invention are composed of a heavy chain
 CC variable region, comprising a modified contiguous sequence from a
 CC FRI-FR3 sequence encoded by a human VH3-33 family gene. The
 CC modifications are contained in CDR1, CDR2 and/or framework regions.
 CC The antibodies may be used to inhibit CTLA-4 and down-regulate the
 CC immune system to treat hyperimmunity disorders (e.g. autoimmune
 CC disease, diabetes and graft rejection) and proliferative disorders
 CC (e.g. cancer). CTLA-4 stimulatory agents may be used to up-regulate
 CC immune system to up-regulate immunodeficient disorders.

XX Sequence 235 AA;

Query Match 98.8%; Score 554; DB 21; Length 235;
 Best Local Similarity 97.2%; Pred. No. 2.5e-34;

Matches 105; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 EIVLTQSPGTLISLSPGERATLSCRASQSVSSFLAWYQQRGQAPRLIYGASRRATGIP 60
 DB 21 EIVLTQSPGTLISLSPGERATLSCRASQSVSSFLAWYQQRGQAPRLIYGASRRATGIP 80
 QY 61 DRFGSGSGGTDFTLTISRLEPEDPAVYYCCQYSSSPWTFGGTKVEIK 108
 DB 81 DRFGSGSGGTDFTLTISRLEPEDPAVYYCCQYSSSPWTFGGTKVEIK 128

RESULT 3

ABB07233 standard; Protein; 109 AA.

AC ABB07233;

DT 26-MAR-2002 (first entry)

XX Anti-IL-4 and IL-13 receptors MAb 27A1 light chain variable region.

KW Human; antibody; interleukin; IL-4; antagonist; receptor; IL-4 receptor;
 KW antiarthritic; dermatological; antitumor; antineoplastic; cytotoxic;
 KW antitickling; immunosuppressive; tuberculosis; ophthalmological;
 KW IL-13; antitumor; antitumor.

OS Homo sapiens.

XX Key Location/Qualifiers
 FH Region 24..35
 FT /note= "complementarity determining region (CDR) 1"
 FT Region 51..57
 FT /note= "complementarity determining region (CDR) 2"
 FT Region 90..99
 FT /note= "complementarity determining region (CDR) 3"

PN WO200192340-A2.

PD 06-DEC-2001.

PP 25-MAY-2001; 2001WO-US17094.

PR 26-MAY-2000; 2000US-0579808.

PR 19-SEP-2000; 2000US-0665343.

PR 15-FEB-2001; 2001US-0785934.

PR 01-MAY-2001; 2001US-0847816.

PA (IMAV) IMMUNEX CORP.

PI Plueneke JD;

DR WPI; 2002-114332/15.
 DR N-PSDB; ABA94333.

Novel human antibody which binds human interleukin (IL)-4 receptor and is capable of inhibiting IL-4 induced biological activity, functions as IL-4 antagonist and is useful for treating septic arthritis, scleroderma

Claim 3; Page 77; 85pp; English.

The invention relates to a human antibody (an interleukin (IL)-4 antagonist) (I) that binds human IL-4 receptor (IL-4R), and is capable of inhibiting an IL-4-induced biological activity. (I) is also useful for inhibiting both IL-4-induced biological activity and IL-13-induced biological activity in vivo in a human, and for treating septic arthritis in a human afflicted with septic arthritis. (I) is also used for treating conditions such as septic/reactive arthritis, dermatitis herpetiformis, urticaria (especially chronic idiopathic urticaria), ulcers, gastric inflammation, mucosal inflammation, ulcerative colitis, Crohn's disease, inflammatory bowel disease, other disorders of the digestive system in which IL-4 plays a role (e.g. IL-4-induced inflammation of part of the gastrointestinal tract), conditions in which IL-4-induced barrier disruption plays a role (e.g. conditions characterized by decreased epithelial barrier function in the lung or gastrointestinal tract), scleroderma, hypertrophic scarring, Whipple's disease, benign prostatic hyperplasia, IL-4-induced pulmonary conditions, allergic reactions to medication, Kawasaki disease, sickle cell disease or crisis, Churg-Strauss syndrome, Grave's disease, pre-eclampsia, Sjogren's syndrome, autoimmune lymphoproliferative syndrome, autoimmune haemolytic anemia, Barrett's esophagus, autoimmune uveitis, tuberculosis, nephrosis, pemphigus vulgaris or bullous pemphigoid (autoimmune blistering diseases), and myasthenia gravis (an autoimmune muscular disease). IL-4 antagonists also find use as adjuvants to allergy immunotherapy and as vaccine adjuvants, especially when directing the immune response toward a TH1 response would be beneficial in treating or preventing the disease. The present sequence represents an anti-IL-4 receptor and anti-IL-13 receptor monoclonal antibody (MAB) 27A1 light chain variable region.

Sequence : 109 AA;

Query Match 97.6%; Score 547.5; DB 23; Length 109;
Best Local Similarity 98.2%; Pred. No. 3.8e-34;
Matches 107; Conservative 1; Mismatches 0; Indels 1; Gaps 1;

1 EIVLTQSPGTLISPGERATISCRASQSVSSFLAWYQKRGQAPRLITYGASSRATGIP 60
1 EIVLTQSPGTLISPGERATISCRASQSVSSFLAWYQKRGQAPRLITYGASSRATGIP 60
61 DRPSGSGSGTDFLTISRLEPEDFAVYVCOYQSSPWTFGQGTKEIK 108
61 DRPSGSGSGTDFLTISRLEPEDFAVYVCOYQSSPWTFGQGTKEIK 109

RESULT 4

AAR38672 ID AAR38672 standard; Protein; 129 AA.

XX AAR38672;

DT 01-NOV-1993 (first entry)

XX VK325-JK2.

Monoclonal antibody; MAb; envelope; glycoprotein; gp120; HIV; AIDS; CD4; receptor; hybridoma; polymerase chain reaction; PCR; heavy; light; chain; epitope; immune deficiency.

OS Homo sapiens.

XX Key Location/Qualifiers

FT Peptide 1..20 /label= sig_peptide

FT Protein 21..129 /label= mat_protein

FT Region 1..116 /label= VK325

FT

FT Region 117..129
FT /label= JK2
FT Region 44..55
FT /label= CDR1
FT Region 71..77
FT /label= CDR2
FT Region 110..117
FT /label= CDR3
FT Misc-difference 1 /note= "Met encoded by ATC (sic)"
FT Misc-difference 35 /note= "Pro encoded by GCA (sic)"
FT Misc-difference 99 /note= "Leu encoded by GTG (sic)"
FT Misc-difference 113 /note= "Gly encoded by GAT (sic)"
FT Misc-difference 114 /note= "Ser encoded by AAC (sic)"
FT Misc-difference 116 /note= "Pro encoded by GTT (sic)"

W09312232-A.
24-JUN-1993.
10-DEC-1992; 92WO-US10928.
10-DEC-1992; 91US-0804652.
10-DEC-1991; 91US-0804652.

(DAND) DANA FARBER CANCER INST INC.
(NEMF-) NEW ENGLAND DEACONNESS HOSPITAL CORP.

Haselaine WA, Marasco WA, Posner MR, Sodroski JG;
WPI; 1993-214174/26.
N-PSDB; AAQ42706.

DNA segments encoding monoclonal antibody - which binds to gp120 and neutralises HIV, for treating AIDS, and for diagnosing and monitoring HIV infection

Disclousure; Page 74-75; 109pp; English.

The nucleotide sequence of F105 VK (AAQ42707 - sequence differs from other F105 VK sequences given elsewhere in the specification) was compared with germline gene HumvK325 (AAQ42706), showing 97.7% similarity. By nucleotide sequence analysis, F105 appears to be derived from a member of the VK III subgroup gene family.

Sequence 129 AA;

Query Match 97.3%; Score 546; DB 14; Length 129;
Best Local Similarity 97.2%; Pred. No. 5.7e-34;
Matches 105; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

1 EIVLTQSPGTLISPGERATISCRASQSVSSFLAWYQKRGQAPRLITYGASSRATGIP 60
21 EIVLTQSPGTLISPGERATISCRASQSVSSFLAWYQKRGQAPRLITYGASSRATGIP 80

61 DRPSGSGSGTDFLTISRLEPEDFAVYVCOYQSSPWTFGQGTKEIK 108
81 DRPSGSGSGTDFLTISRLEPEDFAVYVCOYQSSPWTFGQGTKEIK 128

RESULT 5

AAB62770 ID AAB62770 standard; Protein; 108 AA.

XX AAB62770;

DT 03-ARR-2001 (first entry)

DE Human HIV-1 monoclonal antibody SEQ ID NO: 69.

XX Human immunodeficiency virus-1; HIV-1; human monoclonal antibody;
KW envelope glycoprotein; gp120; diagnosis.
XX Homo sapiens.
XX WO20010678-A1.
XX 04-JAN-2001.
XX 23-JUN-2000; 2000WO-US17327.
XX 30-JUN-1999; 99US-0141701.
XX (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX Watkins BA, Reitz MS;
XX WPI; 2001-112438/12.
XX N-PSDB; AAF29071.
XX Novel human monoclonal antibody immunoreactive with human
PT immunodeficiency virus-1 glycoprotein gp120, useful for detecting HIV-1
PT in biological sample and providing passive immunotherapy to HIV-1
PT infected mammal
XX
XX Claim 1; Page 66; 81pp; English.
XX The present invention provides the protein and coding sequences for the
CC variable regions of human monoclonal antibodies which are immunoreactive
CC with human immunodeficiency virus-1 (HIV-1) envelope glycoprotein gp120.
CC These can be used in diagnosis and therapy of HIV-1 infection.
XX
SQ Sequence 108 AA;
Query Match 97.1%; Score 545; DB 22; Length 108;
Best Local Similarity 97.2%; Pred. No. 5.8e-34;
Matches 104; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
QY 2 IVTQSPGTLSLSPGERATLSCRASQSVSSFLAWYQKPGQAPRLIYGASSRATGIP 61
DB 1 LVLTQSPGTLSLSPGERATLSCRASQSVSSFLAWYQKPGQAPRLIYGASSRATGIP 60
QY 62 RFSGSGSGTDFTLTISRLEPEDFAVYYCCQYGSSPMTFGQTKVEIK 108
DB 61 RFSGSGSGTDFTLTISRLEPEDFAVYYCCQYGSSPMTFGQTKVEIK 107
RESULT 6
AA24101
ID AAM24101 standard; Protein; 384 AA.
XX AAM24101;
XX 12-OCT-2001 (first entry)
XX Human EST encoded protein SEQ ID NO: 1626.
XX
XX Human; sheep; pig; cow; fruit fly; yeast; hamster; macaque; horse;
KW tomato; monkey; dog; sea urchin; expressed sequence tag; EST;
KW diagnostics; forensic test; gene mapping; genetic disorder;
KW biodiversity; gene therapy; nutrition.
XX Homo sapiens.
XX WO200154477-A2.
XX
XX 02-AUG-2001.
XX
XX 25-JAN-2001; 2001WO-US02687.
XX
XX 25-JAN-2000; 2000US-0491404.
XX
XX 17-JUL-2000; 2000US-0617746.

PR 03-AUG-2000; 2000US-0631451.
PR 15-SEP-2000; 2000US-0663670.
XX (HYSE-) HYSEQ INC.
XX
XX Tang YT, Liu C, Zhou P, Qian XB, Wang Z, Chen R, Asundi V;
PI Cao Y, Drmanac RA, Zhang J, Werthman T;
XX WPI; 2001-476164/51.
XX N-PSDB; AAH98760.
XX
XX Isolated polypeptide for treatment of diseases, diagnostics, raising
PT antibodies and research use -
XX
XX Claim 20; Page 1102-1103; 1275pp; English.
XX
XX The present invention provides the protein and coding sequences of novel
CC proteins from a variety of organisms, including human, dog, cat, horse,
CC cow, pig, hamster, monkey, macaque, yeast, bacteria, fruit fly, sea
CC urchin and tomato. These were derived from expressed sequence tags (ESTs)
CC from the organism of interest. They can be used in diagnostics,
CC forensics, gene mapping, identification of mutations, to assess
CC biodiversity and for nutritional purposes. The present sequence is a
CC protein of the invention.
XX
SQ Sequence 384 AA;
Query Match 97.1%; Score 545; DB 22; Length 384;
Best Local Similarity 98.1%; Pred. No. 1.8e-33;
Matches 106; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 EIVLTQSPGTLSLSPGERATLSCRASQSVSSFLAWYQKPGQAPRLIYGASSRATGIP 60
DB 167 EIVLTQSPGTLSLSPGERATLSCRASQSVSSFLAWYQKPGQAPRLIYGASSRATGIP 226
QY 61 DRFSGSGSGTDFTLTISRLEPEDFAVYYCCQYGSSPMTFGQTKVEIK 108
DB 227 DRFSGSGSGTDFTLTISRLEPEDFAVYYCCQYGSSPMTFGQTKVEIK 274
RESULT 7
AA24101
ID AAG33666 standard; Protein; 108 AA.
XX AAG33666;
XX
XX 14-SEP-2001 (first entry)
XX
XX Human anti-Rh(D) antibody clone SH52 protein sequence.
DB
XX Human; anti-Rh(D) antibody; Rh(D) binding protein; immunostimulant;
KW red blood cell; Rh phenotype; diagnosis; therapeutic.
XX
XX Homo sapiens.
XX US625455-B1.
XX
XX 03-JUL-2001.
XX
XX 29-JAN-1999; 99US-0240274.
XX
XX 11-OCT-1996; 96US-0028550.
XX 10-APR-1998; 98US-0081380.
XX 27-JUN-1997; 97US-0864045.
XX
XX (TYPE-) UNIV PENNSYLVANIA.
XX
XX Stiegel DL;
XX
XX WPI; 2001-388931/41.
XX N-PSDB; AAH68723.
XX
XX New isolated protein, preferably a human anti-Rh(D) antibody for use in

[illegible]

DR	N-PSDB; ABA04331.
XX	Novel human antibody which binds human interleukin (IL)-4 receptor and is capable of inhibiting IL-4 induced biological activity, functions as
PT	IL-4 antagonist and is useful for treating septic arthritis,
PT	scleroderma
XX	
PS	Claim 3; Page 74; 85pp; English.
XX	
CC	The invention relates to a human antibody (an interleukin (IL)-4
CC	antagonist) (I) that binds human IL-4 receptor (IL-4R), and is capable of
CC	inhibiting an IL-4-induced biological activity. (I) is also useful for
CC	inhibiting both IL-4-induced biological activity and IL-13-induced
CC	biological activity in vivo in a human, and for treating septic arthritis
CC	in a human afflicted with septic arthritis. (I) is also used for treating
CC	conditions such as septic/reactive arthritis, dermatitis herpetiformis,
CC	urticaria (especially chronic idiopathic urticaria), ulcers, gastric
CC	inflammation, mucosal inflammation, ulcerative colitis, Crohn's disease,
CC	inflammatory bowel disease, other disorders of the digestive system in
CC	which IL-4 plays a role (e.g. IL-4-induced inflammation of part of the
CC	gastrointestinal tract), conditions in which IL-4-induced barrier
CC	disruption plays a role (e.g. conditions characterized by decreased
CC	epithelial barrier function in the lung or gastrointestinal tract),
CC	scleroderma, hypertrophic scarring, Whipple's disease, benign prolate
CC	hyperplasia, IL-4-induced pulmonary conditions, allergic reactions to
CC	medication, Kawasaki disease, sickle cell disease or crisis, Churg-
CC	Strauss syndrome, Grave's disease, pre-eclampsia, Sjogren's syndrome,
CC	autoimmune lymphoproliferative syndrome, autoimmune haemolytic anemia,
CC	Barrett's esophagus, autoimmune uveitis, tuberculosis, nephrosis,
CC	pemphigus vulgaris or bullous pemphigoid (autoimmune blistering
CC	diseases), and myasthenia gravis (an autoimmune muscular disease). IL-4
CC	antagonists also find use as adjuvants to allergy immunotherapy and as
CC	vaccine adjuvants, especially when directing the immune response toward
CC	a TH1 response would be beneficial in treating or preventing the disease.
CC	The present sequence represents an anti-IL-4 receptor monoclonal antibody
CC	(MAb) 12B5 light chain variable region.
XX	
SO	Sequence 109 AA;
XX	
Query Match	96.9%; Score 543.5; DB 23; Length 109;
Best Local Similarity	97.2%; Pred. No. 7,6e-34;
Matches 106; Conservative	2; Mismatches 0; Indels 1; Gaps 1
QY	1 EYLTDSPEFTLSLSPGERATLSCRASGVSSFLATWYQKRGAPRLILYGASSRATGIP 60
DB	1 EYLTDSPEFTLSLSPGERATLSCRASGVSSSYLATWYQKRGAPRLILYGASSRATGIP 60
QY	61 DPFSGSGGTDEFTLTISRLPEEDPAVYVYCCOYGSS-PRTGGCKKVKIK 108
DB	61 DPFSGSGGTDEFTLTISRLPEEDPAVYVYCCOYGSSPPTWGGCKKVKIK 109
RESULT 9	
ID	AAU14461
XX	AAU14461 standard; Protein; 384 AA.
XX	
XX	AAU14461;
DT	24-OCT-2001 (first entry)
DE	Human novel protein #332.
XX	
XX	Human; novel protein; Antinaemic; osteopathic; antiinflammatory;
KM	immunomodulatory; cytosarctic; neuroprotective; vulnerary; nootropic;
KM	anticonvulsant; antiallergic; cerebroprotective; antifungal; antiviral;
KM	antibacterial; antiallergic; dermatological; haemostatic; antiasthmatic;
KM	thrombolytic; immunogen; antibody; gene therapy; neurological disorder;
KM	Parkinson's disease; inflammatory disorder; cancer; asthma; osteoporosis;
KM	tissue regeneration; immune disorder.
XX	
XX	Homo sapiens.
XX	
XX	MO200155437-A2.

XX 24-OCT-2001 (first entry)
DT Human novel protein #334.
XX
XX Human; novel protein; Antianaemic; osteopathic; antiinflammatory;
KW immunomodulatory; cytoskeletal; neuroprotective; vulnery; nocitropic;
KW anticonvulsant; antiallergic; cerebroprotective; antifungal; antiviral;
KW antibacterial; antiallergic; dermatological; haemostatic; antiaesthetic;
KW chondrolytic; immunogen; antibody; gene therapy; neurological disorder;
KW Parkinson's disease; inflammatory disorder; cancer; asthma; osteoporosis;
KW tissue regeneration; immune disorder.
XX
OS Homo sapiens.
XX
XX MO200155437-A2.
XX
XX 02-AUG-2001.
XX
XX 25-JAN-2001; 2001WO-US02623.
XX
XX 25-JAN-2000; 2000US-0491404.
XX
XX (HYSE-) HYSEQ INC.
XX
XX Tang YT, Liu C, Drmanac RT;
XX
XX WPI; 2001-451939/48.
XX
XX N-PSDB; AAS22768.
XX
XX Isolated polypeptides useful for treating anti-inflammatory diseases,
PT nervous system disorders, and for regenerating bone and cartilage -
XX
XX Example 4; Page 826-827; 894pp; English.
XX
XX The invention relates to polynucleotides encoding novel human
CC proteins or their active domains. The polypeptides, polynucleotides and
CC antibodies raised against the polypeptides are used in a method of
CC treatment of a mammal and prevention of disorders caused by the aberrant
CC protein expression or activity. The polypeptides can be used as
CC molecular weight markers, food supplements, and in antibody production.
CC The polypeptides are used to identify compounds which bind to the
CC polypeptides. Polynucleotides of the invention are used as probes and
CC primers, for sequencing, for chromosome or gene mapping, in the
CC production of recombinant proteins, and in generating anti-sense DNA or
CC RNA and in gene therapy. Polypeptides of the invention can be used to
CC target drugs to a tumour, in assays to determine biological activity, to
CC raise antibodies/elicite an immune response, to determine quantitative
CC protein levels, as tissue markers, and to isolate receptors or ligands.
CC Polypeptides of the invention may also be useful in treating platelet
CC disorders, stem cell disorders, regenerating bone, cartilage, tendon,
CC ligament and/or nerve tissue, wound healing, treating burns, promoting
CC the proliferation, differentiation and survival of stem cells, as a
CC contraceptive, treating osteoporosis and osteoarthritis, anaemia,
CC Alzheimer's, Parkinson's and Huntington's diseases, amyotrophic lateral
CC sclerosis, stroke, immune deficiencies resulting from bacterial, viral or
CC fungal infection or from autoimmunity, cancer, allergy, asthma,
CC graft-versus-host disease, eczema, haemophilia, thrombosis,
CC anti-inflammatory diseases, nervous system disorders, and infection.
XX The present sequence represents a protein of the invention.
XX
SQ Sequence 384 AA;
Query Match 96.6%; Score 542; DB 22; Length 384;
Best Local Similarity 97.2%; Pred. No. 3e-33;
Matches 105; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
QY 1 EIVLTGSPGTLISLSPGPAATLSCRAAGVSSGFLAMVQKQKQAPRLIYAGSSATGIP 60
DB 170 EIVLTGSPGTLISLSPGPAATLSCRAAGVSSGFLAMVQKQKQAPRLIYAGSSATGIP 229
QY 61 DRFGSGSGTDFTLTISLSPGPAATLSCRAAGVSSGFLAMVQKQKQAPRLIYAGSSATGIP 108
DRFGSGSGTDFTLTISLSPGPAATLSCRAAGVSSGFLAMVQKQKQAPRLIYAGSSATGIP 229

DB 230 DRFGSGSGTDFTLTISLSPGPAATLSCRAAGVSSGFLAMVQKQKQAPRLIYAGSSATGIP 277
RESULT 12
AAU14464
ID AAU14464 standard; Protein; 384 AA.
XX
XX AAU14464;
AC
XX
XX 24-OCT-2001 (first entry)
DT Human novel protein #335.
XX
XX Human novel protein #335.
XX
XX Human; novel protein; Antianaemic; osteopathic; antiinflammatory;
KW immunomodulatory; cytoskeletal; neuroprotective; vulnery; nocitropic;
KW anticonvulsant; antiallergic; cerebroprotective; antifungal; antiviral;
KW antibacterial; antiallergic; dermatological; haemostatic; antiaesthetic;
KW chondrolytic; immunogen; antibody; gene therapy; neurological disorder;
KW Parkinson's disease; inflammatory disorder; cancer; asthma; osteoporosis;
KW tissue regeneration; immune disorder.
XX
OS Homo sapiens.
XX
XX MO200155437-A2.
XX
XX 02-AUG-2001.
XX
XX 25-JAN-2001; 2001WO-US02623.
XX
XX 25-JAN-2000; 2000US-0491404.
XX
XX (HYSE-) HYSEQ INC.
XX
XX Tang YT, Liu C, Drmanac RT;
XX
XX WPI; 2001-451939/48.
XX
XX N-PSDB; AAS22769.
XX
XX Isolated polypeptides useful for treating anti-inflammatory diseases,
PT nervous system disorders, and for regenerating bone and cartilage -
XX
XX Example 4; Page 827; 894pp; English.
XX
XX The invention relates to polynucleotides encoding novel human
CC proteins or their active domains. The polypeptides, polynucleotides and
CC antibodies raised against the polypeptides are used in a method of
CC treatment of a mammal and prevention of disorders caused by the aberrant
CC protein expression or activity. The polypeptides can be used as
CC molecular weight markers, food supplements, and in antibody production.
CC The polypeptides are used to identify compounds which bind to the
CC polypeptides. Polynucleotides of the invention are used as probes and
CC primers, for sequencing, for chromosome or gene mapping, in the
CC production of recombinant proteins, and in generating anti-sense DNA or
CC RNA and in gene therapy. Polypeptides of the invention can be used to
CC target drugs to a tumour, in assays to determine biological activity, to
CC raise antibodies/elicite an immune response, to determine quantitative
CC protein levels, as tissue markers, and to isolate receptors or ligands.
CC Polypeptides of the invention may also be useful in treating platelet
CC disorders, stem cell disorders, regenerating bone, cartilage, tendon,
CC ligament and/or nerve tissue, wound healing, treating burns, promoting
CC the proliferation, differentiation and survival of stem cells, as a
CC contraceptive, treating osteoporosis and osteoarthritis, anaemia,
CC Alzheimer's, Parkinson's and Huntington's diseases, amyotrophic lateral
CC sclerosis, stroke, immune deficiencies resulting from bacterial, viral or
CC fungal infection or from autoimmunity, cancer, allergy, asthma,
CC graft-versus-host disease, eczema, haemophilia, thrombosis,
CC anti-inflammatory diseases, nervous system disorders, and infection.
XX The present sequence represents a protein of the invention.
XX
SQ Sequence 384 AA;
Query Match 96.6%; Score 542; DB 22; Length 384;
Best Local Similarity 97.2%; Pred. No. 3e-33;

Matches 105; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 EIVLTOSPGTSLSPGERATLSCRASOSVSSSFLAWYQKPGQAPRLIYGAASRRATGIP 60
DB 170 EIVLTOSPGTSLSPGERATLSCRASOSVSSSFLAWYQKPGQAPRLIYGAASRRATGIP 229

QY 61 DRFGSGSGTDFLTILSRLEPEDFAVYVYCCQYSSPWTFGGTVEIK 108
DB 230 DRFGSGSGTDFLTILSRLEPEDFAVYVYCCQYSSPWTFGGTVEIK 277

RESULT 13
AAB62773
ID AAB62773 standard; Protein; 109 AA.
XX
XX AAB62773;
AC
XX
XX 03-APR-2001 (first entry)
DT
XX
XX Human HIV-1 monoclonal antibody SEQ ID NO: 72.
DE
XX
XX Human immunodeficiency virus-1; HIV-1; human monoclonal antibody;
KM envelope glycoprotein; gp120; diagnosis.
XX
XX Homo sapiens.
OS
XX WO20010678-A1.
PN
XX 04-JAN-2001.
PD
XX
XX 23-JUN-2000; 2000WO-US17327.
PF
XX
XX 30-JUN-1999; 99US-0141701.
PR
XX
XX (USSH) US DEPT HEALTH & HUMAN SERVICES.
PA
XX
XX Watkins BA, Reitz MS;
PI
XX
XX WPI; 2001-112438/12.
DR
XX
XX N-PSDB; AAF29074.
NR
XX
XX Novel human monoclonal antibody immunoreactive with human
PT immunodeficiency virus-1 glycoprotein gp120, useful for detecting HIV-1
PT in biological sample and providing passive immunotherapy to HIV-1
PT infected mammal
XX
XX
XX Claim 1; Page 67-68; 81pp; English.
PS
XX
XX The present invention provides the protein and coding sequences for the
CC variable regions of human monoclonal antibodies which are immunoreactive
CC with human immunodeficiency virus-1 (HIV-1) envelope glycoprotein gp120.
CC These can be used in diagnosis and therapy of HIV-1 infection.
CC
XX
XX Sequence 109 AA;
SQ

Query Match 95.9%; Score 538; DB 22; Length 109;
Best Local Similarity 95.4%; Pred. No. 2e-33;
Matches 103; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 EIVLTOSPGTSLSPGERATLSCRASOSVSSSFLAWYQKPGQAPRLIYGAASRRATGIP 60
DB 1 DVLVLTOSPGTSLSPGERATLSCRASOSVSSSFLAWYQKPGQAPRLIYGAASRRATGIP 60

QY 61 DRFGSGSGTDFLTILSRLEPEDFAVYVYCCQYSSPWTFGGTVEIK 108
DB 61 DRFGSGSGTDFLTILSRLEPEDFAVYVYCCQYSSPWTFGGTVEIK 108

RESULT 14
AAB99374
ID AAB99374 standard; Protein; 226 AA.
XX
XX AAB99374;

XX
DT 28-AUG-2001 (first entry)
XX
XX Human interleukin 8 antibody protein sequence M1_231.
DE
XX
XX Human antibody; detection; Fab; immunoglobulin; heterophilic antibody;
KM human anti-mouse antibody; HAMA antibody; interleukin 8; IL-8; herpes;
KM target antigen; bacterial; fungal; viral; pathogen; human disease;
KM hepatitis A; hepatitis B; hepatitis C; influenza; Giardia; Malaria;
KM Leishmania; Staphylococcus aureus; Pseudomonas aeruginosa; diagnosis.
XX
XX Homo sapiens.
OS
XX Synthetic.
OS
XX WO200140306-A1.
PN
XX
XX 07-JUN-2001.
PD
XX
XX 06-DEC-2000; 2000WO-US33042.
PF
XX
XX 06-DEC-1999; 99US-0456090.
PR
XX
XX (BIOS-) BIOSITE DIAGNOSTICS INC.
PA (GENP-) GENPHARM INT.
PI
XX
XX Buechler J, Valikirs G, Gray J, Lomberg N;
PI
XX
XX WPI; 2001-374798/39.
DR
XX
XX

Example 22; Page 94; 135pp; English.

PT Detecting analyte in human sample containing human antibodies binding
PT to nonhuman-antibodies, involves contacting sample with human antibody
PT which binds to antibodies from nonhuman species and detecting binding

PS

XX The present invention describes a method for detecting an analyte in a
XX human sample containing human antibodies that specifically bind to
XX antibodies from a nonhuman species. The method involves contacting the
XX sample with a human antibody (I) which specifically binds to antibodies
XX from a nonhuman species and detecting the binding between (I) and the
XX analyte to indicate presence of the analyte. The method is used for
XX detecting an analyte in a human sample containing human anti-mouse
XX antibody (HAMA) (preferably human anti-mouse idotype antibodies and/or
XX heterophilic antibodies). The method can also be used for detecting any
XX type of target antigen including bacterial, fungal and viral pathogens
XX that cause human diseases e.g., hepatitis (A, B and C), influenza, Herpes,
XX Giardia, Malaria, Leishmania, Staphylococcus aureus, Pseudomonas
XX aeruginosa. Human antibodies can be used as detection reagents for
XX performing clinical diagnostic tests and for performing other in vitro
XX detection assays, including for research purposes. (I) can be used in
XX qualitative assays designed to indicate the presence of one or more
XX target antigens above minimally detectable amounts of antigen in the
XX sample that usually correspond to the sensitivity limitations of the
XX assays for each target antigen. Also, (I) is used to determine the
XX amount of target antigen in a sample in a semi-quantitative or relative
XX sense. Quantification of one or more target antigens in a sample can
XX also be carried out using (I). AHA41612 to AHA41686, and AAB99361 to
XX AAB99399, represent sequences used in the exemplification of the present
XX invention.
XX
XX Sequence 226 AA;
SQ

Query Match 95.5%; Score 535.5; DB 22; Length 226;
Best Local Similarity 96.3%; Pred. No. 5.8e-33;
Matches 105; Conservative 3; Mismatches 0; Indels 1; Gaps 1;

QY 1 EIVLTOSPGTSLSPGERATLSCRASOSVSSSFLAWYQKPGQAPRLIYGAASRRATGIP 60
DB 1 EIVLTOSPGTSLSPGERATLSCRASOSVSSSFLAWYQKPGQAPRLIYGAASRRATGIP 60

QY 61 DRFGSGSGTDFLTILSRLEPEDFAVYVYCCQYSSPWTFGGTVEIK 108
DB 61 DRFGSGSGTDFLTILSRLEPEDFAVYVYCCQYSSPWTFGGTVEIK 108

DB 61 DRFGSGSGTDFTLTISRLEPEDFAVYCCQYGSPPYFGGTKEIK 109

RESULT 15

AAB99397 standard; Protein; 226 AA.

AC AAB99397;

DT 28-AUG-2001 (first entry)

XX Human interleukin 8 antibody protein sequence M2_33L.

XX Human antibody; detection; Fab; immunoglobulin; heterophilic antibody;
XX human anti-mouse antibody; HAMA antibody; interleukin 8; IL-8; Herpes;
XX target antigen; bacterial; fungal; viral; pathogen; human disease;
XX hepatitis A; hepatitis B; hepatitis C; influenza; Giardia; Malaria;
XX Leishmania; Staphylococcus aureus; Pseudomonas aeruginosa; diagnosis.

OS Homo sapiens.
OS Synthetic.

PN M0200140306-A1.

PD 07-JUN-2001.

PF 06-DEC-2000; 2000MO-US33042.

PR 06-DEC-1999; 99US-0456090.

PA (BIOS-) BIOSITE DIAGNOSTICS INC.
PA (GENP-) GENPHARM INT.

PI Buechler J, Valkirs G, Gray J, Lonberg N;

DR WPI; 2001-374798/39.

PT Detecting analyte in human sample containing human antibodies binding
PT to nonhuman-antibodies, involves contacting sample with human antibody
PT which binds to antibodies from nonhuman species and detecting binding

PS Example 22; Page 96; 135pp; English.

XX The present invention describes a method for detecting an analyte in a
XX human sample containing human antibodies that specifically bind to
XX antibodies from a nonhuman species. The method involves contacting the
XX sample with a human antibody (I) which specifically binds to antibodies
XX from a nonhuman species and detecting the binding between (I) and the
XX analyte to indicate presence of the analyte. The method is used for
XX detecting an analyte in a human sample containing human anti-mouse
XX antibody (HAMA) (preferably human anti-mouse idiotype antibodies and/or
XX heterophilic antibodies). The method can also be used for detecting any
XX type of target antigen including bacterial, fungal and viral pathogens
XX that cause human diseases e.g., hepatitis (A,B and C), influenza, Herpes,
XX Giardiasis, Malaria, Leishmania, Staphylococcus aureus, Pseudomonas
XX aeruginosa. Human antibodies can be used as detection reagents for
XX performing clinical diagnostic tests and for performing other in vitro
XX detection assays, including for research purposes. (I) can be used in
XX qualitative assays designed to indicate the presence of one or more
XX target antigens above minimally detectable amounts of antigen in the
XX sample that usually correspond to the sensitivity limitations of the
XX assay for each target antigen. Also, (I) is used to determine the
XX amount of target antigen in a sample in a semi-quantitative or relative
XX sense. Quantification of one or more target antigens in a sample can
XX also be carried out using (I). AAH41612 to AAH4166, and AAB99361 to
XX AAB99399, represent sequences used in the exemplification of the present
XX invention.

SQ Sequence 226 AA;

Query Match 95.5%; Score 535.5; DB 22; Length 226;
Best Local Similarity 96.3%; Pred. No. 5.8e-33;

Matches 105; Conservative 3; Mismatches 0; Indels 1; Gaps 1;

QY 1 EIVLTQSPGTLISLSPGERATLSCRASQSVSSSFLAMYOQKPGQAPRLLIYGASRATGIP 60

DB 1 EIVLTQSPGTLISLSPGERATLSCRASQSVSSSYLAMYOQKPGQAPRLLIYGASRATGIP 60

QY 61 DRFGSGSGTDFTLTISRLEPEDFAVYCCQYGS-PTFGGTKEIK 108

DB 61 DRFGSGSGTDFTLTISRLEPEDFAVYCCQYGSPPYFGGTKEIK 109

Search completed: June 3, 2003, 08:14:43
Job time : 49.6553 secs

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OM protein - protein search, using sw model

Run on: June 3, 2003, 08:21:07 ; Search time 25.6177 Seconds

(without alignments)
426.742 Million cell updates/sec

Title: US-09-644-668A-9

Sequence: 1 EIVLTGSPGTLISPGERAT.....COYGGSPFTGCGTKVEIK 108

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 383519 seqs, 101223694 residues

Total number of hits satisfying chosen parameters: 383519

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: Published Applications AA:*

1: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
6: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
7: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep.*
8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
9: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
10: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep.*
11: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
12: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep.*
13: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
14: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	554	98.8	235	US-10-153-382-7
2	544	97.0	108	US-09-848-798-178
3	535.5	95.5	109	US-10-073-644C-8
4	535.5	95.5	226	US-09-453-234-50
5	535.5	95.5	226	US-09-453-234-86
6	532	94.8	141	US-10-153-382-23
7	528.5	94.2	226	US-09-453-234-80
8	526.5	93.9	226	US-09-453-234-42
9	523.5	93.3	226	US-09-453-234-72
10	522.5	93.1	226	US-09-453-234-74
11	520.5	92.8	226	US-09-453-234-38
12	520.5	92.8	246	US-09-880-748-1264
13	520	92.7	8	US-08-844-215-8
14	520	92.7	253	US-09-880-748-1499
15	517	92.2	150	US-09-782-397-5
16	517	92.2	287	US-09-782-397-17
17	517	92.2	304	US-09-782-397-14
18	516.5	92.1	224	US-09-453-234-52
19	514	91.6	108	US-09-300-425B-21

20	513	91.4	105	US-09-828-708-3	Sequence 3, Appl
21	512.5	91.4	251	US-09-880-748-1219	Sequence 1219, Ap
22	511	91.1	233	US-10-153-382-11	Sequence 11, Appl
23	510.5	91.0	224	US-09-453-234-76	Sequence 76, Appl
24	509	90.7	105	US-09-828-708-7	Sequence 7, Appl
25	509	90.7	107	US-08-844-215-10	Sequence 10, Appl
26	509	90.7	110	US-10-001-934-40	Sequence 40, Appl
27	508.5	90.6	236	US-09-859-053-34	Sequence 34, Appl
28	507.5	90.5	224	US-09-453-234-44	Sequence 44, Appl
29	507.5	90.5	224	US-09-453-234-78	Sequence 78, Appl
30	507.5	90.5	234	US-10-153-382-15	Sequence 15, Appl
31	507.5	90.5	236	US-09-859-053-38	Sequence 38, Appl
32	506.5	90.3	212	US-10-006-593-118	Sequence 118, Ap
33	506	90.2	249	US-09-880-748-1035	Sequence 1035, Ap
34	505.5	90.1	252	US-09-453-234-40	Sequence 40, Appl
35	499.5	89.0	252	US-09-880-748-1534	Sequence 1534, Ap
36	499	88.9	109	US-10-125-687-10	Sequence 10, Appl
37	499	88.9	109	US-10-025-687-10	Sequence 10, Appl
38	497.5	88.7	146	US-10-153-382-28	Sequence 28, Appl
39	491.5	87.6	106	US-08-844-215-14	Sequence 14, Appl
40	491	87.5	96	US-10-194-975-82	Sequence 82, Appl
41	491	87.5	96	US-10-153-382-22	Sequence 22, Appl
42	489	87.2	141	US-10-153-382-74	Sequence 24, Appl
43	488	87.0	107	US-08-844-215-12	Sequence 12, Appl
44	487.5	86.9	254	US-09-880-748-905	Sequence 905, Ap
45	487	86.8	214	US-10-229-567-11	Sequence 11, Appl

ALIGNMENTS

RESULT 1
US-10-153-382-7
Sequence 7, Application US/10153382
Publication No. US20030086930A1
GENERAL INFORMATION:
APPLICANT: PFIZER PRODUCTS INC.
TITLE OF INVENTION: USES OF ANTI-CTLA-4 ANTIBODIES
FILE REFERENCE: PC23019A
CURRENT APPLICATION NUMBER: US/10/153,382
CURRENT FILING DATE: 2002-05-22
PRIOR APPLICATION NUMBER: 60/293042
PRIOR FILING DATE: 2001-05-23
NUMBER OF SEQ ID NOS: 39
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 7
LENGTH: 235
TYPE: PRT
ORGANISM: Homo sapiens
US-10-153-382-7

Query Match 98.8%; Score 554; DB 9; Length 235;
Best Local Similarity 97.2%; Pred. No. 3.2e-32;
Matches 105; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 EIVLTGSPGTLISPGERATLSGRASGVSSFLAWYQKPGAPRLIYGASRRATGIP 60
DB 21 EIVLTGSPGTLISPGERATLSGRASGVSSFLAWYQKPGAPRLIYGASRRATGIP 80

QY 61 DRFGSGSGGTDFTLTISRLEPEDFAVYCCOYGGSPFTGCGTKVEIK 108
DB 81 DRFGSGSGGTDFTLTISRLEPEDFAVYCCOYGGSPFTGCGTKVEIK 128

RESULT 2
US-09-848-798-178
Sequence 178, Application US/09848798
Publication No. US20030040605A1
GENERAL INFORMATION:
APPLICANT: Siegel, Donald L.
TITLE OF INVENTION: RH(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
FILE REFERENCE: 09596-4202

CURRENT APPLICATION NUMBER: US/09/848,798
CURRENT FILING DATE: 2001-05-04
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/240,274
PRIOR FILING DATE: EARLIER FILING DATE: 1999-01-29
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/028,550
PRIOR FILING DATE: EARLIER FILING DATE: 1996-10-11
NUMBER OF SEQ ID NOS: 224
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 178
LENGTH: 108
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: anti-Rh(D) antibody clone SHS2
US-09-848-798-178

Query Match 97.0%; Score 544; DB 9; Length 108;
Best Local Similarity 96.1%; Pred. No. 8,3e-32;
Matches 103; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 4 LTQSPGTLSPGERATLSCRASQSVSSFLAWYQKPGQAPRLIYGASSRATGIP 63
DB 3 LTQSPGTLSPGERATLSCRASQSVSSFLAWYQKPGQAPRLIYGASSRATGIP 62
QY 64 SGSGSGTDFLTITSLRLEPEDFAVYCCQYSSPMTFGGTVEIK 108
DB 63 SGSGSGTDFLTITSLRLEPEDFAVYCCQYSSPMTFGGTVEIK 107

RESULT 3
US-10-073-644C-8
Sequence 8, Application US/10073644C
Publication No. US20030082643A1
GENERAL INFORMATION:
APPLICANT: Hudson, Debra
APPLICANT: van de Winkel, Jan
TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO FC ALPHA
FILE REFERENCE: MXI-211
CURRENT APPLICATION NUMBER: US/10/073,644C
CURRENT FILING DATE: 2002-02-11
PRIOR APPLICATION NUMBER: US 60/338,956
PRIOR FILING DATE: 2001-11-05
PRIOR APPLICATION NUMBER: US 60/268,075
PRIOR FILING DATE: 2001-02-12
NUMBER OF SEQ ID NOS: 8
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 8
LENGTH: 109
TYPE: PRT
ORGANISM: Homo sapiens
US-10-073-644C-8

Query Match 95.5%; Score 535.5; DB 9; Length 109;
Best Local Similarity 96.3%; Pred. No. 3,3e-31;
Matches 105; Conservative 3; Mismatches 0; Indels 1; Gaps 1;

QY 1 EIVLTQSPGTLSPGERATLSCRASQSVSSFLAWYQKPGQAPRLIYGASSRATGIP 60
DB 1 EIVLTQSPGTLSPGERATLSCRASQSVSSFLAWYQKPGQAPRLIYGASSRATGIP 60
QY 61 DRFGSGSGTDFLTITSLRLEPEDFAVYCCQYSSPMTFGGTVEIK 108
DB 61 DRFGSGSGTDFLTITSLRLEPEDFAVYCCQYSSPMTFGGTVEIK 109

RESULT 4
US-09-453-234-50
Sequence 50, Application US/09453234
Publication No. US20030091995A1
GENERAL INFORMATION:
APPLICANT: Buechler, Joe

APPLICANT: Walkiers, Gunars
APPLICANT: Gray, Jeff
APPLICANT: Lomborg, Nils
APPLICANT: Biosite Diagnostics, Inc.
APPLICANT: Genpharm International
TITLE OF INVENTION: Human Antibodies
FILE REFERENCE: 020015-000110US
CURRENT APPLICATION NUMBER: US/09/453,234
CURRENT FILING DATE: 1999-12-01
PRIOR APPLICATION NUMBER: US 60/157,415
PRIOR FILING DATE: 1999-10-02
NUMBER OF SEQ ID NOS: 112
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 50
LENGTH: 226
TYPE: PRT
ORGANISM: Homo sapiens
OTHER INFORMATION: M1-23L
US-09-453-234-50

Query Match 95.5%; Score 535.5; DB 9; Length 226;
Best Local Similarity 96.3%; Pred. No. 6,1e-31;
Matches 105; Conservative 3; Mismatches 0; Indels 1; Gaps 1;

QY 1 EIVLTQSPGTLSPGERATLSCRASQSVSSFLAWYQKPGQAPRLIYGASSRATGIP 60
DB 1 EIVLTQSPGTLSPGERATLSCRASQSVSSFLAWYQKPGQAPRLIYGASSRATGIP 60
QY 61 DRFGSGSGTDFLTITSLRLEPEDFAVYCCQYSSPMTFGGTVEIK 108
DB 61 DRFGSGSGTDFLTITSLRLEPEDFAVYCCQYSSPMTFGGTVEIK 109

RESULT 5
US-09-453-234-86
Sequence 86, Application US/09453234
Publication No. US20030091995A1
GENERAL INFORMATION:
APPLICANT: Buechler, Joe
APPLICANT: Walkiers, Gunars
APPLICANT: Gray, Jeff
APPLICANT: Lomborg, Nils
APPLICANT: Biosite Diagnostics, Inc.
TITLE OF INVENTION: Human Antibodies
FILE REFERENCE: 020015-000110US
CURRENT APPLICATION NUMBER: US/09/453,234
CURRENT FILING DATE: 1999-12-01
PRIOR APPLICATION NUMBER: US 60/157,415
PRIOR FILING DATE: 1999-10-02
NUMBER OF SEQ ID NOS: 112
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 86
LENGTH: 226
TYPE: PRT
ORGANISM: Homo sapiens
OTHER INFORMATION: M2-33L
US-09-453-234-86

Query Match 95.5%; Score 535.5; DB 9; Length 226;
Best Local Similarity 96.3%; Pred. No. 6,1e-31;
Matches 105; Conservative 3; Mismatches 0; Indels 1; Gaps 1;

QY 1 EIVLTQSPGTLSPGERATLSCRASQSVSSFLAWYQKPGQAPRLIYGASSRATGIP 60
DB 1 EIVLTQSPGTLSPGERATLSCRASQSVSSFLAWYQKPGQAPRLIYGASSRATGIP 60
QY 61 DRFGSGSGTDFLTITSLRLEPEDFAVYCCQYSSPMTFGGTVEIK 108
DB 61 DRFGSGSGTDFLTITSLRLEPEDFAVYCCQYSSPMTFGGTVEIK 109

RESULT 6

US-10-153-382-23
; Sequence 23, Application US/10153382
; Publication No. US20030086930A1
; GENERAL INFORMATION:
; APPLICANT: PFEIZER PRODUCTS INC.
; TITLE OF INVENTION: USES OF ANTI-CTLA-4 ANTIBODIES
; FILE REFERENCE: PC33019A
; CURRENT APPLICATION NUMBER: US/10/153,382
; CURRENT FILING DATE: 2002-05-22
; PRIOR APPLICATION NUMBER: 60/293042
; PRIOR FILING DATE: 2001-05-23
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 23
; LENGTH: 141
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-153-382-23

Query Match 94.8%; Score 532; DB 9; Length 141;
Best Local Similarity 97.1%; Pred. No. 7,2e-31;
Matches 100; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

OY 6 OSRGTLSPGRTLSLSPGERATLSCRASQSVSSFLAWYQOKPGQAPRLIYGASSRATGIPDRSG 65
DB 1 EIVWTOSPGTSLSPGERATLSCRASQSVSSFLAWYQOKPGQAPRLIYGASSRATGIPDRSG 60

OY 66 SSGSGTDFLTISRLEPEDFAVYCCOYGSSPMTFGQTKVEIK 108
DB 61 SSGSGTDFLTISRLEPEDFAVYCCOYGSSPMTFGQTKVEIK 103

RESULT 7
US-09-453-234-80
; Sequence 80, Application US/09453234
; Publication No. US20030091995A1
; GENERAL INFORMATION:
; APPLICANT: Buechler, Joe
; APPLICANT: Walkers, Gunars
; APPLICANT: Gray, Jeff
; APPLICANT: Lomborg, Nils
; APPLICANT: Biosite Diagnostics, Inc.
; APPLICANT: Genpharm International
; TITLE OF INVENTION: Human Antibodies
; FILE REFERENCE: 020015-000110US
; CURRENT APPLICATION NUMBER: US/09/453,234
; CURRENT FILING DATE: 1999-12-01
; PRIOR APPLICATION NUMBER: US 60/157,415
; PRIOR FILING DATE: 1999-10-02
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 80
; LENGTH: 226
; TYPE: PRT
; ORGANISM: Homo sapiens
; OTHER INFORMATION: M2-20L
US-09-453-234-80

Query Match 94.2%; Score 528.5; DB 9; Length 226;
Best Local Similarity 94.5%; Pred. No. 1,9e-30;
Matches 103; Conservative 4; Mismatches 1; Indels 1; Gaps 1;

OY 1 EIVLTOSPGTSLSPGERATLSCRASQSVSSFLAWYQOKPGQAPRLIYGASSRATGIP 60
DB 1 EIVWTOSPGTSLSPGERATLSCRASQSVSSFLAWYQOKPGQAPRLIYGASSRATGIP 60

OY 61 DRFGSGSGTDFLTISRLEPEDFAVYCCOYGSSPMTFGQTKVEIK 108
DB 61 DRFGSGSGTDFLTISRLEPEDFAVYCCOYGSSPMTFGQTKVEIK 109

RESULT 8
US-09-453-234-42

; Sequence 42, Application US/09453234
; Publication No. US20030091995A1
; GENERAL INFORMATION:
; APPLICANT: Buechler, Joe
; APPLICANT: Walkers, Gunars
; APPLICANT: Gray, Jeff
; APPLICANT: Lomborg, Nils
; APPLICANT: Biosite Diagnostics, Inc.
; APPLICANT: Genpharm International
; TITLE OF INVENTION: Human Antibodies
; FILE REFERENCE: 020015-000110US
; CURRENT APPLICATION NUMBER: US/09/453,234
; CURRENT FILING DATE: 1999-12-01
; PRIOR APPLICATION NUMBER: US 60/157,415
; PRIOR FILING DATE: 1999-10-02
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 42
; LENGTH: 226
; TYPE: PRT
; ORGANISM: Homo sapiens
; OTHER INFORMATION: M1-5L
US-09-453-234-42

Query Match 93.9%; Score 526.5; DB 9; Length 226;
Best Local Similarity 94.5%; Pred. No. 2,6e-30;
Matches 103; Conservative 4; Mismatches 1; Indels 1; Gaps 1;

OY 1 EIVLTOSPGTSLSPGERATLSCRASQSVSSFLAWYQOKPGQAPRLIYGASSRATGIP 60
DB 1 EIVWTOSPGTSLSPGERATLSCRASQSVSSFLAWYQOKPGQAPRLIYGASSRATGIP 60

OY 61 DRFGSGSGTDFLTISRLEPEDFAVYCCOYGSSPMTFGQTKVEIK 108
DB 61 DRFGSGSGTDFLTISRLEPEDFAVYCCOYGSSPMTFGQTKVEIK 109

RESULT 9
US-09-453-234-74
; Sequence 74, Application US/09453234
; Publication No. US20030091995A1
; GENERAL INFORMATION:
; APPLICANT: Buechler, Joe
; APPLICANT: Walkers, Gunars
; APPLICANT: Gray, Jeff
; APPLICANT: Lomborg, Nils
; APPLICANT: Biosite Diagnostics, Inc.
; APPLICANT: Genpharm International
; TITLE OF INVENTION: Human Antibodies
; FILE REFERENCE: 020015-000110US
; CURRENT APPLICATION NUMBER: US/09/453,234
; CURRENT FILING DATE: 1999-12-01
; PRIOR APPLICATION NUMBER: US 60/157,415
; PRIOR FILING DATE: 1999-10-02
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 74
; LENGTH: 226
; TYPE: PRT
; ORGANISM: Homo sapiens
; OTHER INFORMATION: M2-12L
US-09-453-234-74

Query Match 93.3%; Score 523.5; DB 9; Length 226;
Best Local Similarity 93.6%; Pred. No. 4,3e-30;
Matches 102; Conservative 4; Mismatches 2; Indels 1; Gaps 1;

OY 1 EIVLTOSPGTSLSPGERATLSCRASQSVSSFLAWYQOKPGQAPRLIYGASSRATGIP 60
DB 1 EIVWTOSPGTSLSPGERATLSCRASQSVSSFLAWYQOKPGQAPRLIYGASSRATGIP 60

OY 61 DRFGSGSGTDFLTISRLEPEDFAVYCCOYGSSPMTFGQTKVEIK 108
DB 61 DRFGSGSGTDFLTISRLEPEDFAVYCCOYGSSPMTFGQTKVEIK 109

Db 61 DRFGSGGCTDFTLTISLSEPEDFAVYCCQYGVSSPPYFGGCTKLEIK 109

RESULT 10

US-09-453-234-72
Sequence 72, Application US/09453234
Publication No. US20030091995A1
GENERAL INFORMATION:
APPLICANT: Buechler, Joe
APPLICANT: Valkirs, Gunars
APPLICANT: Gray, Jeff
APPLICANT: Lomborg, Nils
APPLICANT: Bioelite Diagnostics, Inc.
APPLICANT: Genpharm International
TITLE OF INVENTION: Human Antibodies
FILE REFERENCE: 020015-000110US
CURRENT APPLICATION NUMBER: US/09/453,234
CURRENT FILING DATE: 1999-12-01
PRIOR FILING DATE: 1999-10-02
NUMBER OF SEQ ID NOS: 112
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO: 72
LENGTH: 226
TYPE: PRT
ORGANISM: Homo sapiens
OTHER INFORMATION: M2-11L
US-09-453-234-72

Query Match 93.1%; Score 522.5; DB 9; Length 226;
Best Local Similarity 93.6%; Pred. No. 5e-30;
Matches 102; Conservative 4; Mismatches 2; Indels 1; Gaps 1;

Qy 1 EIVLTQSPGTLISLGERATLISCRASQSVSSFLAWYQOKPGQAPRLLIYGASSRATGIP 60
Db 1 EIVMTQSPGTLISLGERATLISCRASQGVSSSYLAWYQOKPGQAPRLLIYGASSRATGIP 60

Qy 61 DRFGSGGCTDFTLTISLSEPEDFAVYCCQYGVSS-PMTFGGCTKLEIK 108
Db 61 DRFGSGGCTDFTLTISLSEPEDFAVYCCQYGVSSPFTFGGCTKVDIK 109

RESULT 11

US-09-453-234-38
Sequence 38, Application US/09453234
Publication No. US20030091995A1
GENERAL INFORMATION:
APPLICANT: Buechler, Joe
APPLICANT: Valkirs, Gunars
APPLICANT: Gray, Jeff
APPLICANT: Lomborg, Nils
APPLICANT: Bioelite Diagnostics, Inc.
TITLE OF INVENTION: Human Antibodies
FILE REFERENCE: 020015-000110US
CURRENT APPLICATION NUMBER: US/09/453,234
CURRENT FILING DATE: 1999-12-01
PRIOR FILING DATE: 1999-10-02
NUMBER OF SEQ ID NOS: 112
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO: 38
LENGTH: 226
TYPE: PRT
ORGANISM: Homo sapiens
OTHER INFORMATION: M1-3L
US-09-453-234-38

Query Match 92.8%; Score 520.5; DB 9; Length 226;
Best Local Similarity 93.6%; Pred. No. 6.9e-30;
Matches 102; Conservative 4; Mismatches 2; Indels 1; Gaps 1;

Qy 1 EIVLTQSPGTLISLGERATLISCRASQSVSSFLAWYQOKPGQAPRLLIYGASSRATGIP 60

Db 1 EIVMTQSPGTLISLGERATLISCRASQSVSSSYLAWYQOKPGQAPRLLIYGASSRATGIP 60

Qy 61 DRFGSGGCTDFTLTISLSEPEDFAVYCCQYGVSS-PMTFGGCTKLEIK 108
Db 61 DRFGSGGCTDFTLTISLSEPEDFAVYCCQYGVSSPFTFGGCTKVDIK 109

RESULT 12

US-09-880-748-1264
Sequence 1264, Application US/09880748
Publication No. US20030059937A1
GENERAL INFORMATION:
APPLICANT: Ruben et al.
TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
FILE REFERENCE: PF523
CURRENT APPLICATION NUMBER: US/09/880,748
CURRENT FILING DATE: 2001-06-15
PRIOR FILING DATE: 2001-06-15
PRIOR FILING DATE: 2000-06-15
PRIOR FILING DATE: 2000-10-17
PRIOR FILING DATE: 2000-10-17
PRIOR FILING DATE: 2001-03-16
PRIOR FILING DATE: 2001-03-16
PRIOR FILING DATE: 2001-03-21
PRIOR FILING DATE: 2001-03-21
PRIOR FILING DATE: 2001-05-25
NUMBER OF SEQ ID NOS: 3239
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO: 1264
LENGTH: 246
TYPE: PRT
ORGANISM: Homo sapiens
US-09-880-748-1264

Query Match 92.8%; Score 520.5; DB 9; Length 246;
Best Local Similarity 96.3%; Pred. No. 7.4e-30;
Matches 104; Conservative 1; Mismatches 2; Indels 1; Gaps 1;

Qy 1 EIVLTQSPGTLISLGERATLISCRASQSVSSFLAWYQOKPGQAPRLLIYGASSRATGIP 60
Db 139 EIVLTQSPGTLISLGERATLISCRASQSVSSSYLAWYQOKPGQAPRLLIYGASSRATGIP 198

Qy 61 DRFGSGGCTDFTLTISLSEPEDFAVYCCQYGVSS-PMTFGGCTKLEIK 108
Db 199 DRFGSGGCTDFTLTISLSEPEDFAVYCCQYGVSS-LTFGGGCTKVEIK 245

RESULT 13

US-08-844-215-8
Sequence 8, Application US/08844215
Patent No. US20020016445A1
GENERAL INFORMATION:
APPLICANT: PERSOON, MATS AXEL
TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES SPECIFIC FOR
TITLE OF INVENTION: HEPATITIS C VIRUS (HCV) E2 ANTIGEN
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
ADDRESSER: ROBINS & ASSOCIATES
STREET: 90 MIDDLEFIELD ROAD, SUITE 200
CITY: MENLO PARK
STATE: CA
COUNTRY: USA
ZIP: 94025
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/844,215

FILING DATE: 17-APR-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/635,109
FILING DATE: 19-APR-1996
ATTORNEY/AGENT INFORMATION:
NAME: MCCracken, THOMAS P.
REGISTRATION NUMBER: 38,548
REFERENCE/DOCKET NUMBER: 80146,002
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 325-7812
TELEFAX: (650) 325-7823
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 107 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-644-215-8

Query Match 92.7%; Score 520; DB 8; Length 107;
Best Local Similarity 94.3%; Pred. No. 4e-30;
Matches 99; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 4 LTGSPGTLISLPGERATISCRASOSVSSFLAWYQKQKGAQPRLLIYGASSRATGIPRF 63
DB 3 LTGSPGTLISLPGERATISCRASOSVSSFLAWYQKQKGAQPRLLIYGASSRATGIPRF 62

QY 64 SSGSGSGTDFTLTISRLEPEDFAVYVYCCQYGGSSPMTFGGQTKVEIK 108
DB 63 SSGSGSGTDFTLTISRLEPEDFAVYVYCCQYGGSSPMTFGGQTKVEIK 107

RESULT 14

US-09-880-748-1499
Sequence 1499, Application US/09880748
Publication No. US20030059937A1

GENERAL INFORMATION:

APPLICANT: Ruben et al.
TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys

FILE REFERENCE: PF523

CURRENT APPLICATION NUMBER: US/09/880,748

PRIOR APPLICATION NUMBER: 60/212,210

PRIOR FILING DATE: 2000-06-15

PRIOR APPLICATION NUMBER: 60/240,816

PRIOR FILING DATE: 2000-10-17

PRIOR APPLICATION NUMBER: 60/276,248

PRIOR FILING DATE: 2001-03-16

PRIOR APPLICATION NUMBER: 60/277,379

PRIOR FILING DATE: 2001-03-21

PRIOR APPLICATION NUMBER: 60/293,499

PRIOR FILING DATE: 2001-05-25

NUMBER OF SEQ ID NOS: 3239

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 1499

LENGTH: 253

TYPE: PRT

ORGANISM: Homo sapiens

US-09-880-748-1499

Query Match 92.7%; Score 520; DB 9; Length 253;
Best Local Similarity 93.5%; Pred. No. 8.3e-30;
Matches 101; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 1 EIVLTGSPGTLISLPGERATISCRASOSVSSFLAWYQKQKGAQPRLLIYGASSRATGIP 60
DB 145 EIVLTGSPGTLISLPGERATISCRASOSVSSFLAWYQKQKGAQPRLLIYGASSRATGIP 204

QY 61 DRFGSGSGTDFTLTISRLEPEDFAVYVYCCQYGGSSPMTFGGQTKVEIK 108
DB 205 DRFGSGSGTDFTLTISRLEPEDFAVYVYCCQYGGSSPMTFGGQTKVEIK 252

RESULT 15
US-09-782-397-5
Sequence 5, Application US/09782397
Publication No. US20030021799A1

GENERAL INFORMATION:

APPLICANT: Dan, Michael D.

Mailli, Pradip K.

Kaplan, Howard A.

TITLE OF INVENTION: ANTIGEN BINDING FRAGMENTS H1, THAT

SPECIFICALLY DETECT CANCER CELLS, NICOTINES ENCODING THE

FRAGMENTS, AND USE THEREOF FOR THE PROPHYLAXIS AND

DETECTION OF CANCERS

NUMBER OF SEQUENCES: 28

CORRESPONDENCE ADDRESS:

ADDRESSEE: Morrison & Foerster LLP

STREET: 755 Page Mill Road

CITY: Palo Alto

STATE: CA

COUNTRY: USA

ZIP: 94304-1018

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/782,397

FILING DATE: 13-Feb-2001

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/862,124

FILING DATE: 1997-05-22

ATTORNEY/AGENT INFORMATION:

NAME: lehnardt, Susan K.

REGISTRATION NUMBER: 33,943

REFERENCE/DOCKET NUMBER: 31608-20001.20

TELECOMMUNICATION INFORMATION:

TELEPHONE: (650) 813-5600

TELEFAX: (650) 494-0792

TELEX: 706141

INFORMATION FOR SEQ ID NO: 5:

SEQUENCE CHARACTERISTICS:

LENGTH: 150 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

SEQUENCE DESCRIPTION: SEQ ID NO: 5:

US-09-782-397-5

Query Match 92.4%; Score 517; DB 9; Length 150;
Best Local Similarity 91.1%; Pred. No. 8.6e-30;
Matches 102; Conservative 4; Mismatches 2; Indels 4; Gaps 1;

QY 1 EIVLTGSPGTLISLPGERATISCRASOSVSSFLAWYQKQKGAQPRLLIYGASSRATGIP 60
DB 25 DIVLTGSPGTLISLPGERATISCRASOSVSSFLAWYQKQKGAQPRLLIYGASSRATGIP 84

QY 61 DRFGSGSGTDFTLTISRLEPEDFAVYVYCCQYGGSSPMTFGGQTKVEIK 108
DB 85 DRFGSGSGTDFTLTISRLEPEDFAVYVYCCQYGGSSPMTFGGQTKVEIK 136

Search completed: June 3, 2003, 08:52:51
Job time: 26.6177 secs

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OM protein - protein search, using sw model

Run on: June 3, 2003, 08:10:19 ; Search time 16.4027 Seconds
(Without alignments)
193.728 Million cell updates/sec

Title: US-09-644-668a-9

Sequence: 1 EIVLTQSPGRLSISPERAT.....COQTGSFPTGQTKVIRK 108

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents AA:*
1: /cgn2_6/ptodata/1/1aa/5A.COMB.pep:*
2: /cgn2_6/ptodata/1/1aa/5B.COMB.pep:*
3: /cgn2_6/ptodata/1/1aa/6A.COMB.pep:*
4: /cgn2_6/ptodata/1/1aa/6B.COMB.pep:*
5: /cgn2_6/ptodata/1/1aa/PCTUS.COMB.pep:*
6: /cgn2_6/ptodata/1/1aa/backfiles.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	546	97.3	109	4	US-09-025-769B-16
2	544	97.0	108	4	US-09-240-274-178
3	542	96.6	108	2	US-08-233-081B-42
4	538	95.9	108	1	US-08-488-113B-150
5	538	95.9	108	1	US-08-477-484B-150
6	538	95.9	108	2	US-08-646-360-150
7	538	95.9	108	4	US-08-839-765-150
8	538	95.9	108	4	US-09-136-389-150
9	538	95.9	108	4	US-09-610-838-150
10	521	92.9	108	1	US-07-634-278-86
11	521	92.9	108	1	US-08-477-728-86
12	521	92.9	108	1	US-08-474-040-86
13	521	92.9	108	1	US-08-487-200-86
14	521	92.9	108	4	US-08-484-537-86
15	517.5	92.2	107	1	US-08-107-669D-14
16	517.5	92.2	107	1	US-08-472-788A-14
17	517.5	92.2	107	2	US-08-477-531B-14
18	517.5	92.2	107	2	US-08-082-842A-14
19	517	92.2	108	1	US-08-276-852-86
20	517	92.2	108	1	US-08-899-575-86
21	517	92.2	108	1	US-08-899-575-86
22	517	92.2	108	5	PCT-US95-08743-86
23	517	92.2	150	4	US-08-862-124-5
24	517	92.2	287	4	US-08-862-124-17
25	516.5	92.1	304	4	US-08-862-124-14
26	516.5	92.1	107	2	US-08-652-558-49
27	508	90.6	108	1	US-08-276-852-99

28	508	90.6	108	1	US-08-899-575-99	Sequence 99, App1
29	508	90.6	108	1	US-08-899-575-99	Sequence 99, App1
30	508	90.6	108	5	PCT-US95-08743-99	Sequence 99, App1
31	507	90.4	129	2	US-08-480-774A-4	Sequence 4, App1
32	505.5	90.1	134	1	US-08-405-034-4	Sequence 4, App1
33	499	88.9	110	4	US-09-025-769B-30	Sequence 30, App1
34	499	88.9	110	4	US-09-025-769B-47	Sequence 47, App1
35	497	88.6	109	1	US-08-162-102C-23	Sequence 23, App1
36	497	88.6	109	5	PCT-US93-08786-23	Sequence 23, App1
37	495.5	88.3	109	1	US-08-276-852-147	Sequence 147, App
38	495.5	88.3	109	1	US-08-899-575-147	Sequence 147, App
39	495.5	88.3	109	1	US-08-899-575-147	Sequence 147, App
40	495.5	88.3	109	5	PCT-US95-08743-147	Sequence 147, App
41	493	87.9	104	1	US-08-276-852-100	Sequence 100, App
42	493	87.9	104	1	US-08-899-575-100	Sequence 100, App
43	493	87.9	104	1	US-08-899-575-100	Sequence 100, App
44	493	87.9	104	5	PCT-US95-08743-100	Sequence 100, App
45	493	87.9	107	1	US-08-276-852-90	Sequence 90, App1

ALIGNMENTS

RESULT 1
US-09-025-769B-16
Sequence 16, Application US/09025769B
Patent No. 6300064
GENERAL INFORMATION:
APPLICANT: Knappik, Achim
APPLICANT: Pack, Peter
APPLICANT: Ilag, Vic
APPLICANT: Ge, Liming
APPLICANT: Moroney, Simon
APPLICANT: Plueckhuhn, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
NUMBER OF SEQUENCES: 373
CORRESPONDENCE ADDRESS:
ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
STREET: 1251 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10021
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/025,769B
FILING DATE: 18-FEB-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: James F. Haley, Jr., Esq.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: MORPHO/5
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)596-9000
TELEFAX: (212)596-9090
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 109 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-025-769B-16
Query Match 97.3%, Score 546, DB 4, Length 109;
Best Local Similarity 97.3%, Pred. No. 8.9e-42;
Matches 105, Conservative 3, Mismatches 0, Gaps 0;

QY 1 EIVLTOSPGLTSLSPGERATLSCRASOSVSSFLAWYQKPGQAPRLIYGAASSRATGIP 60
DB 1 EIVLTOSPGLTSLSPGERATLSCRASOSVSSFLAWYQKPGQAPRLIYGAASSRATGIP 60
QY 61 DRFSGSGGTDFLTITISRLPEPDFAVYCCQYGGSSPMTFGGTKEIK 108
DB 61 DRFSGSGGTDFLTITISRLPEPDFAVYCCQYGGSSPMTFGGTKEIK 108

RESULT 2
US-09-240-274-178

Sequence 178, Application US/09240274
Patent No. 6255455
GENERAL INFORMATION:
APPLICANT: Siegel, Donald L.
TITLE OF INVENTION: RH(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
FILE REFERENCE: 09596-4202
CURRENT APPLICATION NUMBER: US/09/240,274
EARLIER FILING DATE: 1999-01-29
EARLIER APPLICATION NUMBER: 60/081,380
EARLIER FILING DATE: 1998-04-10
EARLIER APPLICATION NUMBER: 60/028,550
NUMBER OF SEQ ID NOS: 224
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 108
LENGTH: 108
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: anti-Rh(D) antibody clone SH52
US-09-240-274-178

Query Match 97.0%; Score 544; DB 4; Length 108;
Best Local Similarity 98.1%; Pred. No. 1.3e-41;
Matches 103; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 4 LTOSTGTLSPGERATLSCRASOSVSSFLAWYQKPGQAPRLIYGAASSRATGIP 63
DB 3 LTOSTGTLSPGERATLSCRASOSVSSFLAWYQKPGQAPRLIYGAASSRATGIP 62
QY 64 SSGSGGTDFLTITISRLPEPDFAVYCCQYGGSSPMTFGGTKEIK 108
DB 63 SSGSGGTDFLTITISRLPEPDFAVYCCQYGGSSPMTFGGTKEIK 107

RESULT 3

US-08-232-081B-42
Sequence 42, Application US/08232081B
Patent No. 5866152
GENERAL INFORMATION:
APPLICANT: NAKATANI, TOMOYUKI
APPLICANT: GOMI, HIDEYUKI
APPLICANT: WIDENES, JOHN
APPLICANT: NOGUCHI, HIROSHI
TITLE OF INVENTION: HUMANIZED B-B10
NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
ADDRESSEE: BIRCH, STEWART, KOLASCH AND BIRCH
STREET: PO BOX 747
CITY: FALLS CHURCH
STATE: VA
COUNTRY: USA
ZIP: 22040-0747
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,081B

FILING DATE:
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: SVENSSON, LEONARD R
REGISTRATION NUMBER: 30,330
REFERENCE/DOCKET NUMBER: 20-3484
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 205-8000
TELEFAX: (703) 205-8050
INFORMATION FOR SEQ ID NO: 42:
SEQUENCE CHARACTERISTICS:
LENGTH: 108 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-232-081B-42

Query Match 96.6%; Score 542; DB 2; Length 108;
Best Local Similarity 97.2%; Pred. No. 2e-41;
Matches 105; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 EIVLTOSPGLTSLSPGERATLSCRASOSVSSFLAWYQKPGQAPRLIYGAASSRATGIP 60
DB 1 EIVLTOSPGLTSLSPGERATLSCRASOSVSSFLAWYQKPGQAPRLIYGAASSRATGIP 60
QY 61 DRFSGSGGTDFLTITISRLPEPDFAVYCCQYGGSSPMTFGGTKEIK 108
DB 61 DRFSGSGGTDFLTITISRLPEPDFAVYCCQYGGSSPMTFGGTKEIK 108

RESULT 4
US-08-488-113B-150

Sequence 150, Application US/08488113B
Patent No. 5744580
GENERAL INFORMATION:
APPLICANT: Better, Marc D.
APPLICANT: Cartoli, Stephen F.
APPLICANT: Stuchlik, Gary M.
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
NUMBER OF SEQUENCES: 169
CORRESPONDENCE ADDRESS:
ADDRESSEE: McAndrews, Held & Malloy, Ltd.
STREET: 500 West Madison Street, 34th floor
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60661
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/488,113B
FILING DATE: 07-JUN-1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/425,336
FILING DATE: 18-APR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/064,691
FILING DATE: 12-MAY-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/988,430
FILING DATE: 09-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/901,707
FILING DATE: 19-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/787,567
FILING DATE: 04-NOV-1991

ATTORNEY/AGENT INFORMATION:

NAME: McNicholas, Janet M.
REGISTRATION NUMBER: 32,918
REFERENCE/DOCKET NUMBER: 11022US07/200-70.P3.C2A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/707-8889
TELEFAX: 312/707-9155
TELEX: 650 388-1248
INFORMATION FOR SEQ ID NO: 150:
SEQUENCE CHARACTERISTICS:
LENGTH: 108 amino acids
TYPE: amino acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-477-484B-150

Query Match 95.9%; Score 538; DB 1; Length 108;
Best Local Similarity 97.2%; Pred. No. 4.5e-41;
Matches 105; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 EIVLTOSPGTSLSPGERATLSCRASQSVSSFLAWYQOKPGQAPRLITYGSSRATGIP 60
DB 1 EIVLTOSPGTSLSPGERATLSCRASQSVSSFLAWYQOKPGQAPRLITYGSSRATGIP 60

QY 61 DRFGSGSGGTDFTLTISRLEPEDFAVYVYCOQYGGSSPMTFGGTVEIK 108
DB 61 DRFGSGSGGTDFTLTISRLEPEDFAVYVYCOQYGGSSPMTFGGTVEIK 108

RESULT 5
US-08-477-484B-150
Sequence 150, Application US/08477484B
Patent No. 5756699

GENERAL INFORMATION:

APPLICANT: Better, Marc D.
APPLICANT: Carroll, Stephen F.
APPLICANT: Studilka, Gary M.
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
NUMBER OF SEQUENCES: 169
CORRESPONDENCE ADDRESS:
ADDRESSEE: McAndrews, Held & Malloy, Ltd.
STREET: 500 West Madison Street, 34th floor
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60661

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/477,484B
FILING DATE: 07-JUN-1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/425,336
FILING DATE: 18-APR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/064,691
FILING DATE: 12-MAY-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/988,430
FILING DATE: 09-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/901,707
FILING DATE: 19-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/787,567
FILING DATE: 04-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: McNicholas, Janet M.

NAME: McNicholas, Janet M.
REGISTRATION NUMBER: 32,918
REFERENCE/DOCKET NUMBER: 11022US07/200-70.P3.C2A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/707-8889
TELEFAX: 312/707-9155
TELEX: 650 388-1248
INFORMATION FOR SEQ ID NO: 150:
SEQUENCE CHARACTERISTICS:
LENGTH: 108 amino acids
TYPE: amino acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-477-484B-150

Query Match 95.9%; Score 538; DB 1; Length 108;
Best Local Similarity 97.2%; Pred. No. 4.5e-41;
Matches 105; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 EIVLTOSPGTSLSPGERATLSCRASQSVSSFLAWYQOKPGQAPRLITYGSSRATGIP 60
DB 1 EIVLTOSPGTSLSPGERATLSCRASQSVSSFLAWYQOKPGQAPRLITYGSSRATGIP 60

QY 61 DRFGSGSGGTDFTLTISRLEPEDFAVYVYCOQYGGSSPMTFGGTVEIK 108
DB 61 DRFGSGSGGTDFTLTISRLEPEDFAVYVYCOQYGGSSPMTFGGTVEIK 108

RESULT 6
US-08-646-360-150
Sequence 150, Application US/08646360
Patent No. 5837491

GENERAL INFORMATION:

APPLICANT: Better, Marc D.
APPLICANT: Carroll, Stephen F.
APPLICANT: Studilka, Gary M.
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
NUMBER OF SEQUENCES: 173
CORRESPONDENCE ADDRESS:
ADDRESSEE: McAndrews, Held & Malloy, Ltd.
STREET: 500 West Madison Street, 34th floor
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60661

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/646,360
FILING DATE: 13-MAY-1996
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/05348
FILING DATE: 12-MAY-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/064,691
FILING DATE: 12-MAY-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/988,430
FILING DATE: 09-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/901,707
FILING DATE: 19-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/787,567
FILING DATE: 04-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: McNicholas, Janet M.

REGISTRATION NUMBER: 32,918
REFERENCE/DOCKET NUMBER: 200-70-P4
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/707-8889
TELEFAX: 312/707-9155
TELEX: 650 388-1248
INFORMATION FOR SEQ ID NO: 150:
SEQUENCE CHARACTERISTICS:
LENGTH: 108 amino acids
TYPE: amino acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-646-360-150

Query Match 95.9%; Score 538; DB 2; Length 108;
Best Local Similarity 97.2%; Pred. No. 4.5e-41;
Matches 105; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 EIVLTSPGTLSPGERATLSCRASQSVSSFLAWYQOKPGAPRLIYGASSRATGIP 60
DB 1 EIVLTSPGTLSPGERATLSCRASQSVSSFLAWYQOKPGAPRLIYGASSRATGIP 60
QY 61 DRSSGSGTDFLTITSLRLEPEDFAVYCCQYGSSTPFGQGTKEIK 108
DB 61 DRSSGSGTDFLTITSLRLEPEDFAVYCCQYGSSTPFGQGTKEIK 108

RESULT 7

US-08-839-765-150
Sequence 150, Application US/08839765
Patent No. 6146631
GENERAL INFORMATION:
APPLICANT: Better, Marc D.
APPLICANT: Carroll, Stephen F.
APPLICANT: Studnika, Gary M.
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
NUMBER OF SEQUENCES: 169
CORRESPONDENCE ADDRESSES:
ADDRESSEE: McAndrews, Held & Malloy, Ltd.
STREET: 500 West Madison Street, 34th floor
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60661
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/839,765
FILING DATE: 15-APR-1997
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/425,316
FILING DATE: 18-APR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/064,651
FILING DATE: 12-MAY-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/988,430
FILING DATE: 09-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/901,707
FILING DATE: 19-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/787,567
FILING DATE: 04-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: McNicholas, Janet M.
REGISTRATION NUMBER: 32,918

REGISTRATION NUMBER: 11022US09/200-70-P3-C3
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/707-8889
TELEFAX: 312/707-9155
TELEX: 650 388-1248
INFORMATION FOR SEQ ID NO: 150:
SEQUENCE CHARACTERISTICS:
LENGTH: 108 amino acids
TYPE: amino acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-839-765-150

Query Match 95.9%; Score 538; DB 4; Length 108;
Best Local Similarity 97.2%; Pred. No. 4.5e-41;
Matches 105; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 EIVLTSPGTLSPGERATLSCRASQSVSSFLAWYQOKPGAPRLIYGASSRATGIP 60
DB 1 EIVLTSPGTLSPGERATLSCRASQSVSSFLAWYQOKPGAPRLIYGASSRATGIP 60
QY 61 DRSSGSGTDFLTITSLRLEPEDFAVYCCQYGSSTPFGQGTKEIK 108
DB 61 DRSSGSGTDFLTITSLRLEPEDFAVYCCQYGSSTPFGQGTKEIK 108

RESULT 8

US-09-136-389-150
Sequence 150, Application US/09136389
Patent No. 6146850
GENERAL INFORMATION:
APPLICANT: Better, Marc D.
APPLICANT: Carroll, Stephen F.
APPLICANT: Studnika, Gary M.
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
NUMBER OF SEQUENCES: 173
CORRESPONDENCE ADDRESSES:
ADDRESSEE: McAndrews, Held & Malloy, Ltd.
STREET: 500 West Madison Street, 34th floor
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60661
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/136,389
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/646,360
FILING DATE: 13-MAY-1996
APPLICATION NUMBER: PCT/US94/05348
FILING DATE: 12-MAY-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/064,691
FILING DATE: 12-MAY-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/988,430
FILING DATE: 09-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/901,707
FILING DATE: 19-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/787,567
FILING DATE: 04-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: McNicholas, Janet M.

REGISTRATION NUMBER: 32,918
REFERENCE/DOCKET NUMBER: 200-70.P4
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/707-8889
TELEFAX: 312/707-9155
TELEX: 650 388-1248
INFORMATION FOR SEQ ID NO: 150:
SEQUENCE CHARACTERISTICS:
LENGTH: 108 amino acids
TYPE: amino acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-136-389-150

Query Match 95.9%; Score 538; DB 4; Length 108;
Best Local Similarity 97.2%; Pred. No. 4.5e-41;
Matches 105; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 EIVLTQSGTSLSPGERATLSCRASQSVSSFLAWYQKPGQAPRLIYGASSRATGIP 60
DB 1 EIVLTQSGTSLSPGERATLSCRASQSVSSFLAWYQKPGQAPRLIYGASSRATGIP 60

QY 61 DRFSGSGGTDFTLTISRLPEDPFAVYVYCOQYGSSPTFGGTKEIK 108
DB 61 DRFSGSGGTDFTLTISRLPEDPFAVYVYCOQYGSSPTFGGTKEIK 108

RESULT 9

US-09-610-838-150
Sequence 150, Application US/09610838

GENERAL INFORMATION:
PATENT NO. 6376217
APPLICANT: Better, Marc D.
APPLICANT: Cartoll, Stephen F.
APPLICANT: Studinka, Gary M.
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
TITLE OF INVENTION: Proteins
NUMBER OF SEQUENCES: 173
CORRESPONDENCE ADDRESS:
ADDRESSEE: McAndrews, Held & Malloy, Ltd.
STREET: 500 West Madison Street, 34th floor
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60661
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/610,838
FILING DATE: 06-JUL-2000
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/136,389
FILING DATE: 18-AUG-1998
APPLICATION NUMBER: 08/546,360
FILING DATE: 13-MAY-1996
APPLICATION NUMBER: PCT/US94/05348
FILING DATE: 12-MAY-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/064,691
FILING DATE: 12-MAY-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/988,430
FILING DATE: 09-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/901,707
FILING DATE: 19-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/787,567

FILING DATE: 04-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: McNicholas, Janet M.
REGISTRATION NUMBER: 32,918
REFERENCE/DOCKET NUMBER: 200-70.P4
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/707-8889
TELEFAX: 312/707-9155
TELEX: 650 388-1248
INFORMATION FOR SEQ ID NO: 150:
SEQUENCE CHARACTERISTICS:
LENGTH: 108 amino acids
TYPE: amino acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-610-838-150

Query Match 95.9%; Score 538; DB 4; Length 108;
Best Local Similarity 97.2%; Pred. No. 4.5e-41;
Matches 105; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 EIVLTQSGTSLSPGERATLSCRASQSVSSFLAWYQKPGQAPRLIYGASSRATGIP 60
DB 1 EIVLTQSGTSLSPGERATLSCRASQSVSSFLAWYQKPGQAPRLIYGASSRATGIP 60

QY 61 DRFSGSGGTDFTLTISRLPEDPFAVYVYCOQYGSSPTFGGTKEIK 108
DB 61 DRFSGSGGTDFTLTISRLPEDPFAVYVYCOQYGSSPTFGGTKEIK 108

RESULT 10

US-07-634-278-86
Sequence 86, Application US/07634278

GENERAL INFORMATION:
PATENT NO. 5530101
APPLICANT: QUEEN, Cary L.
APPLICANT: CO, Man Sung
APPLICANT: SCHNEIDER, William P.
APPLICANT: LANDOLFI, Nicholas F.
APPLICANT: COELING, Kathleen L.
TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
NUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Kourie and Crew
STREET: 379 Lytton Avenue
CITY: Palo Alto
STATE: California
COUNTRY: US
ZIP: 94301
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/634,278
FILING DATE: 19-DEC-1990
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/590,274
FILING DATE: 28-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/310,252
FILING DATE: 13-FEB-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/290,975
FILING DATE: 28-DEC-1988
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William W
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 11823-002600

TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 86:
SEQUENCE CHARACTERISTICS:
LENGTH: 108 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-07-634-278-86

Query Match 92.9%; Score 521; DB 1; Length 108;
Best Local Similarity 94.4%; Pred. No. 1.4e-39;
Matches 102; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 1 EIVLTQSPGTLSTISPGERATLSCRASQSVSSFLAWYQKPGQAPRLIIYGASSRATGIP 60
DB 1 EIVLTQSPGTLSTISPGERATLSCRASQSVSSFLAWYQKPGQAPRLIIYGASSRATGIP 60

QY 61 DRFGSGSGTDFLTITSLRLEPEDPAVYVYCOQYGSPPWTFGGTVEIK 108
DB 61 DRFGSGSGTDFLTITSLRLEPEDPAVYVYCOQYGSPPWTFGGTVEIK 108

RESULT 11

US-08-477-728-86
Sequence 86, Application US/08477728
Patent No. 5585089

GENERAL INFORMATION:

APPLICANT: QUEEN, Cary L.
APPLICANT: SCHNEIDER, William P.
APPLICANT: SELICK, Harold E.
TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
NUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: Palo Alto
STATE: California
COUNTRY: US
ZIP: 94111

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/477,728
FILING DATE: 07-JUN-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/634,278
FILING DATE: 19-DEC-1990

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/590,274
FILING DATE: 28-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/310,252
FILING DATE: 13-FEB-1989

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/290,975
FILING DATE: 28-DEC-1988
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M.
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 11823-002600

TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422

INFORMATION FOR SEQ ID NO: 86:
SEQUENCE CHARACTERISTICS:
LENGTH: 108 amino acids

TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-477-728-86

Query Match 92.9%; Score 521; DB 1; Length 108;
Best Local Similarity 94.4%; Pred. No. 1.4e-39;
Matches 102; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 1 EIVLTQSPGTLSTISPGERATLSCRASQSVSSFLAWYQKPGQAPRLIIYGASSRATGIP 60
DB 1 EIVLTQSPGTLSTISPGERATLSCRASQSVSSFLAWYQKPGQAPRLIIYGASSRATGIP 60

QY 61 DRFGSGSGTDFLTITSLRLEPEDPAVYVYCOQYGSPPWTFGGTVEIK 108
DB 61 DRFGSGSGTDFLTITSLRLEPEDPAVYVYCOQYGSPPWTFGGTVEIK 108

RESULT 12

US-08-474-040-86
Sequence 86, Application US/08474040
Patent No. 5693761

GENERAL INFORMATION:

APPLICANT: QUEEN, Cary L.
APPLICANT: CO, Man Sung
APPLICANT: SCHNEIDER, William P.
APPLICANT: LANDOLFI, Nicholas F.
APPLICANT: COELINGH, Kathleen L.
APPLICANT: SELICK, Harold E.
TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
NUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Kourie and Crew
STREET: 379 Lytton Avenue
CITY: Palo Alto
STATE: California
COUNTRY: US
ZIP: 94301

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/474,040
FILING DATE: 07-JUN-1995
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/634,278
FILING DATE: 19-DEC-1990

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/590,274
FILING DATE: 28-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/310,252
FILING DATE: 13-FEB-1989

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/290,975
FILING DATE: 28-DEC-1988
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M.
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 11823-002600

TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422

INFORMATION FOR SEQ ID NO: 86:
SEQUENCE CHARACTERISTICS:
LENGTH: 108 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide

US-08-474-040-86

Query Match 92.9%; Score 521; DB 1; Length 108;

Best Local Similarity 94.4%; Pred. No. 1.4e-39;

Matches 102; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 1 EIVLTOSGTTSLISGERATLSCRASQSVSSFLAWYQKPGQAPRLIYGASSRATGIP 60

DB 1 EIVLTOSGTTSLISGERATLSCRASQSVSSFLAWYQKPGQAPRLIYGASSRATGIP 60

QY 61 DRFSGSGGTDFTLTISRLEPEDFAVYCCQYGSPPMTFGGQTKYEIK 108
DB 61 DRFSGSGGTDFTLTISRLEPEDFAVYCCQYGSPPMTFGGQTKYEIK 108

RESULT 13

US-08-487-200-86

Sequence 86, Application US/08487200

Patent No. 5693762

GENERAL INFORMATION:

APPLICANT: QUEEN, Cary L.

APPLICANT: CO, Man Sung

APPLICANT: SCHNEIDER, William P.

APPLICANT: LANDOLFI, Nicholas F.

APPLICANT: COELINGH, Kathleen L.

TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS

NUMBER OF SEQUENCES: 113

CORRESPONDENCE ADDRESSES:

ADDRESS: Townsend and Townsend and Crew

STREET: 379 Lytton Avenue

CITY: Palo Alto

STATE: California

COUNTRY: US

ZIP: 94301

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/487,200

FILING DATE: 7-JUN-1995

CLASSIFICATION: 424

PRIOR APPLICATION NUMBER: US 07/634,278

FILING DATE: 19-DEC-1990

APPLICATION NUMBER: 19-DEC-1990

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/590,274

FILING DATE: 28-SEP-1990

APPLICATION NUMBER: US 07/310,252

FILING DATE: 13-FEB-1989

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/290,975

FILING DATE: 28-DEC-1988

ATTORNEY/AGENT INFORMATION:

NAME: Smith, William M

REGISTRATION NUMBER: 30,223

REFERENCE/DOCKET NUMBER: 11823-002610

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 326-2400

TELEFAX: (415) 326-2422

INFORMATION FOR SEQ ID NO: 86:

SEQUENCE CHARACTERISTICS:

LENGTH: 108 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-08-487-200-86

Query Match 92.9%; Score 521; DB 1; Length 108;

Best Local Similarity 94.4%; Pred. No. 1.4e-39;

Matches 102; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 1 EIVLTOSGTTSLISGERATLSCRASQSVSSFLAWYQKPGQAPRLIYGASSRATGIP 60

DB 1 EIVLTOSGTTSLISGERATLSCRASQSVSSFLAWYQKPGQAPRLIYGASSRATGIP 60

QY 61 DRFSGSGGTDFTLTISRLEPEDFAVYCCQYGSPPMTFGGQTKYEIK 108
DB 61 DRFSGSGGTDFTLTISRLEPEDFAVYCCQYGSPPMTFGGQTKYEIK 108

RESULT 14

US-08-484-537-86

Sequence 86, Application US/08484537

Patent No. 6180370

GENERAL INFORMATION:

APPLICANT: QUEEN, Cary L.

APPLICANT: CO, Man Sung

APPLICANT: SCHNEIDER, William P.

APPLICANT: LANDOLFI, Nicholas F.

APPLICANT: COELINGH, Kathleen L.

TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS

NUMBER OF SEQUENCES: 113

CORRESPONDENCE ADDRESSES:

ADDRESS: Townsend and Townsend and Crew

STREET: 379 Lytton Avenue

CITY: Palo Alto

STATE: California

COUNTRY: US

ZIP: 94301

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/484,537

FILING DATE: 13-FEB-1989

CLASSIFICATION: 424

PRIOR APPLICATION NUMBER: US 07/634,278

FILING DATE: 19-DEC-1990

APPLICATION NUMBER: US 07/590,274

FILING DATE: 28-SEP-1990

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/310,252

FILING DATE: 13-FEB-1989

APPLICATION NUMBER: 13-FEB-1989

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/290,975

FILING DATE: 28-DEC-1988

ATTORNEY/AGENT INFORMATION:

NAME: Smith, William M

REGISTRATION NUMBER: 30,223

REFERENCE/DOCKET NUMBER: 11823-002600

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 326-2400

TELEFAX: (415) 326-2422

INFORMATION FOR SEQ ID NO: 86:

SEQUENCE CHARACTERISTICS:

LENGTH: 108 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-08-484-537-86

Query Match 92.9%; Score 521; DB 4; Length 108;

Best Local Similarity 94.4%; Pred. No. 1.4e-39;

Matches 102; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 1 EIVLTOSGTTSLISGERATLSCRASQSVSSFLAWYQKPGQAPRLIYGASSRATGIP 60

Db 1 EIVLTQSPGTLISLSPGERATLSCRASQSVSSGYLGMWQKQGPRLIYGAASSRATGIP 60
QY 61 DRFGSGSGTDFLTLSLSPGERATLSCRASQSVSSGYLGMWQKQGPRLIYGAASSRATGIP 108
Db 61 DRFGSGSGTDFLTLSLSPGERATLSCRASQSVSSGYLGMWQKQGPRLIYGAASSRATGIP 108

RESULT 15

US-08-107-669D-14
Sequence 14, Application US/08107669D
Patent No. 5766886
GENERAL INFORMATION:
APPLICANT: Studnicka, Gary M.
TITLE OF INVENTION: Modified Antibody Variable Domains (as amended)
NUMBER OF SEQUENCES: 67
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein and Fox P.L.L.C.
STREET: 1100 New York Ave., N.W., Suite 600
CITY: Washington
STATE: D.C.
COUNTRY: United States of America
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentln Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/107,669D
FILING DATE: 13-AUG-1993
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/10906
FILING DATE: 14-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/808,464
FILING DATE: 13-DEC-1991
ATTORNEY/AGENT INFORMATION:
NAME: Michele A. Cimbalia
REGISTRATION NUMBER: 33,851
REFERENCE/DOCKET NUMBER: 0610.1000001/MAC
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202/371-2600
TELEFAX: 202/371-2540
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 107 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-107-669D-14

Query Match 92.2%; Score 517.5; DB 1; Length 107;
Best Local Similarity 95.4%; Pred. No. 2,9e-39;
Matches 103; Conservative 1; Mismatches 3; Indels 1; Gaps 1;
QY 1 EIVLTQSPGTLISLSPGERATLSCRASQSVSSGYLGMWQKQGPRLIYGAASSRATGIP 60
Db 1 EIVLTQSPGTLISLSPGERATLSCRASQSVSSGYLGMWQKQGPRLIYGAASSRATGIP 59
QY 61 DRFGSGSGTDFLTLSLSPGERATLSCRASQSVSSGYLGMWQKQGPRLIYGAASSRATGIP 108
Db 60 DRFGSGSGTDFLTLSLSPGERATLSCRASQSVSSGYLGMWQKQGPRLIYGAASSRATGIP 107

Search completed: June 3, 2003, 08:24:15
Job time: 18.4027 secs

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OM protein - protein search, using sw model

Run on: June 3, 2003, 08:09:29 ; Search time 21.3447 Seconds

(without alignments)
531.460 Million cell updates/sec

Title: US-09-644-668A-19

Perfect score: 633
Sequence: 1 QVQLVESGGGVGQVQPERSLRL.....TGMLEPFDYWGQCTLVTVSS 118

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

1: PIR 73:*
2: PIR2:*
3: PIR3:*
4: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	563.5	89.0	121	2	IG heavy chain V r
2	559.5	88.4	121	2	IG heavy chain V r
3	557.5	88.1	135	2	IG heavy chain V r
4	551	87.0	118	2	IG heavy chain - h
5	550	86.9	137	2	IG heavy chain V r
6	549	86.7	122	2	IG heavy chain - h
7	548	86.6	140	2	IG heavy chain pre
8	545.5	86.2	134	2	IG heavy chain V r
9	545	86.1	114	2	IG heavy chain V r
10	544	85.9	122	2	IG heavy chain V r
11	542	85.6	120	2	IG heavy chain - h
12	541.5	85.5	132	2	IG heavy chain V r
13	540.5	85.4	119	2	IG heavy chain V r
14	538.5	85.1	133	2	IG heavy chain V r
15	538	85.0	139	2	IG heavy chain V r
16	537.5	84.9	130	2	IG heavy chain V r
17	524	82.8	114	2	IG heavy chain V r
18	523.5	82.7	130	2	IG heavy chain V r
19	523	82.6	133	2	IG heavy chain pre
20	522	82.5	128	2	IG heavy chain - h
21	521.5	82.4	109	2	IG heavy chain V r
22	517.5	81.8	123	2	IG heavy chain V r
23	517	81.7	122	1	IG heavy chain - h
24	516	81.5	151	2	IG heavy chain V r
25	514	81.2	114	2	IG heavy chain pre
26	512.5	81.0	109	2	IG heavy chain V r
27	510.5	80.6	119	2	IG heavy chain V r
28	506.5	80.0	111	2	IG heavy chain V r
29	506	79.9	122	2	IG V-D-J region (K

30	505.5	79.9	111	2	PH1643	IG heavy chain V r
31	504.5	79.7	143	2	S23624	IG heavy chain V r
32	504	79.6	120	2	S44111	IG heavy chain V-D
33	502.5	79.4	119	2	S31108	IG heavy chain - h
34	502	79.3	118	2	S31677	IG heavy chain V r
35	501.5	79.2	117	2	S78486	IG heavy chain V r
36	500.5	79.1	123	2	S31114	IG heavy chain - h
37	500	79.0	120	2	S48798	IG heavy chain V r
38	499.5	78.9	119	1	G1H0N1	IG heavy chain V r
39	498	78.7	136	2	S31587	IG heavy chain V r
40	497.5	78.6	140	2	B56701	IG heavy chain V r
41	497.5	78.6	140	2	S31686	IG heavy chain V r
42	496.5	78.4	119	2	S31107	IG heavy chain V r
43	496	78.4	108	2	PH1642	IG heavy chain - h
44	495.5	78.3	113	2	S38490	IG heavy chain V r
45	494.5	78.1	125	2	S30531	IG heavy chain V r

ALIGNMENTS

RESULT 1

S19666
IG heavy chain V region (VH3DTH4) - human

C/Species: Homo sapiens (man)
C/Date: 22-Jan-1993 #sequence_rev150n 22-Jan-1993 #text_change 20-Jun-2000

C/Accession: S19666

R/Marks: J.D.; Hoogenboom, H.R.; Bonnert, T.P.; McCafferty, J.; Griffiths, A.D.; Winter

J. Mol. Biol. 222, 581-597, 1991

A/Title: By-passing immunization. Human antibodies from V-gene libraries displayed on I

A/Reference number: S19663; MUID:92085276; PMID:1748994

A/Accession: S19666

A/Molecule type: mRNA

A/Residues: 1-121 <MAR>

A/Cross-references: EMBL:X61646; NID:937688; PIDD:CAA43827.1; PID:9133369

C/Keywords: heterocyclamer; immunoglobulin V region; immunoglobulin homology

P15-98/Domain: Immunoglobulin homology <IMM>

Query Match 89.0%, Score 563.5, DB 2; Length 121;

Best Local Similarity 88.4%, Pred. No. 4.7e-44;

Matches 107; Conservative 6; Mismatches 5; Indels 3; Gaps 1;

QY	1	QVQLVESGGGVGQVQPERSLRLCAASGFTFSYTHMWRQAPGKLEWYFISYDGSNKRY 60
DB	1	QVQLVSGGGVQGRSIRLSCAASGFTFSYGMHWROAPGKLEWVAVISYDGSNKRY 60
QY	61	ADSVKGRFTISRDNKNTLYIQNNSLRADTAITYCAFTG---LSPFDYWGQCTLVTVS 117
DB	61	ADSVKGRFTISRDNKNTLYIQNNSLRADTAITYCAFTG---LSPFDYWGQCTLVTVS 120
QY	118	S 118
DB	121	S 121

RESULT 2

G36005
IG heavy chain V region (M74) - human

C/Species: Homo sapiens (man)
C/Date: 21-Dec-1990 #sequence_rev150n 21-Dec-1990 #text_change 16-Dec-1998

C/Accession: G36005

R/Schroeder Jr., H.W.; Wang, J.Y.
Proc. Natl. Acad. Sci. U.S.A. 87, 6146-6150, 1990

A/Title: Preferential utilization of conserved immunoglobulin heavy chain variable gene

A/Reference number: A36005; MUID:90349571; PMID:2117273

A/Accession: G36005

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-121 <SCH>

A/Cross-references: GB:M34031

C/Genetics: GDB:IGH@, IGHDIY

A/Gene: GDB:IGH@, IGHDIY

A/Cross-references: GDB:118731; OMIM:146910
 A/Map position: 14q32.33-14q32.33
 C/Superfamily: immunoglobulin V region; immunoglobulin homology
 C/Keywords: heterotetramer; immunoglobulin
 F/15-98/Domain: immunoglobulin homology <IMM>

Query Match 88.4%; Score 559.5; DB 2; Length 121;
 Best Local Similarity 88.5%; Pred. No. 1.1e-43;
 Matches 108; Conservative 3; Mismatches 6; Indels 5; Gaps 2;

QY 1 QVQLVSGGAVQPGKSLRLSCAASGFTSSYTMHWROAPGKLEWTFISYDGSNKHY 60
 DB 1 QVQLVSGGAVQPGKSLRLSCAASGFTSSYTMHWROAPGKLEWTFISYDGSNKHY 60
 QY 61 ADSVKGRFTVSRDNRKNTLYLQNNSLRAEDTAIYYCARIGWLGPPDYWGOGTLVTVSS 116
 DB 61 ADSVKGRFTVSRDNRKNTLYLQNNSLRAEDTAIYYCARIGWLGPPDYWGOGTLVTVSS 119
 QY 117 SS 118
 DB 120 SS 121

RESULT 3

Ig heavy chain V region - human
 C/Species: Homo sapiens (man)
 C/Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
 C/Accession: S31598
 R/CuSlnier, A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnelie, C.
 submitted to the EMBL Data Library, June 1992
 A/Description: Mechanisms that generate human immunoglobulin diversity operate from the
 A/Reference number: S31585
 A/Accession: S31598
 A/Status: preliminary
 A/Molecule type: mRNA
 A/Residues: 1-135 <CUI>
 A/Cross-references: EMBL:Z14170; NID:G31001; PIDN:CAA78539.1; PID:G31002
 C/Superfamily: immunoglobulin V region; immunoglobulin homology
 C/Keywords: heterotetramer; immunoglobulin
 F/31-114/Domain: immunoglobulin homology <IMM>

Query Match 88.1%; Score 557.5; DB 2; Length 135;
 Best Local Similarity 88.2%; Pred. No. 1.8e-43;
 Matches 105; Conservative 5; Mismatches 8; Indels 1; Gaps 1;

QY 1 QVQLVSGGAVQPGKSLRLSCAASGFTSSYTMHWROAPGKLEWTFISYDGSNKHY 60
 DB 17 QVQLVSGGAVQPGKSLRLSCAASGFTSSYTMHWROAPGKLEWTFISYDGSNKHY 76
 QY 61 ADSVKGRFTVSRDNRKNTLYLQNNSLRAEDTAIYYCARIGWLGPPDYWGOGTLVTVSS 118
 DB 77 ADSVKGRFTVSRDNRKNTLYLQNNSLRAEDTAIYYCARIGWLGPPDYWGOGTLVTVSS 135

RESULT 4

Ig heavy chain - human
 C/Species: Homo sapiens (man)
 C/Date: 02-Dec-1993 #sequence_revision 26-May-1995 #text_change 17-Mar-1999
 C/Accession: S31116
 R/Raaphorst, F.M.; Timmers, E.; Kenter, M.J.H.; van Tol, M.J.D.; Vossen, J.M.; Schuurman
 Eur. J. Immunol. 22, 247-251, 1992
 A/Title: Restricted utilization of germ-line V(H)3 genes and short diverse third complement
 A/Reference number: S31104; MIMD:92111633; PMID:1730252
 A/Accession: S31116
 A/Status: preliminary; nucleic acid sequence not shown; translation not shown
 A/Molecule type: mRNA
 A/Residues: 1-118 <RAA>
 A/Cross-references: EMBL:X62966
 A/Note: the nucleotide sequence was submitted to the EMBL Data Library, October 1991
 C/Superfamily: immunoglobulin V region; immunoglobulin homology
 C/Keywords: heterotetramer; immunoglobulin

F/15-98/Domain: immunoglobulin homology <IMM>

Query Match 87.0%; Score 551; DB 2; Length 118;
 Best Local Similarity 88.1%; Pred. No. 6.1e-43;
 Matches 104; Conservative 4; Mismatches 10; Indels 0; Gaps 0;

QY 1 QVQLVSGGAVQPGKSLRLSCAASGFTSSYTMHWROAPGKLEWTFISYDGSNKHY 60
 DB 1 QVQLVSGGAVQPGKSLRLSCAASGFTSSYTMHWROAPGKLEWTFISYDGSNKHY 60
 QY 61 ADSVKGRFTVSRDNRKNTLYLQNNSLRAEDTAIYYCARIGWLGPPDYWGOGTLVTVSS 118
 DB 61 ADSVKGRFTVSRDNRKNTLYLQNNSLRAEDTAIYYCARIGWLGPPDYWGOGTLVTVSS 118

RESULT 5

Ig heavy chain V region - human (fragment)
 C/Species: Homo sapiens (man)
 C/Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
 C/Accession: S31701
 R/CuSlnier, A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnelie, C.
 submitted to the EMBL Data Library, June 1992
 A/Description: Mechanisms that generate human immunoglobulin diversity operate from
 A/Reference number: S31585
 A/Accession: S31701
 A/Status: preliminary
 A/Molecule type: mRNA
 A/Residues: 1-137 <CUI>
 A/Cross-references: EMBL:Z14177; NID:G31020; PIDN:CAA78546.1; PID:G31021
 C/Superfamily: immunoglobulin V region; immunoglobulin homology
 C/Keywords: heterotetramer; immunoglobulin
 F/34-117/Domain: immunoglobulin homology <IMM>

Query Match 86.9%; Score 550; DB 2; Length 137;
 Best Local Similarity 86.4%; Pred. No. 8.8e-43;
 Matches 102; Conservative 5; Mismatches 11; Indels 0; Gaps 0;

QY 1 QVQLVSGGAVQPGKSLRLSCAASGFTSSYTMHWROAPGKLEWTFISYDGSNKHY 60
 DB 20 QVQLVSGGAVQPGKSLRLSCAASGFTSSYTMHWROAPGKLEWTFISYDGSNKHY 79
 QY 61 ADSVKGRFTVSRDNRKNTLYLQNNSLRAEDTAIYYCARIGWLGPPDYWGOGTLVTVSS 118
 DB 80 PDSVKGRFTVSRDNRKNTLYLQNNSLRAEDTAIYYCATNMDAFDIWGOGTLVTVSS 137

RESULT 6

Ig heavy chain - human
 C/Species: Homo sapiens (man)
 C/Date: 02-Dec-1993 #sequence_revision 26-May-1995 #text_change 17-Mar-1999
 C/Accession: S31117
 R/Raaphorst, F.M.; Timmers, E.; Kenter, M.J.H.; van Tol, M.J.D.; Vossen, J.M.; Schuurman
 Eur. J. Immunol. 22, 247-251, 1992
 A/Title: Restricted utilization of germ-line V(H)3 genes and short diverse third complement
 A/Reference number: S31104; MIMD:92111633; PMID:1730252
 A/Accession: S31117
 A/Status: preliminary; nucleic acid sequence not shown; translation not shown
 A/Molecule type: mRNA
 A/Residues: 1-122 <RAA>
 A/Cross-references: EMBL:X62967
 A/Note: the nucleotide sequence was submitted to the EMBL Data Library, October 1991
 C/Superfamily: immunoglobulin V region; immunoglobulin homology
 C/Keywords: heterotetramer; immunoglobulin
 F/15-98/Domain: immunoglobulin homology <IMM>

Query Match 86.7%; Score 549; DB 2; Length 122;
 Best Local Similarity 86.9%; Pred. No. 9.6e-43;
 Matches 106; Conservative 4; Mismatches 8; Indels 4; Gaps 1;

QY 1 QVQLVSGGAVQPGKSLRLSCAASGFTSSYTMHWROAPGKLEWTFISYDGSNKHY 60
 |||||

Db 1 QVOLVESGGVGPGRSLRLSCAASGFTSSYGMHWRAQPGKLEWVAIWDGSKKYY 60
QY 61 ADSVKGRFTVSRDNRKNTLYLQNMNLSRAEDTAIYCCARTGMLGP----FDYWGQGLTVTV 116
Db 61 ADSVKGRFTISRDNKNTLYLQNMNLSRAEDTAIYCCARTGMLGP----FDYWGQGLTVTV 120
QY 117 SS 118
Db 121 SS 122

RESULT 7

S70442

Ig heavy chain precursor V region (mu) - human (fragment)
C/Species: Homo sapiens (man)
C/Date: 24-Jul-1998 #sequence_revision 24-Jul-1998 #text_change 21-Jan-2000
C/Accession: S70442
R/Cuisinier, A.M.; Fumoux, F.; Fougereau, M.; Tonnelie, C.
Mol. Immunol. 29, 1363-1373, 1992
A/Title: IGM kappa/lambda EBV human B cell clone: an early step of differentiation of B
A/Reference number: S70442; MUID:93024508; PMID:1383695
A/Accession: S70442
A/Status: not compared with conceptual translation
A/Molecule type: mRNA
A/Residues: 1-140 <CUI>
C/Superfamily: immunoglobulin V region; immunoglobulin homology
F:34-117/Domain: immunoglobulin homology <IMM>

Query Match 86.6%; Score 548; DB 2; Length 140;
Best Local Similarity 87.5%; Pred. No. 1.4e-42;
Matches 105; Conservative 5; Mismatches 8; Indels 2; Gaps 1;

QY 1 QVOLVESGGVGPGRSLRLSCAASGFTSSYGMHWRAQPGKLEWVAIWDGSKKYY 60
Db 20 QVOLVESGGVGPGRSLRLSCAASGFTSSYGMHWRAQPGKLEWVAIWDGSKKYY 79
QY 61 ADSVKGRFTVSRDNRKNTLYLQNMNLSRAEDTAIYCCARTGMLGP--PDYWGQGLTVTVSS 118
Db 80 ADSVKGRFTISRDNKNTLYLQNMNLSRAEDTAIYCCARTGMLGP--PDYWGQGLTVTVSS 139

RESULT 8

S31679

Ig heavy chain V region - human (fragment)
C/Species: Homo sapiens (man)
C/Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C/Accession: S31679
R/Cuisinier, A.M.; Gauthier, L.; Boublil, L.; Fougereau, M.; Tonnelie, C.
submitted to the EMBL Data Library, June 1992
A/Description: Mechanisms that generate human immunoglobulin diversity operate from the
A/Reference number: S31679
A/Accession: S31679
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-1134 <CUI>
C/Cross-references: EMBL:214203; NID:930965; PIDN:CA478572.1; PID:930966
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin
F:34-117/Domain: immunoglobulin homology <IMM>

Query Match 86.2%; Score 545.5; DB 2; Length 134;
Best Local Similarity 89.0%; Pred. No. 2.2e-42;
Matches 105; Conservative 3; Mismatches 7; Indels 3; Gaps 1;

QY 1 QVOLVESGGVGPGRSLRLSCAASGFTSSYGMHWRAQPGKLEWVAIWDGSKKYY 60
Db 20 QVOLVESGGVGPGRSLRLSCAASGFTSSYGMHWRAQPGKLEWVAIWDGSKKYY 79
QY 61 ADSVKGRFTVSRDNRKNTLYLQNMNLSRAEDTAIYCCARTGMLGPFDYWGQGLTVTVSS 118
Db 80 ADSVKGRFTISRDNKNTLYLQNMNLSRAEDTAIYCCARTGMLGPFDYWGQGLTVTVSS 134

RESULT 9

S46390

Ig heavy chain V region - human
C/Species: Homo sapiens (man)
C/Date: 27-Jan-1995 #sequence_revision 27-Jan-1995 #text_change 20-Jun-2000
C/Accession: S46390
R/Figini, M.; Marks, J.D.; Winter, G.; Griffiths, A.D.
J. Mol. Biol. 239, 68-78, 1994
A/Title: In vitro assembly of repertoires of antibody chains on the surface of phage b
A/Reference number: S46390; MUID:94254092; PMID:8196048
A/Accession: S46390
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-114 <FIG>
C/Cross-references: EMBL:231686; NID:9509782; PIDN:CA483491.1; PID:91335143
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 86.1%; Score 545; DB 2; Length 114;
Best Local Similarity 89.0%; Pred. No. 2.1e-42;
Matches 105; Conservative 4; Mismatches 5; Indels 4; Gaps 2;

QY 1 QVOLVESGGVGPGRSLRLSCAASGFTSSYGMHWRAQPGKLEWVAIWDGSKKYY 60
Db 1 EVOLVESGGVGPGRSLRLSCAASGFTSSYGMHWRAQPGKLEWVAIWDGSKKYY 60
QY 61 ADSVKGRFTVSRDNRKNTLYLQNMNLSRAEDTAIYCCARTGMLGPFDYWGQGLTVTVSS 118
Db 61 ADSVKGRFTISRDNKNTLYLQNMNLSRAEDTAIYCCARTGMLGPFDYWGQGLTVTVSS 114

RESULT 10

E36005

Ig heavy chain V region (M72) - human
C/Species: Homo sapiens (man)
C/Date: 21-Dec-1990 #sequence_revision 21-Dec-1990 #text_change 16-Dec-1998
C/Accession: E36005
R/Schroeder Jr., H.W.; Wang, J.Y.
Proc. Natl. Acad. Sci. U.S.A. 87, 6146-6150, 1990
A/Title: Preferential utilization of conserved immunoglobulin heavy chain variable gene
A/Reference number: A36005; MUID:90349571; PMID:2117273
A/Accession: E36005
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-122 <SCH>
C/Cross-references: GB:M34030
C/Genetics:
A/Gene: GDB:IGH@; IGHDI1
A/Cross-references: GDB:118731; OMIM:146910
A/Map position: 14q32.33-14q32.33
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 85.9%; Score 544; DB 2; Length 122;
Best Local Similarity 85.2%; Pred. No. 2.7e-42;
Matches 104; Conservative 4; Mismatches 10; Indels 4; Gaps 1;

QY 1 QVOLVESGGVGPGRSLRLSCAASGFTSSYGMHWRAQPGKLEWVAIWDGSKKYY 60
Db 1 QVOLVESGGVGPGRSLRLSCAASGFTSSYGMHWRAQPGKLEWVAIWDGSKKYY 60
QY 61 ADSVKGRFTVSRDNRKNTLYLQNMNLSRAEDTAIYCCARTGMLGPFDYWGQGLTVTV 116
Db 61 ADSVKGRFTISRDNKNTLYLQNMNLSRAEDTAIYCCARTGMLGPFDYWGQGLTVTV 120

QY 117 SS 118
Db 121 SS 122

RESULT 11

S31112
Ig heavy chain - human
C/Species: Homo sapiens (man)
C/Date: 02-Dec-1993 #sequence_revision 26-May-1995 #text_change 17-Mar-1999
C/Accession: S31112
R/Author: F.M.; Timmers, E.; Kenter, M.J.H.; van Tol, M.J.D.; Voosen, J.M.; Schuurman
Burr, J. Immunol. 22, 247-251, 1992
A/Title: Restricted utilization of germ-line V(H)3 genes and short diverse third complement
A/Reference number: S31104; MUID:92111633; PMID:1730252
A/Accession: S31112
A/Status: preliminary; nucleic acid sequence not shown; translation not shown
A/Molecule type: mRNA
A/Residues: 1-120 <RAA>
A/Cross-references: EMBL:X62961
A/Note: the nucleotide sequence was submitted to the EMBL Data Library, October 1991
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin
F/15-98/Domain: immunoglobulin homology <IMM>

Query Match 85.6%; Score 542; DB 2; Length 120;
Best Local Similarity 87.6%; Pred. No. 4, 1e-42;
Matches 106; Conservative 4; Mismatches 7; Indels 4; Gaps 2;
QY 1 QVQLVSGGAVQPGKSLRLSCAASGFTSSYTMHWVROAPGKLEWVTFISYDGSNKHY 60
Db 1 QVQLVSGGAVQPGKSLRLSCAASGFTSSYTMHWVROAPGKLEWVAVISYDGSNKHY 60
QY 61 ADSVKGKFTISRDNKNTLYLQNSLRADTAIYCARGLG-PEDYWGQGLTVTVSS 117
Db 61 ADSVKGKFTISRDNKNTLYLQNSLRADTAIYCARGLG-PEDYWGQGLTVTVSS 119
QY 118 S 118
Db 120 S 120

RESULT 12
S31603
Ig heavy chain V region - human
C/Species: Homo sapiens (man)
C/Date: 03-Mar-1994 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C/Accession: S31603
R/Cutshier, L.; Gauthier, L.; Boublil, L.; Fougereau, M.; Tonnelie, C.
submitted to the EMBL Data Library, June 1992
A/Description: Mechanisms that generate human immunoglobulin diversity operate from the
A/Reference number: S31585
A/Status: preliminary
A/Accession: S31603
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-132 <CU>
A/Cross-references: EMBL:Z14168; NID:930999; PIDN:CA48537.1; PID:931000
C/Keywords: heterotetramer; immunoglobulin homology
F/30-113/Domain: immunoglobulin homology <IMM>

Query Match 85.5%; Score 541.5; DB 2; Length 132;
Best Local Similarity 88.1%; Pred. No. 5e-42;
Matches 104; Conservative 5; Mismatches 8; Indels 1; Gaps 1;
QY 1 QVQLVSGGAVQPGKSLRLSCAASGFTSSYTMHWVROAPGKLEWVTFISYDGSNKHY 60
Db 1 QVQLVSGGAVQPGKSLRLSCAASGFTSSYTMHWVROAPGKLEWVAVISYDGSNKHY 75
QY 61 ADSVKGKFTISRDNKNTLYLQNSLRADTAIYCARGLG-PEDYWGQGLTVTVSS 118
Db 61 ADSVKGKFTISRDNKNTLYLQNSLRADTAIYCARGLG-PEDYWGQGLTVTVSS 132

RESULT 13
F36005
Ig heavy chain V region (M49) - human
C/Species: Homo sapiens (man)
C/Date: 21-Dec-1990 #sequence_revision 21-Dec-1990 #text_change 16-Dec-1998

C/Accession: F36005
R/Schroeder Jr., H.W.; Wang, J.Y.
Proc. Natl. Acad. Sci. U.S.A. 87, 6146-6150, 1990
A/Title: Preferential utilization of conserved immunoglobulin heavy chain variable
A/Reference number: A36005; MUID:90349571; PMID:2117273
A/Accession: F36005
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-119 <SCH>
A/Cross-references: GB:M34026
A/Genetics:
A/Gene: GDB:IGH; IGHDIY1
A/Cross-references: GDB:118731; OMIM:146910
A/Map position: 14q32.33-14q32.33
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin
F/15-98/Domain: immunoglobulin homology <IMM>

Query Match 85.4%; Score 540.5; DB 2; Length 119;
Best Local Similarity 87.4%; Pred. No. 5.5e-42;
Matches 104; Conservative 4; Mismatches 10; Indels 1; Gaps 1;
QY 1 QVQLVSGGAVQPGKSLRLSCAASGFTSSYTMHWVROAPGKLEWVTFISYDGSNKHY 60
Db 1 QVQLVSGGAVQPGKSLRLSCAASGFTSSYTMHWVROAPGKLEWVAVISYDGSNKHY 60
QY 61 ADSVKGKFTISRDNKNTLYLQNSLRADTAIYCARGLG-PEDYWGQGLTVTVSS 118
Db 61 ADSVKGKFTISRDNKNTLYLQNSLRADTAIYCARGLG-PEDYWGQGLTVTVSS 119

RESULT 14
A49028
Ig heavy chain V-III region - human (fragment)
C/Species: Homo sapiens (man)
C/Date: 21-Jan-1994 #sequence_revision 18-Nov-1994 #text_change 23-Jul-1999
C/Accession: A49028
R/Timmers, E.; Kenter, M.; Thompson, A.; Kraakman, M.E.; Berman, J.E.; Alt, F.W.; S.
Burr, J. Immunol. 21, 2355-2363, 1991
A/Title: Diversity of immunoglobulin heavy chain gene segment rearrangement in B ly
A/Reference number: A49028; MUID:92008140; PMID:1915549
A/Accession: A49028
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-133 <TIM>
A/Cross-references: GB:S64471; NID:9236904; PIDN:AA320011.1; PID:9236905
A/Experimental source: X-linked agammaglobulinemia patients, B lymphoblastoid cell
C/Note: sequence extracted from NCI backbone (NCBI:64471, NCBI:64470)
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin
F/15-98/Domain: immunoglobulin homology <IMM>

Query Match 85.1%; Score 538.5; DB 2; Length 133;
Best Local Similarity 85.4%; Pred. No. 9.3e-42;
Matches 105; Conservative 3; Mismatches 10; Indels 5; Gaps 1;
QY 1 QVQLVSGGAVQPGKSLRLSCAASGFTSSYTMHWVROAPGKLEWVTFISYDGSNKHY 60
Db 1 QVQLVSGGAVQPGKSLRLSCAASGFTSSYTMHWVROAPGKLEWVAVISYDGSNKHY 60
QY 61 ADSVKGKFTISRDNKNTLYLQNSLRADTAIYCARGLG-PEDYWGQGLTVTVSS 115
Db 61 ADSVKGKFTISRDNKNTLYLQNSLRADTAIYCARGLG-PEDYWGQGLTVTVSS 120
QY 116 VSS 118
Db 121 VSS 123

RESULT 15
S31674
Ig heavy chain V region - human (fragment)
C/Species: Homo sapiens (man)

C>Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999

C/Accession: S31674

R/CuiSinter: A.M.; Gauthier, L.; Boudil, L.; Fougereau, M.; Tonnelie, C.

Submitted to the EMBL Data Library, June 1992

A/Description: Mechanisms that generate human immunoglobulin diversity operate from the

A/Reference number: S31585

A/Accession: S31674

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-139 <CUI>

A/Cross-references: EMBL:214204; NID:g30967; PID:CAA78573.1; PID:g30968

C/Superfamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: heterotetramer; immunoglobulin

F/34-117/Domain: immunoglobulin homology <IMM>

Query Match 85.0%; Score 538; DB 2; Length 139;
Best Local Similarity 85.4%; Pred. No. 1.1e-41;
Matches 105; Conservative 4; Mismatches 6; Indels 8; Gaps 2;

QY 1 QVQLVESGGGVVQPGRSLRLSCAASGFTPSSTYTMHWROAPGKGLEWTFISYDGSNKHY 60
|||
20 QVQLVESGGGVVQPGRSLRLSCAASGFTPSSTYTMHWROAPGKGLEWTFISYDGSNKHY 79
|||

QY 61 ADSVKGRTFSRDNSKNTLYLOMSLRADDTAIYCARNG----WLGPEDYWGQGLTYT 115
|||
80 ADSVKGRTFSRDNSKNTLYLOMSLRADDTAIYCARNGGLGFNW---FDPWGQGLTYT 136
|||

QY 116 VSS 118
|||
137 VSS 139

Search completed: June 3, 2003, 08:22:39
Job time : 21.3447 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 3, 2003, 08:02:44 ; Search time 10.8737 Seconds
(without alignments)
450.095 Million cell updates/sec

Title: US-09-644-668A-19
Perfect score: 633
Sequence: 1 QVQLVESGGGVQVQGRSLRL.....TGMLEPPYWGQGLTVTVSS 118

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	517	81.7	122 1	HV3G_HUMAN
2	499.5	78.9	119 1	HV3I_HUMAN
3	492	77.7	122 1	HV3H_HUMAN
4	488	77.1	126 1	HV3K_HUMAN
5	483.5	76.4	121 1	HV3J_HUMAN
6	465	73.5	116 1	HV3T_HUMAN
7	458	72.4	114 1	HV3B_HUMAN
8	458	72.4	136 1	HV16_MOUSE
9	449.5	71.0	119 1	HV3L_HUMAN
10	433	68.4	120 1	HV3U_HUMAN
11	432	68.2	119 1	HV3M_HUMAN
12	430	67.9	119 1	HV3N_HUMAN
13	429	67.8	117 1	HV3C_HUMAN
14	426	67.3	119 1	HV38_MOUSE
15	425.5	67.2	120 1	HV3E_HUMAN
16	424.5	67.1	115 1	HV3D_HUMAN
17	421	66.5	122 1	HV3A_HUMAN
18	419	66.2	117 1	HV3O_HUMAN
19	418	66.0	119 1	HV37_MOUSE
20	417	65.9	114 1	HV01_CANPA
21	413.5	65.3	115 1	HV32_MOUSE
22	413.5	65.3	115 1	HV3F_HUMAN
23	411.5	65.0	113 1	HV30_MOUSE
24	411.5	65.0	116 1	HV05_CARAU
25	408	64.5	119 1	HV40_MOUSE
26	407.5	64.4	118 1	HV39_MOUSE
27	406.5	64.2	113 1	HV27_MOUSE
28	403.5	63.7	113 1	HV31_MOUSE
29	402.5	63.6	115 1	HV33_MOUSE
30	402	63.5	111 1	HV35_MOUSE
31	401.5	63.4	116 1	HV30_HUMAN
32	401.5	63.4	142 1	HV01_RAT
33	400.5	63.3	113 1	HV28_MOUSE

34	399.5	63.1	113 1	HV34_MOUSE	P01803 mus musculus
35	399.5	63.1	117 1	HV02_CANPA	P01785 canis fam1
36	397.5	62.8	117 1	HV41_MOUSE	P01811 mus musculus
37	397	62.7	119 1	HV3P_HUMAN	P01772 homo sapien
38	396.5	62.6	113 1	HV29_MOUSE	P01798 mus musculus
39	394.5	62.3	117 1	HV17_MOUSE	P01786 mus musculus
40	392	61.9	117 1	HV54_MOUSE	P18525 mus musculus
41	392	61.9	122 1	HV20_MOUSE	P01789 mus musculus
42	391.5	61.8	116 1	HV3R_HUMAN	P01779 homo sapien
43	389.5	61.5	123 1	HV25_MOUSE	P01794 mus musculus
44	388.5	61.4	123 1	HV24_MOUSE	P01793 mus musculus
45	388	61.3	118 1	HV3V_HUMAN	P80419 homo sapien

ALIGNMENTS

RESULT 1	
HV3G_HUMAN	
ID HV3G_HUMAN	STANDARD; PRT; 122 AA.
AC P01768;	
DT 21-JUL-1986 (Rel. 01, Created)	
DT 21-JUL-1986 (Rel. 01, Last sequence update)	
DT 15-JUL-1999 (Rel. 38, Last annotation update)	
DS 19 heavy chain V-II region CM.	
OS Homo sapiens (Human).	
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	
OX NCBI_TaxID=9606;	
RN [1]	
RP SEQUENCE.	
RX MEDLINE=81013859; PubMed=6774332;	
RA Lehman D.W., Putnam F.W.,	
RT "Amino acid sequence of the variable region of a human mu chain:	
RL Proc. Natl. Acad. Sci. U.S.A. 77:3239-3243(1980).	
CC -1- MISCELLANEOUS: THIS MU CHAIN WAS ISOLATED FROM THE PLASMA OF A	
CC PATIENT WITH MACROGLOBULINEMIA.	
DR PIR; A02051; M3HUM.	
DR HSSP; P01772; 2FB4.	
DR InterPro; IPR003006; Ig_MHC.	
DR InterPro; IPR003596; Ig_V.	
DR Pfam; PF00047; Ig; 1.	
DR SMART; SM00406; IgV; 1.	
KW Immunoglobulin V region.	
FT MOD_RES 1 1	
FT NON_TER 122 122	
FT SEQUENCE 122 AA; 13668 MW; A42DOF17D252FIC2 CRC64;	
Query Match	81.7%; Score 517; DB 1; Length 122;
Best Local Similarity	77.9%; Pred. No. 3,2e-46;
Matches 95; Conservative 11; Mismatches 10; Indels 4; Gaps 1;	
QY 1 QVQLVESGGGVQVQGRSLRLSCAASGFTSSYTMWVRQAPGKGLEWVTFISYDGSKHY 60	
DB 1 QVQLVESGGGVQVQGRSLRLSCAASGFTSSYTMWVRQAPGKGLEWVAVISYGBBKXY 60	
QY 61 ADVSKGFTTSPDNRKTYLQNNSLRAEDTATYYCART-----GMLEPPYWGQGLTVTV 116	
DB 61 ABSYKGFITTSRDSKRTLYLQNNSLRAEDTAVYYCARDPYGVRAFYWGQGLTVTV 120	
QY 117 SS 118	
DB 121 SS 122	
RESULT 2	
HV3I_HUMAN	
ID HV3I_HUMAN	STANDARD; PRT; 119 AA.
AC P01770;	
DT 21-JUL-1986 (Rel. 01, Created)	
DT 21-JUL-1986 (Rel. 01, Last sequence update)	
DT 15-JUL-1999 (Rel. 38, Last annotation update)	

DB Ig heavy chain V-III region NIE.
 OS Homo sapiens (Human).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=77070269; PubMed=826475;
 RA Ponstingl H., Hilschmann N.;
 RT "The rule of antibody structure. The primary structure of a
 RT monoclonal IgG1 immunoglobulin (myeloma protein NIE). II. The
 RT chymotryptic peptides of the H-chain, alignment of the tryptic
 RT peptides and discussion of the complete structure.";
 RL Hoppe-Seyler's Z. Physiol. Chem. 357:1571-1604(1976).
 RN [2]
 RP DISULFIDE BOND.
 RX MEDLINE=77070267; PubMed=1002129;
 RA Dreker L., Schwarz J., Reichel W., Hilschmann N.;
 RT "Rule of antibody structure. The primary structure of a monoclonal
 RT IgG1 immunoglobulin (myeloma protein NIE). I: Purification and
 RT characterization of the protein, the L- and H-chains, the
 RT cyanoogen bromide cleavage products, and the disulfide bridges.";
 RL Hoppe-Seyler's Z. Physiol. Chem. 357:1515-1540(1976).
 CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGGL MYELOMA
 PROTEIN.
 CC PIR; A02053; G1HUM1.
 DR HSSP; P01772; 2PB4.
 DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR003596; Ig_V.
 DR Pfam; PF00047; Ig; 1.
 DR SMART; SM00406; IgV; 1.
 KW Immunoglobulin V region.
 FT MOD RES 1 1
 FT DISULFID 22 96
 FT NON TER 119 119
 FT SEQUENCE 119 AA; 13242 MW; C96935A655E165B CRC64;
 SQ
 Query Match 78.3%; Score 499.5; DB 1; Length 119;
 Best Local Similarity 78.3%; Pred. No. 2e-44;
 Matches 95; Conservative 10; Mismatches 11; Indels 5; Gaps 2;
 QY 1 QVQLVDSGGGVVOPGSRSLRSCAASGFTFSSTYTMHWVROAPGKGLMVFPIISDGNKH 60
 DB 1 QVQLVDSGGGVVOPGSRSLRSCAASGFTFSSTYTMHWVROAPGKGLMVFPIISDGNKH 60
 QY 61 ADSVKGRTVSRDINSKNTLYLQNSLRADPTAIYYCAR--TGLMFPDYWGQGLTVTVS 117
 DB 61 ADSVNGRTISRDSKNTLYLQNSLRADPTAIYYCAR--TGLMFPDYWGQGLTVTVS 117
 QY 118 S 118
 DB 119 S 119
 RESULT 3
 HV3K HUMAN STANDARD; PRT; 122 AA.
 ID P01772;
 AC P01772;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE 15 heavy chain V-III region GA.
 DR Homo sapiens (Human).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=74175307; PubMed=4208843;
 RA Florent G., Lehman D., Putnam F.W.;
 RT "The switch point in mu heavy chains of human Igm immunoglobulins.";
 RT Biochemistry 13:2482-2498(1974).
 CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A WALDENSTROM'S

CC MACROGLOBULIN.
 DR PIR; A02052; M3HUGA.
 DR HSSP; P01772; 2PB4.
 DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR003596; Ig_V.
 DR Pfam; PF00047; Ig; 1.
 DR SMART; SM00406; IgV; 1.
 KW Immunoglobulin V region.
 FT MOD RES 1 1
 FT NON TER 122 122
 FT SEQUENCE 122 AA; 13166 MW; 745B6595BE4100A CRC64;
 SQ
 Query Match 77.7%; Score 492; DB 1; Length 122;
 Best Local Similarity 71.3%; Pred. No. 1.2e-43;
 Matches 87; Conservative 23; Mismatches 8; Indels 4; Gaps 2;
 QY 1 QVQLVDSGGGVVOPGSRSLRSCAASGFTFSSTYTMHWVROAPGKGLMVFPIISDGNKH 60
 DB 1 QVQLVDSGGGVVOPGSRSLRSCAASGFTFSSTYTMHWVROAPGKGLMVFPIISDGNKH 60
 QY 61 ADSVKGRTVSRDINSKNTLYLQNSLRADPTAIYYCARFG-WLGPFDYWGQGLTVTV 116
 DB 61 ADSVNGRTISRDSKNTLYLQNSLRADPTAIYYCARFG-WLGPFDYWGQGLTVTV 120
 QY 117 SS 118
 DB 121 SS 122
 RESULT 4
 HV3K HUMAN STANDARD; PRT; 126 AA.
 ID P01772;
 AC P01772;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE 15 heavy chain V-III region KOL.
 DR Homo sapiens (Human).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE, AND DISULFIDE BONDS.
 RX MEDLINE=83289131; PubMed=6844994;
 RA Schmidt W.E., Jung H.-D., Palm W., Hilschmann N.;
 RT "Three-dimensional structure determination of antibodies. Primary
 RT structure of crystallized monoclonal immunoglobulin IgG1 KOL, I.";
 RL Hoppe-Seyler's Z. Physiol. Chem. 364:713-747(1983).
 RN [2]
 RP X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS).
 RX MEDLINE=81072295; PubMed=7441755;
 RA Marguier M., Delgenhofer J., Huber R., Palm W.;
 RT "Crystallographic refinement and atomic models of the intact
 RT immunoglobulin molecule KOL and its antigen-binding fragment at 3.0 A
 RT and 1.0-A resolution.";
 RL J. Mol. Biol. 141:369-391(1980).
 DR PDB; 2PB4; 12-JUL-89.
 DR PDB; 2IG2; 12-JUL-89.
 DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR003596; Ig_V.
 DR Pfam; PF00047; Ig; 1.
 DR SMART; SM00406; IgV; 1.
 KW Immunoglobulin V region; 3D-structure.
 FT MOD RES 1 1
 FT DISULFID 22 96
 FT DISULFID 105 110
 FT STRAND 3 7
 FT STRAND 11 12
 FT TURN 14 15
 FT STRAND 18 25
 FT HELIX 29 31
 FT STRAND 34 39

FT TURN 41 42
 FT STRAND 46 51
 FT TURN 53 54
 FT STRAND 58 60
 FT TURN 62 67
 FT STRAND 68 73
 FT TURN 74 77
 FT STRAND 78 83
 FT HELIX 88 90
 FT STRAND 92 99
 FT STRAND 106 106
 FT TURN 107 108
 FT STRAND 109 109
 FT STRAND 113 113
 FT STRAND 120 124
 FT NON TER 126
 SQ SEQUENCE 126 AA; 13718 MW; 84D71B52B16F8776 CRC64;

Query Match 77.1%; Score 488; DB 1; Length 126;
 Best Local Similarity 74.8%; Pred. No. 3.1e-43;
 Matches 95; Conservative 10; Mismatches 12; Indels 10; Gaps 2;

OY 1 QVQLVSGGAVVQPGSRSLRLSCAASGFTPSYTMHWROAPGKLEWVTFISYGSNKHY 60
 DB 1 QVQLVSGGAVVQPGSRSLRLSCSSSGFTFSSYAMTWROAPGKLEWVAIIWDDGSDQHY 60
 OY 61 ADVKGRFTVSRDINSKNTLYLQNMNLSRAEDTAIYYCARTG-----WLGPFDPYWGQ 111
 DB 61 ADVKGRFTISRDNKNTLFLQMDSLRPEDTGVFCARDGGHGFCSASCFEP-DYWGQ 119
 OY 112 TLNVVSS 118
 DB 120 TPVTSS 126

RESULT 5
 HV3J HUMAN STANDARD; PRT; 121 AA.

DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Ig heavy chain V-II region H1L.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 NCBI_Taxid=9606;

RP SEQUENCE.
 RX MEDLINE=79124695; PubMed=420800;
 RA Chiu Y.-Y.H., Lopez de Castro J.A., Poljak R.J.;
 RT "Amino acid sequence of the VH region of human myeloma
 RL B10chem18:553-560(1979).
 CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IG1 MYELOMA
 CC PROTEIN.

PIR; A02054; GIHQUL.
 DR HSSP; P01772; 2FB4.
 DR InterPro; IPR003006; IG_MHC.
 DR InterPro; IPR003596; IG_V.
 DR Pfam; PF00047; Ig; 1.
 DR SMART; SM00406; IGV; 1.
 KW Immunoglobulin V region.
 FT MOD RES 1 1
 FT NON TER 121 121
 SQ SEQUENCE 121 AA; 13566 MW; 480FC3610E9FDAB CRC64;

Query Match 76.4%; Score 483.5; DB 1; Length 121;
 Best Local Similarity 74.8%; Pred. No. 8.7e-43;
 Matches 92; Conservative 11; Mismatches 13; Indels 7; Gaps 2;

OY 1 QVQLVSGGAVVQPGSRSLRLSCAASGFTPSYTMHWROAPGKLEWVTFISYGSNKHY 60
 DB 1 QVQLVSGGAVVQPGSRSLRLSCSSSGFTFSSYAMTWROAPGKLEWVAIIWDDGSDQHY 60

DB 1 QVQLVQAGGAVVQPGSRSLRLSCIASGFTPSYTMHWROAPGKLEWVAIIVNGSRITY 60
 OY 61 ADVKGRFTVSRDINSKNTLYLQNMNLSRAEDTAIYYCAR-----TGLGPFDPYWGQGLVT 115
 DB 61 ADVKGRFTISRDNKNTLYWZMSLRPEDIATVYICARDPDLIRF--SPDYWGQGLVT 118
 OY 116 VSS 118
 DB 119 VSS 121

RESULT 6

ID HV3J HUMAN STANDARD; PRT; 116 AA.
 AC P01781;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Ig heavy chain V-II region GAL.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 NCBI_Taxid=9606;

RP SEQUENCE.
 RX MEDLINE=75059123; PubMed=4803843;
 RA Watanabe S., Barnikol H.U., Horn J., Berttram J., Hilschmann N.;
 RT "The primary structure of a monoclonal IgM-immunoglobulin
 (macroglobulin Gal.), II: the amino acid sequence of the H-chain (mu-
 type), subgroup H II. Architecture of the complete IgM-molecule."
 RL Hoppe-Seyler's Z. Physiol. Chem. 354:1505-1509(1973).
 [2]
 RP REVISION TO 28-33.

RA Hilschmann N.;
 RL Submitted (JUN-1975) to the PIR data bank.
 CC -1- MISCELLANEOUS: THIS MU CHAIN WAS ISOLATED FROM A WALDENSTROM'S
 CC MACROGLOBULIN.

CC PIR; A02064; M3HUGL.
 DR HSSP; P01772; 2FB4.
 DR InterPro; IPR003006; IG_MHC.
 DR InterPro; IPR003596; IG_V.
 DR Pfam; PF00047; Ig; 1.
 DR SMART; SM00406; IGV; 1.
 KW Immunoglobulin V region.
 FT NON TER 116 116
 SQ SEQUENCE 116 AA; 12730 MW; 2C67CA9AAAA1282 CRC64;

Query Match 73.5%; Score 465; DB 1; Length 116;
 Best Local Similarity 76.3%; Pred. No. 6.5e-41;
 Matches 90; Conservative 9; Mismatches 17; Indels 2; Gaps 2;

OY 1 QVQLVSGGAVVQPGSRSLRLSCAASGFTPSYTMHWROAPGKLEWVTFISYGSNKHY 60
 DB 1 EVQLVSGGAVVQPGSRSLRLSCAASGFTFSSYAMTWROAPGKLEWVAIIKZBSZBY 60
 OY 61 ADVKGRFTVSRDINSKNTLYLQNMNLSRAEDTAIYYCARTGWLGPDPYWGQGLVTYVS 118
 DB 61 VDSYKGRFTISRDNKNTLYLQNMNLSRAEDTAIYYCAR-GH-GGSDYWGQGLVTYVS 116

RESULT 7

ID HV3J HUMAN STANDARD; PRT; 114 AA.
 AC P01763;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Ig heavy chain V-II region WEA.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

NCBI_Taxid=9606;
 RN [1]

RP SEQUENCE.
RX MEDLINE=83273707; PubMed=6410398;
RA Goni F., Frangione B.,
RT "Amino acid sequence of the Fv region of a human monoclonal IGM
RT (protein WEA) with antibody activity against 3,4-pyruvylated
RT galactose in Klebsiella polysaccharides K30 and K33.",
RL Proc. Natl. Acad. Sci. U.S.A. 80:4837-4841(1983).
CC -1- MISCELLANEOUS: THIS CHAIN WAS OBTAINED FROM A MONOCLONAL ANTIBODY
CC AGAINST 3,4-PYRUVYLATED GALACTOSE AND ISOLATED FROM A PATIENT WITH
CC WALDENSTROM'S MACROGLOBULINEMIA.
CC PIR; A02046; MAHWE.
DR HSSP; P01772; 2FB4.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IgV; 1.
KW Immunoglobulin V region.
FT MOD RES 1 1
FT NON TER 114 114
SQ SEQUENCE 114 AA; 12256 MW; D88294FB418A07B7 CRC64;

Query Match 72.4%; Score 458; DB 1; Length 114;
Best Local Similarity 75.4%; Pred. No. 3.3e-40;
Matches 89; Conservative 15; Mismatches 10; Indels 4; Gaps 2;

QY 1 QVQLVESGGGVQPGKSLRLSCAASGFTSSITMHWVROAPGKLEWTFISTGSKHY 60
DB 1 QVQLVDSGGGLVPGGSLRLSCAASGFTSSANDMHWROAPGKLEWTFISTGSGSTIYY 60
QY 61 ADSVKGRFTVSRDINSKNTLYIQNMSLRADDTAIYYCARFGWLPFDYWGGLTVTVSS 118
DB 61 ADSVKGRFTISRHSKNSLYIQNMSLRADDTAVYCAR-GWL--LNMGGTLTVTVSS 114

RESULT 8
HVL6 MOUSE STANDARD; PRT; 136 AA.
AC P01783;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V region MOPC 21 precursor (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_Taxid=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=81234548; PubMed=6788376;
RA Botwell A.L.M., Faskind M., Reih M., Imanishi-Kari T., Rajewsky K.,
RA Baltimore D.;
RT "Heavy chain variable region contribution to the NPb family of
RT antibodies: somatic mutation evident in a gamma 2a variable region.";
RT Cell 24:625-637(1981).
RN [2]
RP SEQUENCE OF 17-136.
RX MEDLINE=77100368; PubMed=401950;
RA Adetungbo K., Milstein C., Secher D.S.;
RT "Molecular analysis of spontaneous somatic mutants";
RT Nature 265:299-304(1977).
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DR EMBL; J00522; AAD15290.1; -
DR PIR; A02066; GIMS21.
DR HSSP; P01772; 2FB4.
DR InterPro; IPR003006; Ig_MHC.

DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IgV; 1.
KW Immunoglobulin V region; Signal.
FT CHAIN 1 1
FT NON TER 1 1
FT SIGNAL <1 16
FT DOMAIN 17 136
FT DOMAIN 115 119
FT DOMAIN 120 136
FT DISULFID 38 112
FT CONFLICT 75 78
FT CONFLICT 89 90
FT CONFLICT 115 115
FT CONFLICT 120 120
FT NON TER 136 136
SQ SEQUENCE 136 AA; 15071 MW; 2276A98DBDBF016 CRC64;

Query Match 72.4%; Score 458; DB 1; Length 136;
Best Local Similarity 75.0%; Pred. No. 4e-40;
Matches 90; Conservative 10; Mismatches 16; Indels 4; Gaps 2;

QY 2 VQLVESGGGVQPGKSLRLSCAASGFTSSITMHWVROAPGKLEWTFISTGSKHYA 61
DB 18 VQLVESGGGVQPGKSLRLSCAASGFTSSFGMHWVROAPGKLEWVAIISGSSITLHYA 77
QY 62 DSVKGRFTVSRDINSKNTLYIQNMSLRADDTAIYYCARFGWLPFDYWGGLTVTVSS 118
DB 78 DTVKGRFTISRDNPKNTLYIQNMSLRSDDTAVYCARWGNV-PYAMDYWGGLTVTVSS 136

RESULT 9
HVL3 HUMAN STANDARD; PRT; 119 AA.
AC P01773;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V-III region BUR.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_Taxid=9606;
RN [1]
RP SEQUENCE (MYELOMA PROTEIN BUR).
RX MEDLINE=79151016; PubMed=107164;
RA Putnam F.W., Liu Y.-S.V., Low T.L.K.;
RT "Primary structure of a human IgM1 immunoglobulin. IV. Streptococcal
RT IgM1 protease, digestion, Fab and Fc fragments, and the complete
RT amino acid sequence of the alpha 1 heavy chain.";
RT J. Biol. Chem. 254:2865-2874(1979).
RL PIR; A02056; A1HUBR.
DR HSSP; P01772; 2FB4.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IgV; 1.
KW Immunoglobulin V region; Glycoprotein.
FT MOD RES 1 1
FT DISULFID 22 96
FT CARBOHYD 28 28
FT NON TER 119 119
SQ SEQUENCE 119 AA; 12981 MW; 12A709A75344D024 CRC64;

Query Match 71.0%; Score 449.5; DB 1; Length 119;
Best Local Similarity 70.3%; Pred. No. 2.6e-39;
Matches 83; Conservative 13; Mismatches 21; Indels 1; Gaps 1;

QY 1 QVQLVESGGGVQPGKSLRLSCAASGFTSSITMHWVROAPGKLEWTFISTGSKHY 60
DB 1 QVQLVESGGGVQAGTSLRLCTASAFYLSYAMHWVROAPGKLEWVALISGGSSTIYY 60
QY 61 ADSVKGRFTVSRDINSKNTLYIQNMSLRADDTAIYYCAR-TGWLFPDYWGGLTVTVSS 117

Db 61 ADVKGRFTISRBSIKNTLYLZMKLTREDTAVYCAKLIAVAGTRBFGQGLTVTS 118

RESULT 10

HV3U HUMAN STANDARD; PRT; 120 AA.

AC P01782;

DT 21-JUL-1986 (Rel. 01, Created)

DT 21-JUL-1986 (Rel. 01, Last sequence update)

DT 15-JUL-1999 (Rel. 38, Last annotation update)

DE Ig heavy chain V-II region DOB.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

OC NCBI_Taxid=9606;

RN (1)

RX MEDLINE=80020920; PubMed=114208;

RA Steiner L.A., Garcia Pardo A., Margolies M.N.;

RT "Amino acid sequence of the heavy-chain variable region of the crystallizable human myeloma protein Dob.";

RL Biochemistry 18:4068-4080(1979).

RN (2)

RP CRYSTALLIZATION.

RX MEDLINE=80020920; PubMed=114208;

RA Steiner L.A., Lopes A.D.;

RT "The crystallizable human myeloma protein Dob has a hinge-region deletion.";

RL Biochemistry 18:4054-4067(1979).

CC -I- MISCELLANEOUS: THIS GAMMA-1 MYELOMA PROTEIN HAS A DELETION IN THE HINGE REGION. THERE ARE NO LIGHT-HEAVY OR INTER-HEAVY CHAIN DISULFIDE BONDS.

DR PIR; A02065; GIHDB.

DR HSSP; P01772; 2FB4.

DR InterPro; IPR003006; IG_MHC.

DR InterPro; IPR003596; IG_V.

DR Pfam; PF00047; Ig_1.

DR SMART; SM00406; IGV; 1.

DR Immunoglobulin V region.

FW NON TER 120

SQ SEQUENCE 120 AA; 13440 MW; 880DDE307C4B2627 CRC64;

Query Match 68.4%; Score 433; DB 1; Length 120;

Best Local Similarity 70.0%; Pred. No. 1.3e-37;

Matches 84; Conservative 13; Mismatches 21; Indels 2; Gaps 2;

QY 1 QVQLVESGGGVQVPGRSLRLSCAASGFTFSSTYTMHWVQAPEKGLIEWYTFISYDGSNKH 60

DB 1 EVQLVESGGDLVQPKRSIRLSCAASGFNPNHEYNMHWLQPGKGPGEWSTITWNGSVLY 60

QY 61 ADVKGRFTISRBSIKNTLYLQMSLRADTAIYYCAATG-WLGP-FDYWGQGLTVTS 118

DB 61 ADVKGRFTISRBSIKNTLYLQMSLRADTAIYYCAATG-WLGP-FDYWGQGLTVTS 118

61 ADVKGRFTISRBSIKNTLYLQMSLRADTAIYYCAATG-WLGP-FDYWGQGLTVTS 120

RESULT 11

HV3M HUMAN STANDARD; PRT; 119 AA.

ID HV3M HUMAN

AC P01774;

DT 21-JUL-1986 (Rel. 01, Created)

DT 21-JUL-1986 (Rel. 01, Last sequence update)

DT 15-JUL-1999 (Rel. 38, Last annotation update)

DE Ig heavy chain V-III region POM.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

OC NCBI_Taxid=9606;

RN (1)

RX MEDLINE=75046755; PubMed=4139708;

RA Capra J.D., Kehoe J.M.;

RT "Structure of antibodies with shared idiotypic: the complete sequence of the heavy chain variable regions of two immunoglobulin M

RT anti-gamma globulins.";

RL Proc. Natl. Acad. Sci. U.S.A. 71:4032-4036(1974).

CC -I- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM IGM WITH ANTI-GAMMA GLOBULIN ACTIVITY.

DR PIR; A02057; M3HUPM.

DR HSSP; P01772; 2FB4.

DR InterPro; IPR003006; IG_MHC.

DR InterPro; IPR003596; IG_V.

DR Pfam; PF00047; Ig_1.

DR SMART; SM00406; IGV; 1.

FW Immunoglobulin V region.

FT VARIANT 54

FT 54

N -> D (PROBABLY DUE TO DEAMINATION DURING ISOLATION).

FTD=VAR_003966.

FT NON TER 119

SQ SEQUENCE 119 AA; 12953 MW; 2E018AF4DCEB2610 CRC64;

Query Match 68.2%; Score 432; DB 1; Length 119;

Best Local Similarity 69.4%; Pred. No. 1.6e-37;

Matches 84; Conservative 16; Mismatches 13; Indels 8; Gaps 2;

QY 1 QVQLVESGGGVQVPGRSLRLSCAASGFTFSSTYTMHWVQAPEKGLIEWYTFISYDGSNKH 60

DB 1 EVQLVESGGGLVQPGKSLRLSCAASGFTFSASMSVQAPEKGLIEWAMKXENGNDKH 60

QY 61 ADVKGRFTISRBSIKNTLYLQMSLRADTAIYYCAATGWLGP-FDYWGQGLTV 114

DB 61 ADVKGRFTISRBSIKNTLYLQMSLRADTAIYYCAATGWLGP-FDYWGQGLTV 114

61 ADVKGRFTISRBSIKNTLYLQMSLRADTAIYYCAATGWLGP-FDYWGQGLTV 118

QY 115 T 115

DB 119 T 119

RESULT 12

HV3N HUMAN STANDARD; PRT; 119 AA.

ID HV3N HUMAN

AC P01775;

DT 21-JUL-1986 (Rel. 01, Created)

DT 21-JUL-1986 (Rel. 01, Last sequence update)

DT 15-JUL-1999 (Rel. 38, Last annotation update)

DE Ig heavy chain V-III region LAY.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

OC NCBI_Taxid=9606;

RN (1)

RX MEDLINE=75046755; PubMed=4139708;

RA Capra J.D., Kehoe J.M.;

RT "Structure of antibodies with shared idiotypic: the complete sequence of the heavy chain variable regions of two immunoglobulin M anti-gamma globulins.";

RL Proc. Natl. Acad. Sci. U.S.A. 71:4032-4036(1974).

CC -I- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM IGM WITH ANTI-GAMMA GLOBULIN ACTIVITY.

DR PIR; A02058; M3HULY.

DR HSSP; P01772; 2FB4.

DR InterPro; IPR003006; IG_MHC.

DR InterPro; IPR003596; IG_V.

DR Pfam; PF00047; Ig_1.

DR SMART; SM00406; IGV; 1.

FW Immunoglobulin V region.

FT NON TER 119

SQ SEQUENCE 119 AA; 12858 MW; D6338098794DCFE5 CRC64;

Query Match 67.9%; Score 430; DB 1; Length 119;

Best Local Similarity 70.0%; Pred. No. 2.6e-37;

Matches 84; Conservative 14; Mismatches 14; Indels 8; Gaps 2;

QY 2 VQLVESGGGVQVPGRSLRLSCAASGFTFSSTYTMHWVQAPEKGLIEWYTFISYDGSNKH 61

DB 2 VQLVESGGGLVQPGKSLRLSCAASGFTFSASMSVQAPEKGLIEWAMKXENGNDKH 61

```

QY 62 DSVKGRFTVSRDNRKNTLYLQWNSLRADTAIYCCARTGWLGP-----FDYWGCGTLVT 115
DB 62 DSVKGRFTISDNRKNTLYLQWNSLRADTAIYCCARTGWLGP-----FDYWGCGTLVT 115
RESULT 13
HV3C_HUMAN STANDARD; PRT; 117 AA.
ID HV3C_HUMAN
AC P01764;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V-II region VH26 precursor.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP MEDLINE=81101090; PubMed=6450418;
RA "Structure and multiplicity of genes for the human immunoglobulin
RT heavy chain variable region."
RL Proc. Natl. Acad. Sci. U.S.A. 77:6561-6565(1980).
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CC or send an email to license@ebi.ch).
DR EMBL; J00236; AA35316.1;
DR EMBL; M35415; AA35735.1;
DR PIR; A02047; H3H26.
DR HSSP; P01772; 2PB4.
DR Genew; HGNC:5545; IGHV.
DR InterPro; IPR003006; IGH_MHC.
DR InterPro; IPR003596; IGH_V.
DR Pfam; PF00047; IGH_1.
DR SMART; SM00406; IGH_1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 117 IG HEAVY CHAIN V-II REGION VH26.
FT NON TER 117 117
SQ SEQUENCE 117 AA; 12582 MW; E826733F1A3CB0P1 CRC64;
Query Match 67.8%; Score 429; DB 1; Length 117;
Best Local Similarity 81.6%; Pred. No. 3.2e-37;
Matches 80; Conservative 9; Mismatches 9; Indels 0; Gaps 0;
QY 1 QVQLVDSGGGVQPGSRSLRSCAAGFTFSYTHWVRQAPGKLEWTFISYDGSNKHY 60
DB 20 EVQLVESGGGLVQPGGSLRLSCAAGFTFSYTHWVRQAPGKLEWTFISYDGSNKHY 79
QY 61 ADSVKGRFTVSRDNRKNTLYLQWNSLRADTAIYCCARTGWLGP-----FDYWGCGTLVT 98
DB 80 GDSVGRFTISDNRKNTLYLQWNSLRADTAIYCCARTGWLGP-----FDYWGCGTLVT 117
RESULT 14
HV38_MOUSE STANDARD; PRT; 119 AA.
ID HV38_MOUSE
AC P01808;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V region T601.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

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OX NCBI_TaxID=10090;
RN [1]
RP MEDLINE=79223895; PubMed=111245;
RA Rao D.N., Rudikoff S., Krutzsch H., Potter M.;
RT "Structural evidence for independent joining region gene in
RT immunoglobulin heavy chains from anti-galactan myeloma proteins and
RT its potential role in generating diversity in
RT complementarity-determining regions."
RL Proc. Natl. Acad. Sci. U.S.A. 76:2890-2894(1979).
CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGA MYELOMA PROTEIN
CC THAT BINDS GALACTAN.
DR PIR; A02078; AWMST6.
DR HSSP; P01810; 2PB7.
DR InterPro; IPR003006; IGH_MHC.
DR InterPro; IPR003596; IGH_V.
DR Pfam; PF00047; IGH_1.
DR SMART; SM00406; IGH_1.
KW Immunoglobulin V region.
FT NON TER 119 119
SQ SEQUENCE 119 AA; 13169 MW; BC38CC84E6EA00E8 CRC64;
Query Match 67.3%; Score 426; DB 1; Length 119;
Best Local Similarity 66.9%; Pred. No. 6.6e-37;
Matches 79; Conservative 17; Mismatches 22; Indels 0; Gaps 0;
QY 1 QVQLVDSGGGVQPGSRSLRSCAAGFTFSYTHWVRQAPGKLEWTFISYDGSNKHY 60
DB 1 EVQLVESGGGLVQPGGSLRLSCAAGFTFSYTHWVRQAPGKLEWTFISYDGSNKHY 60
QY 61 ADSVKGRFTVSRDNRKNTLYLQWNSLRADTAIYCCARTGWLGP-----FDYWGCGTLVT 118
DB 61 TPELKKRFTISDNRKNTLYLQWNSLRADTAIYCCARTGWLGP-----FDYWGCGTLVT 118
RESULT 15
HV3E_HUMAN STANDARD; PRT; 120 AA.
ID HV3E_HUMAN
AC P01766;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V-II region BRO.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP MEDLINE=77117674; PubMed=65324;
RA Capra J.D., Hopper J.E.;
RT "Comparative studies on monocytic Ig lambda and Ig kappa from an
RT individual patient. III. The complete amino acid sequence of the VH
RT region of the Igm paraprotein."
RL Immunochimistry 13:995-999(1976).
CC -1- MISCELLANEOUS: THIS CHAIN WAS OBTAINED FROM IGM ISOLATED FROM THE
CC SERUM OF A PATIENT WITH MALIGNANT LYMPHOMA OF THE WALDENSTROM
CC TYPE.
DR PIR; A02049; M3HUBW.
DR HSSP; P01772; 2PB4.
DR InterPro; IPR003006; IGH_MHC.
DR InterPro; IPR003596; IGH_V.
DR Pfam; PF00047; IGH_1.
DR SMART; SM00406; IGH_1.
KW Immunoglobulin V region.
FT NON TER 120 120
SQ SEQUENCE 120 AA; 13227 MW; D3F0428F7C2E6410 CRC64;
Query Match 67.2%; Score 425.5; DB 1; Length 120;
Best Local Similarity 70.2%; Pred. No. 7.5e-37;
Matches 85; Conservative 13; Mismatches 14; Indels 9; Gaps 3;
QY 1 QVQLVDSGGGVQPGSRSLRSCAAGFTFSYTHWVRQAPGKLEWTFISYDGSNKHY 60

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Db 1 EVQVBSGGGLVQPGSLRLSCHASGFTSYNNMNRQVTGKGLKEMVSHIGTAG-DQY 59
Qy 61 ADSVGRFTVSRDNRKNTLYLQNNSLRAEDTAIYYCART-----GMLGPF--DYWGOGT 112
Db 60 ADSVGRFTISRNDNRKNTLYLNNNSLRAEDTAIYYCARSPVSLVDGMLYYYGVSVMGOGT 119
Qy 113 L 113
Db 120 L 120

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OM protein - protein search, using sw model

Run on: June 3, 2003, 08:07:54 ; Search time 58.7986 Seconds
(without alignments)
413.506 Million cell updates/sec

Title: US-09-644-668a-19
Perfect score: 633
Sequence: 1 QVAVESGGVQVQPRSLRL.....TQWLGPFDYWGQGLTVTSS 118

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 segs, 206047115 residues
Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

SPTREMBL.21.*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_virus:*
16: sp_bacteriap:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	543.5	85.9	116	4 Q9UL93	Q9UL93 homo sapien
2	540	85.3	113	4 Q8WUK1	Q8WUK1 homo sapien
3	531.5	84.0	113	4 Q9UL90	Q9UL90 homo sapien
4	494	78.0	122	4 Q9UL84	Q9UL84 homo sapien
5	494	78.0	147	4 Q9Y509	Q9Y509 homo sapien
6	488.5	77.2	121	4 Q9UL71	Q9UL71 homo sapien
7	478	75.5	118	4 Q8WU38	Q8WU38 homo sapien
8	475.5	75.4	118	4 Q9UL91	Q9UL91 homo sapien
9	475.5	75.1	597	4 Q96B89	Q96B89 homo sapien
10	471	74.4	471	4 Q8IC77	Q8IC77 homo sapien
11	464	73.3	473	11 Q91Z05	Q91Z05 mus musculu
12	463	73.1	118	4 Q9UL72	Q9UL72 homo sapien
13	458	72.4	112	4 Q9HCC1	Q9HCC1 homo sapien
14	442	69.8	494	4 Q96K68	Q96K68 homo sapien
15	435.5	68.8	119	11 Q920E7	Q920E7 mus musculu
16	435	68.7	487	11 Q99KA4	Q99KA4 mus musculu

17	424.5	67.1	479	11 Q91WP5	Q91WP5 mus musculu
18	420	66.4	95	4 Q9UL86	Q9UL86 homo sapien
19	413.5	65.3	131	4 Q9UL88	Q9UL88 homo sapien
20	406	64.1	469	11 Q8R3V9	Q8R3V9 mus musculu
21	405	64.0	298	11 Q9QYF0	Q9QYF0 mus musculu
22	395	62.4	484	11 Q8VEA0	Q8VEA0 mus musculu
23	392.5	62.0	104	4 Q9UL87	Q9UL87 homo sapien
24	389.5	61.5	480	11 Q91XE1	Q91XE1 mus musculu
25	387.5	61.2	486	11 Q91Z07	Q91Z07 mus musculu
26	387	61.1	124	4 Q9UL92	Q9UL92 homo sapien
27	376	59.4	437	11 Q9R1A4	Q9R1A4 mus musculu
28	371.5	58.7	112	4 Q9UGP3	Q9UGP3 homo sapien
29	359.5	56.8	125	4 Q9UL95	Q9UL95 homo sapien
30	356.5	56.3	119	4 Q9UL94	Q9UL94 homo sapien
31	352	55.6	124	6 Q9N0M4	Q9N0M4 oryctolagus
32	351.5	55.5	484	11 Q9JLA6	Q9JLA6 mus musculu
33	349	55.1	124	6 Q9N0M5	Q9N0M5 oryctolagus
34	346.5	54.7	614	4 Q96GAC	Q96GAC homo sapien
35	345.5	54.6	142	11 Q92AQ1	Q92AQ1 mus musculu
36	343	54.2	241	11 Q921A6	Q921A6 mus musculu
37	342.5	54.1	119	4 Q9UL73	Q9UL73 homo sapien
38	335	52.9	145	11 Q924Q7	Q924Q7 mus musculu
39	334	52.8	159	4 Q96C50	Q96C50 homo sapien
40	332.5	52.5	473	11 Q9DBL4	Q9DBL4 mus musculu
41	331.5	52.4	146	11 Q924Q8	Q924Q8 mus musculu
42	331	52.3	482	11 Q91X92	Q91X92 mus musculu
43	330	52.1	109	11 Q9JL75	Q9JL75 mus musculu
44	329.5	52.1	146	11 Q924R8	Q924R8 mus musculu
45	329.5	52.1	481	11 Q91WT1	Q91WT1 mus musculu

ALIGNMENTS

RESULT 1
Q9UL93 PRELIMINARY; PRT: 116 AA.
AC Q9UL93;
DT 01-MAY-2000 (TRENBLREL. 13, Created)
DT 01-MAY-2000 (TRENBLREL. 13, Last sequence update)
DT 01-DEC-2001 (TRENBLREL. 19, Last annotation update)
DE Myosin-reactive immunoglobulin heavy chain variable region (Fragment).
DE (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxId=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M., Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal fetus";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035021; AAD56257.1; -
DR HSSP; P01772; 2F84.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
FT NON_TER
FT NON_TER
SQ SEQUENCE 116 AA; 12434 MW; 0DA0348154DD06061 CRC64;

Query Match 85.9%; Score 543.5; DB 4; Length 116;
Best Local Similarity 89.7%; Pred. No. 2e-49;
Matches 105; Conservative 3; Mismatches 8; Indels 1; Gaps 1;

QY 2 VOLVESGGVQVQPRSLRLCAASGFTFSSTYTMWVQAPKGIEMVTFISYDSNKHYA 61
DB 1 QVAVESGGVQVQPRSLRLSCAASGFTFSSTYAMWVQAPKGIEMVAVISYDSNKHYYA 60

QY 62 DSVKGRFTVSRDNRKNTLYLQMSLRADTAIYYCARTGWLGPDPYWGQGLTVYSS 118
 DB 61 DSVKGRFTVSRDNRKNTLYLQMSLRADTAIYYCARTGWLGPDPYWGQGLTVYSS 116

RESULT 2
 Q8WUK1 PRELIMINARY; PRT; 613 AA.
 ID Q8WUK1
 AC Q8WUK1
 DT 01-MAR-2002 (Tremblrel. 20, Created)
 DT 01-MAR-2002 (Tremblrel. 20, Last sequence update)
 DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)
 DE Hypothetical 67.3 kDa protein.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 NC NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=TONSIL;
 RA Strauberg R.;
 RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC020240; AAH20240.1; -
 DR InterPro; IPR003599; IG_1
 DR InterPro; IPR003597; IG_C1
 DR InterPro; IPR003006; IG_MHC
 DR InterPro; IPR003596; IG_V
 DR Pfam; PF00047; IG_5
 DR SMART; SM00409; IG_2
 DR SMART; SM00407; IG_C1; 4
 DR SMART; SM00406; IG_V; 1
 DR PROSITE; PS00290; IG_MHC; UNKNOWN_3
 KM Hypothetical protein
 SQ SEQUENCE 613 AA; 67296 MW; 60C7F5950671E315 CRC64;

Query Match 85.3%; Score 540; DB 4; Length 613;
 Best Local Similarity 86.0%; Pred. No. 3.9e-48;
 Matches 104; Conservative 6; Mismatches 7; Indels 4; Gaps 2;

QY 1 QVOLVESGGGVOPGSLRLSCAAGFTSSYTMHWVRQAPGKLEWVTFISYDGSNKHY 60
 DB 20 QVOLVESGGGVOPGSLRLSCAAGFTSSYTMHWVRQAPGKLEWVAVIISYDGSNKHY 79

QY 61 ADVKGRFTVSRDNRKNTLYLQMSLRADTAIYYCARTGWLGPDPYWGQGLTVYSS 117
 DB 80 ADVKGRFTVSRDNRKNTLYLQMSLRADTAIYYCARTGWLGPDPYWGQGLTVYSS 138

QY 118 S 118
 DB 139 S 139

RESULT 3
 Q9UL90 PRELIMINARY; PRT; 113 AA.
 ID Q9UL90
 AC Q9UL90
 DT 01-MAY-2000 (Tremblrel. 13, Created)
 DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
 DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
 DE Myosin-reactive immunoglobulin heavy chain variable region (Fragment).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 NC NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC MEDLINE=98277139; PubMed=9614934;
 RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
 RA Young D.C.;
 RT "Myosin-reactive autoantibodies in rheumatic carditis and normal fetus."
 RL Clin. Immunol. Immunopathol. 87:184-192 (1998).

DR EMBL; AF035024; AAD56260.1; -
 DR HSSP; P01772; 2FB4
 DR InterPro; IPR003006; IG_MHC
 DR InterPro; IPR003596; IG_V
 DR Pfam; PF00047; IG_1
 DR SMART; SM00406; IG_V; 1
 FT NON_TER 1
 FT NON_TER 113
 SQ SEQUENCE 113 AA; 12437 MW; ED57FDD19086D07F CRC64;

Query Match 84.0%; Score 531.5; DB 4; Length 113;
 Best Local Similarity 85.6%; Pred. No. 3.5e-48;
 Matches 101; Conservative 6; Mismatches 6; Indels 5; Gaps 1;

QY 1 QVOLVESGGGVOPGSLRLSCAAGFTSSYTMHWVRQAPGKLEWVTFISYDGSNKHY 60
 DB 1 EVOLVESGGGVOPGSLRLSCAAGFTSSYTMHWVRQAPGKLEWVAVIISYDGSNKHY 60

QY 61 ADVKGRFTVSRDNRKNTLYLQMSLRADTAIYYCARTGWLGPDPYWGQGLTVYSS 118
 DB 61 ADVKGRFTVSRDNRKNTLYLQMSLRADTAIYYCARTGWLGPDPYWGQGLTVYSS 113

RESULT 4
 Q9UL84 PRELIMINARY; PRT; 122 AA.
 ID Q9UL84
 AC Q9UL84
 DT 01-MAY-2000 (Tremblrel. 13, Created)
 DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
 DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
 DE Myosin-reactive immunoglobulin heavy chain variable region (Fragment).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 NC NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC MEDLINE=98277139; PubMed=9614934;
 RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
 RA Young D.C.;
 RT "Myosin-reactive autoantibodies in rheumatic carditis and normal fetus."
 RL Clin. Immunol. Immunopathol. 87:184-192 (1998).

QY 1 QVOLVESGGGVOPGSLRLSCAAGFTSSYTMHWVRQAPGKLEWVTFISYDGSNKHY 60
 DB 1 EVOLVESGGGVOPGSLRLSCAAGFTSSYTMHWVRQAPGKLEWVAVIISYDGSNKHY 60

QY 61 ADVKGRFTVSRDNRKNTLYLQMSLRADTAIYYCARTGWLGPDPYWGQGLTVYSS 116
 DB 61 ADVKGRFTVSRDNRKNTLYLQMSLRADTAIYYCARTGWLGPDPYWGQGLTVYSS 120

QY 117 SS 118
 DB 121 SS 122

RESULT 5
 Q9Y509

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ID 09Y509 PRELIMINARY; PRT; 147 AA.
AC 09Y509;
DT 01-NOV-1999 (TRENBLrel. 12, Created)
DT 01-NOV-1999 (TRENBLrel. 12, Last sequence update)
DT 01-DEC-2001 (TRENBLrel. 19, Last annotation update)
DE Vh3 protein (Fragment).
GN Vh3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euteria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96071149; PubMed=7475288;
RA Cao J., Vascio R.A., Rettig M.B., Hong C.H., Kim A., Lee J.C.,
RA Lichtenstein A.K., Berenson J.R.;
RT "A CD10-positive subset of malignant cells is identified in multiple
RT myeloma using PCR with patient-specific immunoglobulin gene primers."
RL Leukemia 9:1348-1953(1995).
DR EMBL; S80860; AAD14339.1; -
DR HSSP; P01772; 2FB4.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; IG_1.
DR SMART; SM00406; IGv; 1.
FT NON_TER 1
SQ SEQUENCE 147 AA; 15768 MW; 8489FCMAA7BC925C CRC64;

Query Match
Best Local Similarity 78.0%; Score 494; DB 4; Length 147;
Matches 94; Conservative 9; Mismatches 15; Indels 8; Gaps 1;

QY 1 QVAVESGGGVVQPGSRSLRLSCAAGFTFSSTYTMHWROAPKGLWYTFISYDGSNKH 60
DB 1 QVAVESGGGVVQPGSRSLRLSCAAGFTFSSTYTMHWROAPKGLWYTFISYDGSNKH 60
QY 61 ADVYKGRFTVSRDNRKNTLYLQNSLRADPTAIYCAR--WLGPFYWGQGT 112
DB 61 AGSYKGRFTISRDNKNTLYLQNTSLRVEDTAVVYCAKDGNYDSVGYAGIDYWGQGT 120
QY 113 LTVSS 118
DB 121 LTVSS 126

RESULT 6
Q9UL71 PRELIMINARY; PRT; 121 AA.
AC Q9UL71;
DT 01-MAY-2000 (TRENBLrel. 13, Created)
DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TRENBLrel. 19, Last annotation update)
DE Myosin-reactive immunoglobulin heavy chain variable region
DE (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euteria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kallis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus."
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035043; AAD56279.1; -
DR HSSP; P01772; 2FB4.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; IG_1.
DR SMART; SM00406; IGv; 1.
FT NON_TER 1

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FT NON_TER 121
SQ SEQUENCE 121 AA; 13154 MW; 2F045CCFA5D50736 CRC64;

Query Match
Best Local Similarity 77.2%; Score 488.5; DB 4; Length 121;
Matches 94; Conservative 9; Mismatches 15; Indels 3; Gaps 1;

QY 1 QVAVESGGGVVQPGSRSLRLSCAAGFTFSSTYTMHWROAPKGLWYTFISYDGSNKH 60
DB 1 EVQVLESGGGVVQPGSRSLRLSCAAGFTFDGAMHWROAPKGLWYSLISGDGSTRY 60
QY 61 ADVYKGRFTVSRDNRKNTLYLQNSLRADPTAIYCAR--TWLGPPDYWGQGT 117
DB 61 ADVYKGRFTISRDNKNTLYLQNSLRADPTAIYCAKGVTTIYDRFDIWGQGT 120
QY 118 S 118
DB 121 S 121

RESULT 7
Q9UL71 PRELIMINARY; PRT; 573 AA.
AC Q9UL71;
DT 01-MAR-2002 (TRENBLrel. 20, Created)
DT 01-MAR-2002 (TRENBLrel. 20, Last sequence update)
DT 01-JUN-2002 (TRENBLrel. 21, Last annotation update)
DE Hypothetical 63.0 kDa protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euteria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA TISSUE=TONSIL;
RA Strausberg R.;
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC021276; AAH21276.1; -
DR InterPro; IPR003599; IG_1.
DR InterPro; IPR003597; IG_1.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; IG_4.
DR SMART; SM00409; IG; 1.
DR SMART; SM00407; IGCL; 3.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW Hypothetical protein.
SQ SEQUENCE 573 AA; 62967 MW; FD072344033AC530 CRC64;

Query Match
Best Local Similarity 75.5%; Score 478; DB 4; Length 573;
Matches 92; Conservative 14; Mismatches 12; Indels 6; Gaps 2;

QY 1 QVAVESGGGVVQPGSRSLRLSCAAGFTFSSTYTMHWROAPKGLWYTFISYDGSNKH 60
DB 20 EVQVLESGGGVVQPGSRSLRLSCAAGFTFDGAMHWROAPKGLWYSLISGDGSTRY 79
QY 61 ADVYKGRFTVSRDNRKNTLYLQNSLRADPTAIYCAR--WLGPFYWGQGT 114
DB 80 ADVYKGRFTISRDNKNTLYLQNSLRADPTAIYCAKGVTTIYDRFDIWGQGT 139
QY 115 TVSS 118
DB 140 TVSS 143

RESULT 8
Q9UL91 PRELIMINARY; PRT; 118 AA.
AC Q9UL91;
DT 01-MAY-2000 (TRENBLrel. 13, Created)
DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)

```

DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
 DE Myosin-reactive immunoglobulin heavy chain variable region
 OS Homo sapiens (Human)
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98277139; Pubmed=9614934;
 RA Wu X., Liu B., Van der Meewe P.L., Kalis N.N., Berney S.M.,
 RA Young D.C.;
 RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
 RT fetus";
 RL Clin. Immunol. Immunopathol. 87:184-192 (1998).
 DR EMBL; AF035023; AAD56259.1;
 DR HSSP; P01772; 2FBA
 DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR003596; Ig_V.
 DR Pfam; PF00047; Ig_1.
 DR SMART; SM00406; IgV_1.
 FT NON TER 1
 FT 118
 SQ SEQUENCE 118 AA; 12843 MW; D0633949F2AC149D CRC64;

Query Match 75.4%; Score 477; DB 4; Length 118;
 Best Local Similarity 77.8%; Pred. No. 1.9e-42;
 Matches 91; Conservative 12; Mismatches 14; Indels 0; Gaps 0;

QY 1 QVQLVSGGQVQPGKSLRLSCAASGFTFSYTMHWVQAQPGKLEWYTFISYDGSNKH 60
 DB 1 EVQLVSGGGLVQPGKSLRLSCAASGFTFSYTMHWVQAQPGKLEWYTFISYDGSNKH 60
 QY 61 ADSVGRFTVSNDNSKNTLYLQMSLRADTAIYCARGMGLGPFYWGQGLTV 117
 DB 61 ADSVGRFTISRDNAKNSLYLQMSLRADTAIYCARDDSSRAFDIMWGQGLTV 117

RESULT 9

Q96BB9 PRELIMINARY; PRT; 597 AA.

AC Q96BB9;
 DT 01-DEC-2001 (TReMBLrel. 19, Created)
 DT 01-DEC-2001 (TReMBLrel. 19, Last sequence update)
 DT 01-MAR-2002 (TReMBLrel. 20, Last annotation update)
 DE Hypothetical 65.0 kDa protein.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-B CELL;
 RA Strausberg R.;
 RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC015760; AAH15760.1;
 DR InterPro; IPR003006; Ig_MHC.
 DR Pfam; PF00047; Ig_5.
 DR PROSITE; PS00290; IG_MHC; UNKNOWN_3.
 KW Hypothetical protein.
 SQ SEQUENCE 597 AA; 65039 MW; 4FCA3AD8E6CE263D9 CRC64;

Query Match 75.1%; Score 475.5; DB 4; Length 597;
 Best Local Similarity 73.6%; Pred. No. 2.1e-41;
 Matches 92; Conservative 14; Mismatches 12; Indels 7; Gaps 1;

QY 1 QVQLVSGGQVQPGKSLRLSCAASGFTFSYTMHWVQAQPGKLEWYTFISYDGSNKH 60
 DB 20 EVQLVSGGGLVQPGKSLRLSCAASGFTFSYTMHWVQAQPGKLEWYTFISYDGSNKH 60
 QY 61 ADSVGRFTVSNDNSKNTLYLQMSLRADTAIYCAR-----TGMLGPFYWGQGLTV 113
 DB 80 ADSVGRFTISRDNAKNSLYLQMSLRADTAIYCARDPGSGYASGAYTREDYWGQGLTV 139

QY 114 TVVSS 118
 DB 140 TVVSS 144

RESULT 10

Q8TC77 PRELIMINARY; PRT; 471 AA.

AC Q8TC77;
 DT 01-JUN-2002 (TReMBLrel. 21, Created)
 DT 01-JUN-2002 (TReMBLrel. 21, Last sequence update)
 DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)
 DE Hypothetical 51.8 kDa protein.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-SPLEEN;
 RA Strausberg R.;
 RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC024289; AAH24289.1;
 KW Hypothetical protein.
 SQ SEQUENCE 471 AA; 51791 MW; 388F7F4CF588660E CRC64;

Query Match 74.4%; Score 471; DB 4; Length 471;
 Best Local Similarity 74.2%; Pred. No. 4.7e-41;
 Matches 92; Conservative 14; Mismatches 10; Indels 8; Gaps 2;

QY 1 QVQLVSGGQVQPGKSLRLSCAASGFTFSYTMHWVQAQPGKLEWYTFISYDGSNKH 60
 DB 20 EVQLVSGGGLVQPGKSLRLSCAASGFTFSYTMHWVQAQPGKLEWYTFISYDGSNKH 60
 QY 61 ADSVGRFTVSNDNSKNTLYLQMSLRADTAIYCAR-----TGMLGPFYWGQGLTV 114
 DB 80 ADSVGRFTISRDNAKNSLYLQMSLRADTAIYCARDDSSRAFDIMWGQGLTV 137

QY 115 TVSS 118
 DB 138 TVSS 141

RESULT 11

Q91Z05 PRELIMINARY; PRT; 473 AA.

AC Q91Z05;
 DT 01-DEC-2001 (TReMBLrel. 19, Created)
 DT 01-DEC-2001 (TReMBLrel. 19, Last sequence update)
 DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)
 DE Hypothetical 51.9 kDa protein.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Strausberg R.;
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC010327; AAH10327.1;
 DR MGI; MGI:2144967; A0044919.
 DR InterPro; IPR000345; CytC_heme_bind.
 DR InterPro; IPR003006; Ig_MHC.
 DR Pfam; PF00047; Ig_3.
 DR PROSITE; PS00190; CYTOCHROME C; UNKNOWN_1.
 DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
 KW Hypothetical protein.
 SQ SEQUENCE 473 AA; 51946 MW; CF625F008932AF12 CRC64;

Query Match 73.3%; Score 464; DB 11; Length 473;
 Best Local Similarity 72.0%; Pred. No. 2.6e-40;

Matches 85; Conservative 15; Mismatches 18; Indels 0; Gaps 0;

QY 1 QVQLVESGGGVVQPGSRSLRLSCAASGFTFSSTYTMHWYRQAPGKLEWTFISYDGSNKH 60
 DB 20 EVQLVESGGGVVQPGSRSLRLSCAASGFTFSSTYTMHWYRQAPGKLEWTFISYDGSNKH 79

QY 61 ADVYKGRFTVSRDNRKNTLYLQNNSLRAEDTAIYCAATGWLGPDPYWGQGLTVVSS 118
 DB 80 ADVYKGRFTVSRDNRKNTLYLQNNSLRAEDTAIYCAATGWLGPDPYWGQGLTVVSS 137

RESULT 12

Q9UL72 PRELIMINARY; PRT; 118 AA.

AC Q9UL72
 DT 01-MAY-2000 (TREMblrel. 13, Created)
 DT 01-MAY-2000 (TREMblrel. 13, Last sequence update)
 DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)
 DE Myosin-reactive immunoglobulin heavy chain variable region (Fragment).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=9827139; PubMed=9614934;
 RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Betney S.M.,
 RA Young D.C.;
 RT "Myosin-reactive autoantibodies in rheumatic carditis and normal fetus."
 RL Clin. Immunol. Immunopathol. 87:184-192(1998).
 DR EMBL; AF035042; AAD56278.1;
 DR HSSP; P01772; 2F84.
 DR InterPro; IPR03006; IG_MHC.
 DR InterPro; IPR03596; IG_v.
 DR Pfam; PF00047; IG_1.
 DR SMART; SM00406; IGV; 1.
 DR NON_TER 1
 FT NON_TER 118
 SQ SEQUENCE 118 AA; 12872 MW; B4D1A5944B2D5CCA CRC64;

Query Match 73.1%; Score 463; DB 4; Length 118;
 Best Local Similarity 78.3%; Pred. No. 5.6e-41;
 Matches 94; Conservative 10; Mismatches 12; Indels 4; Gaps 3;

QY 1 QVQLVESGGGVVQPGSRSLRLSCAASGFTFSSTYTMHWYRQAPGKLEWTFISYDGSNKH 60
 DB 1 EVQLVESGGGVVQPGSRSLRLSCAASGFTFSSTYTMHWYRQAPGKLEWTFISYDGSNKH 59

QY 61 ADVYKGRFTVSRDNRKNTLYLQNNSLRAEDTAIYCAATGWLGPDPYWGQGLTVVSS 118
 DB 60 ADVYKGRFTVSRDNRKNTLYLQNNSLRAEDTAIYCAATGWLGPDPYWGQGLTVVSS 118

RESULT 13

Q9HCCI PRELIMINARY; PRT; 112 AA.

AC Q9HCCI
 DT 01-MAR-2001 (TREMblrel. 16, Created)
 DT 01-MAR-2001 (TREMblrel. 16, Last sequence update)
 DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)
 DE Single chain Fv (Fragment).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Kikuchi M., Takeda C., Tsujimoto Y., Asada S., Nagata K.;
 RT "An antibody fragment2A3 specific for native lyszyme : isolation from a human synthetic phage display library and characterization.";
 RT Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.

DR EMBL; AB049915; BAB16829.1;
 DR HSSP; P01772; 2F84.
 DR InterPro; IPR03599; IG.
 DR InterPro; IPR03600; IG_1like.
 DR InterPro; IPR03006; IG_MHC.
 DR InterPro; IPR03596; IG_v.
 DR Pfam; PF00047; IG_1.
 DR SMART; SM00409; IG; 1.
 DR SMART; SM00406; IGV; 1.
 DR SMART; SM00410; IG_1like; 1.
 DR NON_TER 1
 FT NON_TER 112
 SQ SEQUENCE 112 AA; 12243 MW; 24F1A45EC3B84768 CRC64;

Query Match 72.4%; Score 458; DB 4; Length 112;
 Best Local Similarity 75.4%; Pred. No. 1.8e-40;
 Matches 86; Conservative 13; Mismatches 13; Indels 2; Gaps 1;

QY 1 QVQLVESGGGVVQPGSRSLRLSCAASGFTFSSTYTMHWYRQAPGKLEWTFISYDGSNKH 60
 DB 1 EVQLVESGGGVVQPGSRSLRLSCAASGFTFSSTYTMHWYRQAPGKLEWTFISYDGSNKH 60

QY 61 ADVYKGRFTVSRDNRKNTLYLQNNSLRAEDTAIYCAATGWLGPDPYWGQGLTV 114
 DB 61 ADVYKGRFTVSRDNRKNTLYLQNNSLRAEDTAIYCAATGWLGPDPYWGQGLTV 112

RESULT 14

Q96K68 PRELIMINARY; PRT; 494 AA.

AC Q96K68
 DT 01-DEC-2001 (TREMblrel. 19, Created)
 DT 01-DEC-2001 (TREMblrel. 19, Last sequence update)
 DT 01-JUN-2002 (TREMblrel. 21, Last annotation update)
 DE CDNA FLJ14473 fis, clone MAMMA1001080, highly similar to Homo
 DE sapiens SMC73 protein (SMC73) mRNA.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=MAMMARY GLAND;
 RA Isogai T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,
 RA Nishitawa T., Nagai K., Sugano S., Shiratori A., Sudo H.,
 RA Magatsuma M., Hosoi T., Kaku Y., Kodaira H., Kondo H., Sugawara M.,
 RA Takahashi M., Chiba Y., Ichida S., Murakawa K., Ono Y., Takiguchi S.,
 RA Watanabe S., Kimura K., Murakami K., Ishii S., Kawai Y., Saito K.,
 RA Yamamoto J., Wakamatsu A., Nakamura Y., Nagahara K., Masuno Y.,
 RA Ninomiya K., Iwayanagi T.;
 RT "NEDO human cDNA sequencing project.";
 RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AK027379; BAB55072.1;
 DR InterPro; IPR03006; IG_MHC.
 DR Pfam; PF00047; IG; 4.
 DR PROSITE; PS00290; IG_MHC; UNKOWN_1.
 SQ SEQUENCE 494 AA; 53088 MW; 9A1D7A85A8E4C0E CRC64;

Query Match 69.8%; Score 442; DB 4; Length 494;
 Best Local Similarity 70.5%; Pred. No. 5.5e-38;
 Matches 86; Conservative 13; Mismatches 19; Indels 4; Gaps 1;

QY 1 QVQLVESGGGVVQPGSRSLRLSCAASGFTFSSTYTMHWYRQAPGKLEWTFISYDGSNKH 60
 DB 20 EVQLVESGGGVVQPGSRSLRLSCAASGFTFSSTYTMHWYRQAPGKLEWTFISYDGSNKH 79

QY 61 ADVYKGRFTVSRDNRKNTLYLQNNSLRAEDTAIYCAATGWLGPDPY---WGQGLTV 116
 DB 80 RDSYKGRFTVSRDNRKNTLYLQNNSLRAEDTAIYCAATGWLGPDPY---WGQGLTV 139

QY 117 SS 118
 DB 140 SS 141

```

RESULT 15
Q920E7 PRELIMINARY; PRT; 119 AA.
ID Q920E7
AC Q920E7;
DT 01-DEC-2001 (TREMblrel. 19, Created)
DT 01-DEC-2001 (TREMblrel. 19, Last sequence update)
DT 01-MAR-2002 (TREMblrel. 20, Last annotation update)
DE Pterin-mimicking anti-idiotope heavy chain variable region
DS (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Atkin J.D., Iape A., Jennings I.G., Horvath O., Cotton R.G.H.;
RT "Definition of the idiotope of Pterin-Mimicking Antibodies Expressed
in Mammalian Cells."
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF307937; AAL09421.1;
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; Ig; 1.
FT NON_TER 1
FT NON_TER 1
SQ SEQUENCE 119 AA; 13025 MW; F6E90404381CA7C CRC64;

Query Match 68.8%; Score 435.5; DB 11; Length 119;
Best Local Similarity 72.3%; Pred. No. 4,3e-38;
Matches 86; Conservative 13; Mismatches 19; Indels 1; Gaps 1;

QY 1 QVQLVESGGGVQPGKSLRLSCAASGFTFSYTMHWROAPGKGLWYTFISYDGSNKH 60
   :|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 1 EVQLVESGGDLVKPGGSLKLSCAASGFTFSYGMWVROTPDKRLWVATISSGGSYY 60
   :|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:

QY 61 ADSVKGRTVSRRNSKNTLYLQMSLRADTAIYYCARTG-WLSPFDYWGQCTLYTVSS 118
   :|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 61 PDSVKGRTFTSRDKNKNTLYLQMSLSKSEDTAMYYCARHGDYDVGFAFYWGQCTLYTVSA 119
   :|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:

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Search completed: June 3, 2003, 08:20:47
 Job time : 58.7986 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 3, 2003, 08:02:14 ; Search time 53.1604 Seconds
(without alignments)
295.776 Million cell updates/sec

Title: US-09-644-668A-19

Sequence: 1 QVQLVSGGAVGVPGRSLRL.....TGMILPDPYMGQGLTVTVSS 118

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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2: /SID2/gcgdata/geneseq/geneseq-emb1/AA1981.DAT.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	633	100.0	118	22	AA867509
2	633	100.0	118	22	AA867514
3	623	98.4	118	22	AA867508
4	623	98.4	118	22	AA867513
5	567	89.6	247	23	ABP4913
6	566	89.4	463	21	AA933707
7	566	89.4	463	21	AA933732
8	559.5	88.4	225	22	AA893359
9	559.5	88.4	225	22	AA893360
10	559.5	88.4	225	22	AA875002

11	559.5	88.4	225	22	AA875013
12	559	88.3	252	23	ABP45508
13	558.5	88.2	225	22	AA893388
14	558.5	88.2	225	22	AA875021
15	557	88.0	254	23	ABP44972
16	557	88.0	463	21	AA933701
17	557	88.0	463	21	AA933727
18	557	88.0	463	21	AA933728
19	555.5	87.8	120	15	AA852064
20	554.5	87.6	119	22	AAU02515
21	554	87.5	252	23	ABP45190
22	553.5	87.4	225	22	AA893387
23	553.5	87.4	225	22	AA875020
24	552.5	87.3	519	23	AAU81993
25	551.5	87.1	225	22	AA893367
26	551.5	87.1	225	22	AA893389
27	551.5	87.1	225	22	AA875000
28	551.5	87.1	225	22	AA875022
29	551	87.0	118	23	ABP07230
30	551	87.0	254	21	AA956287
31	551	87.0	490	21	AA956287
32	549.5	86.8	225	22	AA893385
33	549.5	86.8	225	22	AA875018
34	548.5	86.7	115	21	AA895519
35	547	86.4	252	23	ABP45616
36	546.5	86.3	119	17	AA895216
37	546	86.3	118	23	ABG30463
38	546	86.3	249	23	ABP45098
39	545.5	86.2	225	22	AA893381
40	545.5	86.2	225	22	AA875014
41	545.5	86.0	119	22	AA867516
42	543.5	85.9	248	23	ABP45410
43	543	85.8	122	22	AA872883
44	542	85.6	223	20	AA908598
45	541	85.5	118	23	AA851167

ALIGNMENTS

RESULT 1	AA867509	standard; peptide; 118 AA.
ID	AA867509	
AC	AA867509	
XX	29-MAY-2001	(first entry)
XX		
DE	Light chain variable region of anti-CTLA-4 antibody 4B6.	
XX		
KW	Complementarily determining region; CDR; immune response; antibody;	
KW	cytotoxic T lymphocyte associated antigen-4; CTLA-4; B7 ligand; cancer;	
KW	autoimmune disease; infectious disease; inflammation; allergy;	
KW	rheumatoid arthritis; myasthenia gravis; lupus erythematosus;	
KW	multiple sclerosis; insulin-dependent diabetes mellitus; inflammation;	
KW	transplant rejection; graft versus host disease.	
XX		
OS	Homo sapiens	
XX		
XX	Key	Location/Qualifiers
FT	Region	31..35
FT	/note= "CDR1"	
FT	Region	50..66
FT	/note= "CDR2"	
FT	Region	99..107
FT	/note= "CDR3"	
XX		
XX	MO200114424-A2.	
XX	01-MAR-2001.	
XX	24-AUG-2000; 2000MO-US23356.	

Anti-IL8 monoclonal
Human BlyS binding
Human interleukin
Anti-IL8 monoclonal
Human BlyS binding
The heavy chain of
The heavy chain of
The heavy chain of
Heavy chain variab
Anti-adipocyte mon
Human BlyS binding
Human interleukin
Anti-IL8 monoclonal
Human secreted pro
Human interleukin
Human interleukin
Anti-IL8 monoclonal
Anti-IL8 monoclonal
Anti-IL-4 receptor
hCAT clone 25 ant
Anti-IL8 monoclonal
Anti-IL8 monoclonal
Human BlyS binding
Human foetal immun
Human anti-CD40 mo
Human BlyS binding
Human interleukin
Anti-IL8 monoclonal
Anti-IL8 monoclonal
Heavy chain variab
Human BlyS binding
Human anti-HER2/ne
Anti-human TNF- α
Human DE-46 heavy

PR	24-AUG-1999;	99US-0150452.
XX		
PA	(MEDA-) MEDAREX INC.	
PI	Korman AJ, Halk EL, Lonberg N,	
XX		
DR	WPI: 2001-202933/20.	
XX		
PT	Novel human sequence antibody that binds to human cytotoxic T	
PT	lymphocyte associated antigen-4, useful for inducing, augmenting or	
PT	prolonging immune response to antigen or for suppressing immune	
XX	response in patient	
PS	Claim 26; Fig 7; 127pb; English.	
XX		
CC	The present sequence represents the light chain variable region of	
CC	human antibody 486. This antibody specifically binds to human	
CC	cytotoxic T lymphocyte associated antigen-4 (CTLA-4). Such antibodies	
CC	are used in methods for inducing, augmenting or prolonging an immune	
CC	response to an antigen in a patient, where the antibodies block	
CC	binding of human CTLA-4 to human B7 ligands. The antibodies are	
CC	also useful for treating autoimmune disease in a subject caused or	
CC	exacerbated by increased activity of T cells and for treating prostate	
CC	cancer, melanoma or epithelial cancer. A polyvalent or polyclonal	
CC	antibody preparation comprising two antibodies of the invention are	
CC	useful for suppressing a immune response in a patient. They are used for	
CC	treating cancer, infectious diseases and promoting beneficial autoimmune	
CC	reactions for the treatment of diseases with inflammatory or allergic	
CC	components. The polyvalent or polyclonal preparations are useful for	
CC	treating autoimmune diseases such as rheumatoid arthritis, myasthenia	
CC	gravis and lupus erythematosus, multiple sclerosis, insulin-dependent	
CC	diabetes mellitus, transplant rejection, and inflammation, graft versus	
CC	host disease.	
XX		
SO	Sequence 118 AA;	
XX		
QY	Query Match 100.0%; Score 633; DB 22; Length 118;	
Db	Best Local Similarity 100.0%; Pred. No. 6.3e-49;	
	Matches 118; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
QY	1 QVQLVESGGGVQPGKSLRLSCAASGFTFSYTHMWVQAPGKGLWYPTISYSGSNCHY 60	
Db	1 QVQLVESGGGVQPGKSLRLSCAASGFTFSYTHMWVQAPGKGLWYPTISYSGSNCHY 60	
QY	61 ADSVKGRTVSRRNSKNTLYIQMNSLRAEDTAIYYCATGMIGPFDPYGGGTLVTSS 118	
Db	61 ADSVKGRTVSRRNSKNTLYIQMNSLRAEDTAIYYCATGMIGPFDPYGGGTLVTSS 118	
RESULT 2		
AAAB67514		
ID	AAAB67514 standard; peptide; 118 AA.	
XX		
AC	AAAB67514;	
XX		
DT	29-MAY-2001 (first entry)	
XX		
DE	Heavy chain variable region of anti-CTLA-4 antibody 10D1.	
XX		
XX	Complementarity determining region; CDR; immune response; antibody;	
KW	cytotoxic T lymphocyte associated antigen-4; CTLA-4; B7 ligand; cancer;	
KW	autoimmune disease; infectious disease; inflammation; allergy;	
KW	rheumatoid arthritis; myasthenia gravis; lupus erythematosus;	
KW	multiple sclerosis; insulin-dependent diabetes mellitus; inflammation;	
KW	transplant rejection; graft versus host disease.	
XX		
OS	Homo sapiens.	
FT	Key	
FT	Region	
FT	Location/Qualifiers	
FT	31..35	
FT	/note= "CDR1"	
FT	50..66	
FT	/note= "CDR2"	

FT	Region	99.107
FT		/note="CDR3"
XX	WO200114424-A2.	
XX	01-MAR-2001.	
XX	24-AUG-2000; 2000WO-US23356.	
XX	24-AUG-1999; 99US-0150452.	
XX	(MEDA-) MEDAREX INC.	
XX	Korman AJ, Halk EL, Lonberg N;	
XX	WPI; 2001-202933/20.	
XX	Novel human sequence antibody that binds to human cytotoxic T	
XX	lymphocyte associated antigen-4, useful for inducing, augmenting or	
XX	prolonging immune response to antigen or for suppressing immune	
XX	response in patient	
XX	Claim 26; Fig 8; 127p; English.	
XX	The present sequence represents the heavy chain variable region of	
XX	human antibody 10D1. This antibody specifically binds to human	
XX	cytotoxic T lymphocyte associated antigen-4 (CTLA-4). Such antibodies	
XX	are used in methods for inducing, augmenting or prolonging an immune	
XX	response to an antigen in a patient, where the antibodies block	
XX	binding of human CTLA-4 to human B7 ligands. The antibodies are	
XX	also useful for treating autoimmune disease in a subject caused or	
XX	exacerbated by increased activity of T cells and for treating prostate	
XX	cancer, melanoma or epithelial cancer. A polyvalent or polyclonal	
XX	antibody preparation comprising two antibodies of the invention are	
XX	useful for suppressing an immune response in a patient. They are used for	
XX	treating cancer, infectious diseases and promoting beneficial autoimmune	
XX	reactions for the treatment of diseases with inflammatory or allergic	
XX	components. The polyvalent or polyclonal preparations are useful for	
XX	treating autoimmune diseases such as rheumatoid arthritis, myasthenia	
XX	gravis and lupus erythematosus, multiple sclerosis, insulin-dependent	
XX	diabetes mellitus, transplant rejection, and inflammation, graft versus	
XX	host disease.	
XX	Sequence 118 AA;	
XX	Query Match 100.0%; Score 633; DB 22; Length 118;	
XX	Best Local Similarity 100.0%; Pred. NO. 6.3e-48;	
XX	Matches 118; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
QY	1 QVQLVESGSGGVWPGQSRSLRLSCAASGTFSSYTHAWVRQAPGKGLEWTFISYDGSNGY 60	
DB	1 QVQLVESGGGVWPGQGRSLRLSCAASGTFSSYTHAWVRQAPGKGLEWTFISYDGSNGY 60	
QY	61 ADSVKGRFTYSRDNSKNTLYLQWNSLAEDTAIYYCARTGMLGPDWVGQGLTVTSS 118	
DB	61 ADSVKGRFTYSRDNSKNTLYLQWNSLAEDTAIYYCARTGMLGPDWVGQGLTVTSS 118	
RESULT 3		
AAAB67508	standard; peptide; 118 AA.	
AAAB67508;		
DT	29-MAY-2001 (first entry)	
DE	Light chain variable region of anti-CTLA-4 antibody 10D1.	
XX	Complementarity determining region; CDR; immune response; antibody;	
XX	cytotoxic T lymphocyte associated antigen-4; CTLA-4; B7 ligand; cancer;	
XX	autoimmune disease; infectious disease; inflammation; allergy;	
XX	rheumatoid arthritis; myasthenia gravis; lupus erythematosus;	
XX	multiple sclerosis; insulin-dependent diabetes mellitus; inflammation;	

transplant rejection; graft versus host disease.

Homo sapiens.

Key Location/Qualifiers

Region 31..35
/note= "CDR1"

Region 50..66
/note= "CDR2"

Region 99..107
/note= "CDR3"

MO200114424-A2.

01-MAR-2001.

24-AUG-2000; 2000WO-US23356.

24-AUG-1999; 99US-0150452.

(MEDA-) MEDAREX INC.

Korman AJ, Halk EL, Lonberg N;

WPI; 2001-202933/20.

Novel human sequence antibody that binds to human cytotoxic T lymphocyte associated antigen-4, useful for inducing, augmenting or prolonging immune response to antigen or for suppressing immune response in patient

Claim 25; Fig 7; 127pp; English.

The present sequence represents the light chain variable region of human antibody 10D1. This antibody specifically binds to human cytotoxic T lymphocyte associated antigen-4 (CTLA-4). Such antibodies are used in methods for inducing, augmenting or prolonging an immune response to an antigen in a patient, where the antibodies block binding of human CTLA-4 to human B7 ligands. The antibodies are also useful for treating autoimmune disease in a subject caused or exacerbated by increased activity of T cells and for treating prostate cancer, melanoma or epithelial cancer. A polyvalent or polyclonal antibody preparation comprising two antibodies of the invention are useful for suppressing a immune response in a patient. They are used for treating cancer, infectious diseases and promoting beneficial autoimmune components. The polyvalent or polyclonal preparations are useful for treating autoimmune diseases such as rheumatoid arthritis, myasthenia gravis and lupus erythematosus, multiple sclerosis, insulin-dependent diabetes mellitus, transplant rejection, and inflammation, graft versus host disease.

Sequence 118 AA;

Query Match 98.4%; Score 623; DB 22; Length 118;
Best Local Similarity 97.5%; Pred. No. 4.7e-47;
Matches 115; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

1 QVQLVESGGGVVQGRSLRLSCAASGFTFSYTMHWYROAPGKGLEWYFISYDGNKHY 60
1 QVQLVESGGGVVQGRSLRLSCAASGFTFSYTMHWYROAPGKGLEWYFISYDGNKHY 60

61 ADVKGRFTVSRDNSKQTLVQLQNSLRRAEDTAIYYCARTGMGLGPDYWGQGLTVTVSS 118
61 ADVKGRFTVSRDNSKQTLVQLQNSLRRAEDTAIYYCARTGMGLGPDYWGQGLTVTVSS 118

RESULT 4
AAB67513 standard; peptide; 118 AA.

AAB67513;
AC AAB67513;
XX

29-MAY-2001 (first entry)

Heavy chain variable region of anti-CTLA-4 antibody 10D1.

Complementarity determining region; CDR; immune response; antibody; cytotoxic T lymphocyte associated antigen-4; CTLA-4; B7 ligand; cancer; autoimmune disease; infectious disease; inflammation; allergy; rheumatoid arthritis; myasthenia gravis; lupus erythematosus; multiple sclerosis; insulin-dependent diabetes mellitus; inflammation; transplant rejection; graft versus host disease.

Homo sapiens.

Key Location/Qualifiers

Region 31..35
/note= "CDR1"

Region 50..66
/note= "CDR2"

Region 99..107
/note= "CDR3"

MO200114424-A2.

01-MAR-2001.

24-AUG-2000; 2000WO-US23356.

24-AUG-1999; 99US-0150452.

(MEDA-) MEDAREX INC.

Korman AJ, Halk EL, Lonberg N;

WPI; 2001-202933/20.

Novel human sequence antibody that binds to human cytotoxic T lymphocyte associated antigen-4, useful for inducing, augmenting or prolonging immune response to antigen or for suppressing immune response in patient

Claim 25; Fig 8; 127pp; English.

The present sequence represents the heavy chain variable region of human antibody 10D1. This antibody specifically binds to human cytotoxic T lymphocyte associated antigen-4 (CTLA-4). Such antibodies are used in methods for inducing, augmenting or prolonging an immune response to an antigen in a patient, where the antibodies block binding of human CTLA-4 to human B7 ligands. The antibodies are also useful for treating autoimmune disease in a subject caused or exacerbated by increased activity of T cells and for treating prostate cancer, melanoma or epithelial cancer. A polyvalent or polyclonal antibody preparation comprising two antibodies of the invention are useful for suppressing a immune response in a patient. They are used for treating cancer, infectious diseases and promoting beneficial autoimmune components. The polyvalent or polyclonal preparations are useful for treating autoimmune diseases such as rheumatoid arthritis, myasthenia gravis and lupus erythematosus, multiple sclerosis, insulin-dependent diabetes mellitus, transplant rejection, and inflammation, graft versus host disease.

Sequence 118 AA;

Query Match 98.4%; Score 623; DB 22; Length 118;
Best Local Similarity 97.5%; Pred. No. 4.7e-47;
Matches 115; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

1 QVQLVESGGGVVQGRSLRLSCAASGFTFSYTMHWYROAPGKGLEWYFISYDGNKHY 60
1 QVQLVESGGGVVQGRSLRLSCAASGFTFSYTMHWYROAPGKGLEWYFISYDGNKHY 60

61 ADVKGRFTVSRDNSKQTLVQLQNSLRRAEDTAIYYCARTGMGLGPDYWGQGLTVTVSS 118
61 ADVKGRFTVSRDNSKQTLVQLQNSLRRAEDTAIYYCARTGMGLGPDYWGQGLTVTVSS 118

Db 61ADSVAGRFITSRDMSKNTLYLQNNLSRAEDTALTYCARTQWLGSPFDYWGGLTVYSS 118

RESULT 5
 ID ABP44913
 ABP44913 standard; Protein; 247 AA.
 AC ABP44913;
 XX 19-AUG-2002 (first entry)
 DT 19-AUG-2002 (first entry)
 DE Human Blys binding ecFv SEQ ID 924.
 XX
 KW Blys; B lymphocyte stimulator; TNF superfamily; human; cytostatic;
 KW tumour necrosis factor; B cell proliferation; B cell differentiation;
 KW immunosuppressive; immunostimulant; immunomodulatory; antirheumatic;
 KW antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;
 KW systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;
 KW common variable immunodeficiency; acquired immunodeficiency syndrome.
 XX
 OS Homo sapiens.
 XX
 MO WO200202641-A1.
 XX
 PD 10-JAN-2002.
 XX
 PF 15-JUN-2001; 2001WO-US19110.
 XX
 PR 16-JUN-2000; 2000US-212210P.
 PR 17-OCT-2000; 2000US-240816P.
 PR 16-MAR-2001; 2001US-276248P.
 PR 21-MAR-2001; 2001US-277379P.
 PR 25-MAY-2001; 2001US-293499P.
 XX
 PA (HUMA-) HUMAN GENOME SCI INC.
 PA (CAMP-) CAMBRIDGE ANTIBODY TECHNOLOGY.
 XX
 PI Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;
 XX
 DR WPI; 2002-114799/15.
 XX
 PT Antibodies against B lymphocyte stimulating polypeptides, useful for
 PT the diagnosis and treatment of cancers and immune disorders -
 XX
 XX Claim 1; Page 1504-1505; 3148pp; English.
 XX
 PS This invention describes novel antibodies that immunospecifically bind to
 CC B lymphocyte stimulator (Blys) polypeptides. Blys is a member of the
 CC tumour necrosis factor (TNF) super family and induces B cell
 CC proliferation and differentiation. The antibodies of the invention have
 CC cytostatic, immunosuppressive, immunostimulant, immunomodulatory,
 CC antirheumatic and antiAIDS activity and can be used in vaccines to
 CC inhibit the expression and activity of Blys. The antibodies bind to Blys
 CC and so may be used to detect and quantitate the presence of Blys in
 CC biological samples and may be used in this way to diagnose disease
 CC associated with aberrant expression of Blys. They may also be
 CC administered to treat diseases associated with aberrant Blys expression
 CC and activity such as cancer, immune, and autoimmune disorders and
 CC diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,
 CC immunodeficiency (e.g. common variable immunodeficiency (CVID) and
 CC acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent
 CC the invention.
 XX

SQ Sequence 247 AA;
 XX

Query Match 89.6%; Score 567; DB 23; Length 247;
 Best Local Similarity 87.9%; Pred. No. 7.6e-42;
 Matches 109; Conservative 4; Mismatches 5; Indels 6; Gaps 1;

1 QVQLVSGGCVGQPGKSLRLSCAASGPFSSYTWMHWAOADPGKLEMTFTSYGSSNRY 60
 1 QVQLVSGGCVGQPGKSLRLSCAASGPFSSYTWMHWAOADPGKLEMTFTSYGSSNRY 60

Qy		61	ADSVKGRFLVSSDNGNTLYLQNNSLRADFTAIYCAR-----TGMAGPPDYWGCTIV	118
Db		61	ADSVKGRFLTISDNSKNTLYLQNNSLRADFTAIYCARPSYDLIGLYLPDYWGCTIV	120
Qy		115	TWSS 118 121 TWSS 124	
Db				
		RESULT 6		
ID	AAY93707	standard; Protein; 463 AA.		
XX	AAY93707;			
AC				
XX				
DT	03-OCT-2000	(first entry)		
XX				
DE	The heavy chain of immunoglobulin clone 6.1.1.			
XX				
KM	Cytotoxic T-lymphocyte antigen-4; CTLA-4; antibody; immune system;			
KW	hyperimmunity disorder; autoimmune disease; diabetes; graft rejection;			
KX	proliferative disorder; cancer; immunodeficient disorder.			
OS	Homo sapiens.			
PN	WO200037504-A2.			
PD	29-JUN-2000.			
PF	23-DEC-1999; 99WO-US30895.			
PR	23-DEC-1998; 98US-0113647.			
PA	(PFIZ) PFIZER INC.			
PA	(ABGE-) ABERNIX INC.			
PI	Hanson DC, Neveu MD, Mueller EE, Hanke JH, Gilman SC, Davis CG;			
PI	Corvalan JR;			
DR	WPI; 2000-442647/38.			
N-PDB:	AAA46870.			
PT	Novel antibodies capable of binding cytotoxic T-lymphocyte antigen			
PT	(CTLA)-4 containing specified heavy and light chain sequences, useful			
PT	for treating, e.g. immune disorders -			
ES	Claim 2; Fig 1D; 157P; English.			
XX				
XX	The present sequence represents a heavy chain of an antibody of the			
CC	invention. The antibody is directed cytotoxic T-lymphocyte antigen			
CC	(CTLA)-4. Antibodies of the invention are composed of a heavy chain			
CC	variable region, comprising a modified contiguous sequence from a			
CC	FRI-FR3 sequence encoded by a human VH3-33 family gene. The			
CC	modifications may be used to inhibit CTLA-4 and/or framework regions.			
CC	The antibodies may be used to treat hyperimmunity disorders (e.g. autoimmune			
CC	disease, diabetes and graft rejection) and proliferative disorders			
CC	(e.g. cancer). CTLA-4 stimulatory agents may be used to up-regulate			
CC	immune system to up-regulate immunodeficient disorders.			
XX				
SQ	Sequence 463 AA;			
Query Match	89.4%; Score 566; DB 21; Length 463;			
Best Local Similarity	89.8%; Pred. No. 1.8e-41;			
Matches 106; Conservative	3; Mismatches 9; Indels 0; Gaps 0;			
Qy		1	QVLVESGGGVVDPGSRISRISCASGFTFSSTTHMWVRQAPKGKLEMTFISYDGSKHY	60
Db		20	QVLVESGGGVVERGSRISRISCASGFTFSSTGYGHMWRQAPKGKLEWVAIWMYGSKNH	79
Qy		61	ADSVKGRFLVSSDNGNTLYLQNNSLRADFTAIYCARTGMLAPPDYWGCTIVTSS	118

DB 80 ADSAKGRFTISRDNKNTLYLQWNSLRADPTAVVYCARAGLLGPDYWGQGLTVTVSS 137

RESULT 7
ID AAY93732
XX AAY93732 standard; Protein; 463 AA.
AC AAY93732;
XX
XX
DT 03-OCT-2000 (first entry)
XX
XX The heavy chain of immunoglobulin clone 6.1.1.
DE
XX
XX Cytotoxic T-lymphocyte antigen-4; CTLA-4; antibody; immune system;
KW hyperimmunity disorder; autoimmune disease; diabetes; graft rejection;
KW proliferative disorder; cancer; immunodeficient disorder.
XX
XX Homo sapiens.
OS
XX
XX Key Location/Qualifiers
FH 1.19
FT Peptide /note="signal peptide"
FT
XX
XX WO20037504-A2.
XX
XX 29-JUN-2000.
XX
XX 23-DEC-1999; 99WO-US30895.
XX
XX 23-DEC-1999; 98US-0113647.
XX
XX (PF2) PFIZER INC.
XX (ABGE-) ABGENIX INC.
XX
XX Hanson DC, Neveu MJ, Mueller EE, Hanke JH, Gilman SC, Davis CG;
PI Corvatan JR;
XX
XX MPI; 2000-442647/38.
XX N-PSDB; AAA46896.
XX
XX Novel antibodies capable of binding cytotoxic T-lymphocyte antigen
PT (CTLA-4 containing specified heavy and light chain sequences, useful
PT for treating, e.g. immune disorders -
XX
XX Claim 2; Fig 22m; 157pp; English.
XX
XX The present sequence represents a heavy chain of an antibody of the
CC invention. The antibody is directed cytotoxic T-lymphocyte antigen
CC (CTLA-4). Antibodies of the invention are composed of a heavy chain
CC variable region, comprising a modified contiguous sequence from a
CC FRI-FR3 sequence encoded by a human VH3-33 family gene. The
CC modifications are contained in CDR1, CDR2 and/or framework regions.
CC The antibodies may be used to inhibit CTLA-4 and down-regulate the
CC immune system to treat hyperimmunity disorders (e.g. autoimmune
CC disease, diabetes and graft rejection) and proliferative disorders
CC (e.g. cancer). CTLA-4 stimulatory agents may be used to up-regulate
CC immune system to up-regulate immunodeficient disorders.
XX
XX Sequence 463 AA;
SQ

Query Match 89.4%; Score 566; DB 21; Length 463;
Best Local Similarity 89.8%; Pred. No. 1.8e-41;
Matches 106; Conservative 3; Mismatches 9; Indels 0; Gaps 0;
OY 1 QVQLVSGGAVQPGRLRLSCAAGFTFSYTHMVRQAPGKGLEWTFISYDGSNKH 60
DB 20 QVQLVSGGAVVEPERSRLSTASGFTFSYGMHWVQAPEKGLHWAVIWTDSNKH 79

61 ADSYKGRFTVRDNSKNTLYLQWNSLRADPTAVVYCARAGLLGPDYWGQGLTVTVSS 118
DB 80 ADSAKGRFTISRDNKNTLYLQWNSLRADPTAVVYCARAGLLGPDYWGQGLTVTVSS 137

RESULT 8
ID AAB99369
XX AAB99369 standard; Protein; 225 AA.
AC AAB99369;
XX
XX
DT 26-AUG-2001 (first entry)
XX
XX Human Interleukin 8 antibody protein sequence M1_5H.
DE
XX
XX Human antibody; detection; Fab; immunoglobulin; heterophilic antibody;
KW human anti-mouse antibody; Interleukin 8; IL-8; Herpes;
KW target antigen; bacterial; fungal; viral; pathogen; human disease;
KW hepatitis A; hepatitis B; hepatitis C; influenza; Giardia; Malaria;
KW Leishmania; Staphylococcus aureus; Pseudomonas aeruginosa; diagnosis.
XX
XX Homo sapiens.
OS
XX
XX Synthetic.
XX
XX WO200140306-A1.
XX
XX 07-JUN-2001.
XX
XX 06-DEC-2000; 2000WO-US33042.
XX
XX 06-DEC-1999; 99US-0456090.
XX
XX (BIOS-) BIOSITE DIAGNOSTICS INC.
XX (GENP-) GENPHARM INT.
XX
XX Buechler J, Valakis G, Gray J, Lonberg N;
PI MPI; 2001-374798/39.
XX
XX Detecting analyte in human sample containing human antibodies binding
PT to nonhuman antibodies, involves contacting sample with human antibody
PT which binds to antibodies from nonhuman species and detecting binding
XX
XX Example 22; Page 93; 135pp; English.
XX
XX The present invention describes a method for detecting an analyte in a
CC human sample containing human antibodies that specifically bind to
CC antibodies from a nonhuman species. The method involves contacting the
CC sample with a human antibody (I) which specifically binds to antibodies
CC from a nonhuman species and detecting the binding between (I) and the
CC analyte to indicate presence of the analyte. The method is used for
CC detecting an analyte in a human sample containing human anti-mouse
CC antibody (HMA) (preferably human anti-mouse idiotype antibodies and/or
CC heterophilic antibodies). The method can also be used for detecting any
CC type of target antigen including bacterial, fungal and viral pathogens
CC that cause human diseases e.g., hepatitis (A, B and C), influenza, Herpes,
CC Giardia, Malaria, Leishmania, Staphylococcus aureus, Pseudomonas
CC aeruginosa. Human antibodies can be used as detection reagents for
CC performing clinical diagnostic tests and for performing other in vitro
CC detection assays, including for research purposes. (I) can be used in
CC qualitative assays designed to indicate the presence of one or more
CC target antigens above minimally detectable amounts of antigen in the
CC sample that usually correspond to the sensitivity limitations of the
CC assays for each target antigen. Also, (I) is used to determine the
CC amount of target antigen in a sample in a semi-quantitative or relative
CC sense. Quantification of one or more target antigens in a sample can
CC also be carried out using (I). AAH41612 to AAH41666, and AAB99361 to
CC AAB99399, represent sequences used in the exemplification of the present
CC invention.
XX
XX Sequence 225 AA;
SQ

Query Match 88.4%; Score 559.5; DB 22; Length 225;
Best Local Similarity 89.8%; Pred. No. 3.1e-41;
Matches 106; Conservative 5; Mismatches 6; Indels 1; Gaps 1;
OY 1 QVQLVSGGAVQPGRLRLSCAAGFTFSYTHMVRQAPGKGLEWTFISYDGSNKH 60

DB 1 QVQLVSGGGVVPGRSLRLSCAASGFTFSYSGMHWRAQPGKLEWTLITYDGDKKY 60
 QY 61 ADVKGRFTVSRDNRKNTLYLQMSLRADTAIYYCARGMGLPDPYWGGLTVYSS 118
 DB 61 ADVKGRFTVSRDNRKNTLYLQMSLRADTAIYYCARDG-IGYFDYWGGLTVYSS 117

RESULT 9
 AAB9380
 ID AAB9380 standard; Protein; 225 AA.
 XX AAB9380;
 AC AAB9380;
 DT 28-AUG-2001 (first entry)
 XX

DE Human interleukin 8 antibody protein sequence M2.1H.
 XX
 KW Human antibody; detection; Fab; immunoglobulin; heterophilic antibody;
 KW human anti-mouse antibody; HAMA antibody; interleukin 8; IL-8; Herpes;
 KW target antigen; bacterial; fungal; viral; pathogen; human disease;
 KW hepatitis A; hepatitis B; hepatitis C; influenza; giardia; malaria;
 KW Leishmania; Staphylococcus aureus; Pseudomonas aeruginosa; diagnosis.
 XX
 OS Homo sapiens.
 OS Synthetic.
 OS
 PN WO200140306-A1.
 XX
 PD 07-JUN-2001.
 XX
 PF 06-DEC-2000; 2000WO-US33042.
 XX
 PR 06-DEC-1999; 99US-0456090.
 XX
 PA (BIO-) BIOSITE DIAGNOSTICS INC.
 PA (GENP-) GENPHARM INT.
 XX
 PI Buechler J, Valkirs G, Gray J, Lonberg N;
 PI WPI; 2001-374798/39.
 DR
 XX
 PT Detecting analyte in human sample containing human antibodies binding
 PT to nonhuman-antibodies, involves contacting sample with human antibody
 PT which binds to antibodies from nonhuman species and detecting binding
 PT

Example 22; Page 94-95; 135pp; English.

The present invention describes a method for detecting an analyte in a human sample containing human antibodies that specifically bind to antibodies from a nonhuman species. The method involves contacting the sample with a human antibody (I) which specifically binds to antibodies from a nonhuman species and detecting the binding between (I) and the analyte to indicate presence of the analyte. The method is used for detecting an analyte in a human sample containing human anti-mouse antibody (HAMA) (preferably human anti-mouse idotype antibodies and/or heterophilic antibodies). The method can also be used for detecting any type of target antigen including bacterial, fungal and viral pathogens that cause human diseases e.g., hepatitis (A, B and C), influenza, Herpes, giardia, malaria, leishmania, staphylococcus aureus, pseudomonas aeruginosa. Human antibodies can be used as detection reagents for performing clinical diagnostic tests and for performing other in vitro detection assays, including for research purposes. (I) can be used in qualitative assays designed to indicate the presence of one or more target antigens above minimally detectable amounts of antigen in the sample that usually correspond to the sensitivity limitations of the assays for each target antigen. Also, (I) is used to determine the amount of target antigen in a sample in a semi-quantitative or relative sense. Quantification of one or more target antigens in a sample can also be carried out using (I). AAH41612 to AAH41686, and AAB93361 to AAB93399, represent sequences used in the exemplification of the present invention.

XX
 SQ Sequence 225 AA.
 QY Query Match 88.4%; Score 559.5; DB 22; Length 225;
 DB Best Local Similarity 89.8%; Pred. No. 3.1e-41;
 DB Matches 106; Conservative 5; Mismatches 6; Indels 1; Gaps 1;

QY 1 QVQLVSGGGVVPGRSLRLSCAASGFTFSYSGMHWRAQPGKLEWTLITYDGDKKY 60
 DB 1 QVQLVSGGGVVPGRSLRLSCAASGFTFSYSGMHWRAQPGKLEWTLITYDGDKKY 60
 QY 61 ADVKGRFTVSRDNRKNTLYLQMSLRADTAIYYCARGMGLPDPYWGGLTVYSS 118
 DB 61 ADVKGRFTVSRDNRKNTLYLQMSLRADTAIYYCARDG-IGYFDYWGGLTVYSS 117

RESULT 10
 AAB75002
 ID AAB75002 standard; Protein; 225 AA.
 XX AAB75002;
 AC AAB75002;
 DT 19-JUL-2001 (first entry)
 XX
 DE Anti-IL8 monoclonal antibody protein fragment M1.5H.
 XX
 KW Human; antibody; immunoglobulin; interleukin 8; IL8; immunogen;
 KW human antibody phage display library; immunisation; transgenic animal.
 XX
 OS Homo sapiens.
 OS Synthetic.
 OS
 PN WO200125492-A1.
 XX
 PD 12-APR-2001.
 XX
 PF 02-OCT-2000; 2000WO-US27237.
 XX
 PR 02-OCT-1999; 99US-0157415.
 XX
 PR 01-DEC-1999; 99US-0453234.
 XX
 PA (BIO-) BIOSITE DIAGNOSTICS INC.
 PA (GENP-) GENPHARM INT SUBSIDIARY OF MEDAREX INC.
 XX
 PI Buechler J, Valkirs G, Gray J, Lonberg N;
 PI WPI; 2001-335567/35.
 DR
 XX
 PT Producing a human antibody phage display library comprises providing a
 PT transgenic animal whose genome comprises human immunoglobulin genes and
 PT isolating nucleic acids encoding antibody chains from lymphatic cells.
 XX
 PS Example 22; Page 97; 161pp; English.

The present invention describes a method (M1) for producing a human antibody phage display library (I), comprising: (1) providing a nonhuman transgenic animal (II) whose genome comprises human immunoglobulin genes; (2) isolating nucleic acids encoding human antibody chains (III) from lymphatic cells; and (3) forming a library of display packages whose members comprise a nucleic acid encoding (III) which is displayed from the package. The method is used for producing a human antibody display library, e.g., a Fab phage display library. The display method may be used to screen nucleic acids encoding antibody chains obtained from immunised nonhuman transgenic animals, and from this a population of antibodies may be prepared. Production of a human monoclonal antibodies display library using this method means there is no need to immunise humans with antigens, and the difficulties faced with immortalising B cells are avoided. AAH29958 to AAH30066 and AAB74994 to AAB75056 represent sequences used in the exemplification of the present invention.

Query Match 88.4%; Score 559.5; DB 22; Length 225;

Best Local Similarity 89.8%; Pred. No. 3,1e-41;
Matches 106; Conservative 5; Mismatches 6; Indels 1; Gaps 1;

QY 1 QVQLVESGGGVVQPKRSRLSCAASGFTFSYTHMWRQAPGKGLVWTFISYDGNKHY 60
Db 1 QVQLVESGGGVVQPKRSRLSCAASGFTFSYTHMWRQAPGKGLVWTFISYDGNKHY 60
61 ADVYKGRFTISRDNKNTLYLQMSLRADPAIYYCARFGMLGPPDYWGQGLTVTVSS 118
61 ADVYKGRFTISRDNKNTLYLQMSLRADPAIYYCARDG-IGFDYWGQGLTVTVSS 117

Db 61 ADVYKGRFTISRDNKNTLYLQMSLRADPAIYYCARDG-IGFDYWGQGLTVTVSS 117
RESULT 11
AAB75013
ID AAB75013 standard; Protein; 225 AA.

AC AAB75013;
XX
XX 19-JUN-2001 (first entry)

DE Anti-IL8 monoclonal antibody protein fragment M2_11H.
XX Human; antibody; immunoglobulin; interleukin 8; IL8; immunogen;
KM human antibody phage display library; immunisation; transgenic animal.
XX Homo sapiens.
OS Synthetic.
XX MO200125492-A1.
PN 12-APR-2001.

XX 02-OCT-2000; 2000WO-US27237.
XX 02-OCT-1999; 99US-0157415.
PR 01-DEC-1999; 99US-0453234.

XX (BIOS-) BIOSITE DIAGNOSTICS INC.
PA (GENP-) GENPHARM INT SUBSIDIARY OF MEDAREX INC.
XX Buechler J, Valkire G, Gray J, Lomberg N;
XX WPI; 2001-335567/35.

PT Producing a human antibody phage display library comprises providing a
transgenic animal whose genome comprises human immunoglobulin genes and
isolating nucleic acids encoding antibody chains from lymphatic cells -
XX Example 22; Page 98-99; 161pp; English.

XX The present invention describes a method (M1) for producing a human
antibody phage display library (I), comprising: (i) providing a nonhuman
transgenic animal (II) whose genome comprises human immunoglobulin genes;
(2) isolating nucleic acids encoding human antibody chains (III) from
lymphatic cells; and (3) forming a library of display packages whose
members comprise a nucleic acid encoding (III) which is displayed from
the package. The method is used for producing a human antibody display
library, e.g., a Fab phage display library. The display method may be
used to screen nucleic acids encoding antibody chains obtained from
immunised nonhuman transgenic animals, and from this a population of
antibodies may be prepared. Production of a human monoclonal antibodies
display library using this method means there is no need to immunise
humans with antigens, and the difficulties faced with immortalising B
cells are avoided. AAH29958 to AAH30066 and AAB74994 to AAB75056
represent sequences used in the exemplification of the present invention.

XX Sequence 225 AA;

Query Match 88.4%; Score 559.5; DB 22; Length 225;
Best Local Similarity 89.8%; Pred. No. 3,1e-41;
Matches 106; Conservative 5; Mismatches 6; Indels 1; Gaps 1;

QY 1 QVQLVESGGGVVQPKRSRLSCAASGFTFSYTHMWRQAPGKGLVWTFISYDGNKHY 60

Db 1 QVQLVESGGGVVQPKRSRLSCAASGFTFSYTHMWRQAPGKGLVWTFISYDGNKHY 60
QY 61 ADVYKGRFTISRDNKNTLYLQMSLRADPAIYYCARFGMLGPPDYWGQGLTVTVSS 118
Db 61 ADVYKGRFTISRDNKNTLYLQMSLRADPAIYYCARDG-IGFDYWGQGLTVTVSS 117

RESULT 12
ABP45508
ID ABP45508 standard; Protein; 252 AA.

AC ABP45508;
XX
XX 19-AUG-2002 (first entry)

DE Human Blys binding scFv SEQ ID 1519.

XX Blys; B lymphocyte stimulator; TNF superfamily; human; cytostatic;
KM tumour necrosis factor; B cell proliferation; B cell differentiation;
KM immunosuppressive; immunostimulant; immunomodulatory; antirheumatic;
KV antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;
KM systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;
XX common variable immunodeficiency; acquired immunodeficiency syndrome.

XX Homo sapiens.
OS
XX MO200202641-A1.
PN 10-JAN-2002.

XX 15-JUN-2001; 2001WO-US19110.
XX 16-JUN-2000; 2000US-212210P.
PR 17-OCT-2000; 2000US-240815P.
PR 16-MAR-2001; 2001US-276248P.
PR 21-MAR-2001; 2001US-277379P.
PR 25-MAY-2001; 2001US-293499P.

XX (HUMA-) HUMAN GENOME SCI INC.
PA (CAMP-) CAMBRIDGE ANTIBODY TECHNOLOGY.
XX Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;
XX WPI; 2002-114799/15.

PT Antibodies against B lymphocyte stimulating polypeptides, useful for
the diagnosis and treatment of cancers and immune disorders -
XX Claim 1; Page 2215-2216; 3148pp; English.

XX This invention describes novel antibodies that immunospecifically bind to
B lymphocyte stimulator (Blys) polypeptides. Blys is a member of the
tumour necrosis factor (TNF) super family and induces B cell
proliferation and differentiation. The antibodies of the invention have
cytostatic, immunosuppressive, immunostimulant, immunomodulatory,
antirheumatic and antiAIDS activity and can be used in vaccines to
inhibit the expression and activity of Blys. The antibodies bind to Blys
and so may be used to detect and quantitate the presence of Blys in
biological samples and may be used in this way to diagnose disease
associated with aberrant expression of Blys. They may also be
administered to treat diseases associated with aberrant Blys expression
and activity such as cancer, immune, and autoimmune disorders and
diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,
immunodeficiency (e.g. common variable immunodeficiency (CVID) and
acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent
the antibodies and fragments of the antibodies described in the method
of the invention.

XX Sequence 252 AA;

Query Match 88.3%; Score 559; DB 23; Length 252;
Best Local Similarity 85.5%; Pred. No. 3,8e-41;

CC humans with antigens, and the difficulties faced with immortalizing B
 CC cells are avoided. AAH29958 to AAH30066 and AAB74994 to AAB75056
 CC represent sequences used in the exemplification of the present invention.
 XX

XX SQ Sequence 225 AA;

Query Match 88.2%; Score 558.5; DB 22; Length 225;

Best Local Similarity 89.0%; Pred. No. 3.8e-41; Indels 1; Gaps 1;
 Matches 105; Conservative 5; Mismatches 7;

QY 1 QVALVESGGGVVQPPRSRLRLSCASGFTFSSTYTMWVROAPGKLEWYTFISYDGSNKRY 60
 DB 1 QVALVESGGGVVQPPRSRLRLSCASGFTFSSTYTMWVROAPGKLEWYTFISYDGSNKRY 60

QY 61 ADSVKGRTFSRDNSKNTLYLQMSLRADTAIYYCARTGWLGPEDYWGQGLTVTVSS 118
 DB 61 ADSVKGRTFSRDNSKNTLYLQMSLRADTAIYYCARTGWLGPEDYWGQGLTVTVSS 117

RESULT 15

ABP44972 standard; Protein; 254 AA.

AC ABP44972;

DT 19-AUG-2002 (first entry)

DE Human Blys binding scfv SEQ ID 983.

XX Blys; B lymphocyte stimulator; TNF superfamily; human; cytosolic;
 KW tumour necrosis factor; B cell proliferation; B cell differentiation;
 KW immunosuppressive; immunostimulant; immunomodulator; antirheumatic;
 KW antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;
 KW systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;
 KW common variable immunodeficiency; acquired immunodeficiency syndrome.

OS Homo sapiens.

PN WO200202641-A1.

PD 10-JAN-2002.

PE 15-JUN-2001; 2001WO-US19110.

PR 16-JUN-2000; 2000US-212210P.

PR 17-OCT-2000; 2000US-240816P.

PR 16-MAR-2001; 2001US-276248P.

PR 21-MAR-2001; 2001US-277379P.

PR 25-MAY-2001; 2001US-293499P.

PA (HUMA-) HUMAN GENOME SCI INC.
 (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.

PI Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;

DR WPI; 2002-114799/15.

PT Antibodies against B lymphocyte stimulating polypeptides, useful for
 PT the diagnosis and treatment of cancers and immune disorders -

PS Claim 1; Page 1574-1575; 3148pp; English.

XX This invention describes novel antibodies that immunospecifically bind to
 CC B lymphocyte stimulator (Blys) polypeptides. Blys is a member of the
 CC tumour necrosis factor (TNF) super family and induces B cell
 CC proliferation and differentiation. The antibodies of the invention have
 CC cytosolic, immunosuppressive, immunostimulant, immunomodulatory,
 CC antirheumatic and antiAIDS activity and can be used in vaccines to
 CC inhibit the expression and activity of Blys. The antibodies bind to Blys
 CC and so may be used to detect and quantitate the presence of Blys in
 CC biological samples and may be used in this way to diagnose disease
 CC associated with aberrant expression of Blys. They may also be
 CC administered to treat diseases associated with aberrant Blys expression

CC and activity such as cancer, immune, and autoimmune disorders and
 CC diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,
 CC immunodeficiency (e.g. common variable immunodeficiency (CVID) and
 CC acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent
 CC the antibodies and fragments of the antibodies described in the method
 CC of the invention.

XX SQ Sequence 254 AA;

Query Match 88.0%; Score 557; DB 23; Length 254;

Best Local Similarity 83.6%; Pred. No. 5.8e-41; Indels 10; Gaps 2;
 Matches 107; Conservative 6; Mismatches 5;

QY 1 QVALVESGGGVVQPPRSRLRLSCASGFTFSSTYTMWVROAPGKLEWYTFISYDGSNKRY 60
 DB 1 QVALVESGGGVVQPPRSRLRLSCASGFTFSSTYTMWVROAPGKLEWYTFISYDGSNKRY 60

QY 61 ADSVKGRTFSRDNSKNTLYLQMSLRADTAIYYCAR-----TGMLEP--FDYWGQ 110
 DB 61 ADSVKGRTFSRDNSKNTLYLQMSLRADTAIYYCAR-----TGMLEP--FDYWGQ 120

QY 111 GTLVTVSS 118

DB 121 GTMTVSS 128

Search completed: June 3, 2003, 08:14:47
 Job time : 54.1604 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: June 3, 2003, 08:21:07 ; Search time 27.9898 Seconds

(without alignments)
426.742 Million cell updates/sec

Title: US-09-644-668A-19

Perfect score: 633

Sequence: 1 QVQLVESGGGVQGRSLRL.....TGMGLPFDYWGQGLTVTVSS 118

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 383519 seqs, 101223694 residues

Total number of hits satisfying chosen parameters: 383519

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first: 45 summaries

Database : Published Applications AA:*

- 1: /cgn2_6/ptodata/1/pubppa/US08_NEW_PUB.rep.*
- 2: /cgn2_6/ptodata/1/pubppa/FCI_NEW_PUB.rep.*
- 3: /cgn2_6/ptodata/1/pubppa/US06_NEW_PUB.rep.*
- 4: /cgn2_6/ptodata/1/pubppa/US07_NEW_PUB.rep.*
- 5: /cgn2_6/ptodata/1/pubppa/US07_PUBCOMB.rep.*
- 6: /cgn2_6/ptodata/1/pubppa/US07_PUBCOMB.rep.*
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- 9: /cgn2_6/ptodata/1/pubppa/US09_NEW_PUB.rep.*
- 10: /cgn2_6/ptodata/1/pubppa/US09_PUBCOMB.rep.*
- 11: /cgn2_6/ptodata/1/pubppa/US10_NEW_PUB.rep.*
- 12: /cgn2_6/ptodata/1/pubppa/US10_PUBCOMB.rep.*
- 13: /cgn2_6/ptodata/1/pubppa/US60_NEW_PUB.rep.*
- 14: /cgn2_6/ptodata/1/pubppa/US60_PUBCOMB.rep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	567	89.6	247	US-09-880-748-924	Sequence 924, App
2	566	89.4	463	US-10-153-382-13	Sequence 13, Appl
3	559.5	88.4	225	US-09-453-234-60	Sequence 60, Appl
4	559.5	88.4	225	US-09-453-234-92	Sequence 92, Appl
5	559	88.3	252	US-09-880-748-1519	Sequence 1519, Ap
6	558.5	88.2	225	US-09-453-234-108	Sequence 108, App
7	557	88.0	254	US-09-880-748-983	Sequence 983, App
8	557	88.0	463	US-10-153-382-3	Sequence 3, Appl
9	557	88.0	463	US-10-153-382-5	Sequence 5, Appl
10	554	87.5	252	US-09-880-748-1201	Sequence 1201, Ap
11	553.5	87.4	225	US-09-453-234-106	Sequence 106, App
12	551.5	87.1	225	US-09-453-234-55	Sequence 55, Appl
13	551.5	87.1	225	US-09-453-234-110	Sequence 110, App
14	549.5	86.8	225	US-09-453-234-102	Sequence 102, App
15	547	86.4	252	US-09-880-748-1627	Sequence 1627, Ap
16	546	86.3	249	US-09-880-748-1109	Sequence 1109, Ap
17	545.5	86.2	225	US-09-453-234-94	Sequence 94, Appl
18	543.5	85.9	248	US-09-880-748-1421	Sequence 1421, Ap
19	541.5	85.5	119	US-10-073-644C-6	Sequence 6, Appl

20	540.5	85.4	464	US-10-153-382-9	Sequence 9, Appl
21	539.5	85.2	119	US-10-073-644C-2	Sequence 2, Appl
22	538.5	85.1	241	US-09-880-748-2055	Sequence 2055, Ap
23	538	85.0	253	US-09-880-748-1200	Sequence 1200, Ap
24	537	84.8	252	US-09-880-748-956	Sequence 956, App
25	536	84.7	249	US-09-880-748-512	Sequence 512, App
26	535.5	84.6	125	US-09-848-798-9	Sequence 9, Appl
27	534.5	84.4	125	US-09-848-798-24	Sequence 24, Appl
28	534	84.4	254	US-09-880-748-977	Sequence 977, App
29	532.5	84.1	252	US-09-880-748-1731	Sequence 1731, Ap
30	531.5	84.0	123	US-10-243-265-2	Sequence 2, Appl
31	531.5	84.0	225	US-09-453-234-68	Sequence 68, Appl
32	531.5	84.0	225	US-09-453-234-100	Sequence 100, App
33	529	83.6	244	US-09-880-748-1910	Sequence 1910, Ap
34	529	83.6	247	US-09-880-748-1330	Sequence 1330, Ap
35	527	83.3	251	US-09-848-798-149	Sequence 149, App
36	527	83.3	251	US-09-880-748-1512	Sequence 1512, Ap
37	527	83.3	254	US-09-880-748-1554	Sequence 1554, Ap
38	527	83.3	254	US-09-880-748-881	Sequence 881, App
39	526.5	83.2	240	US-09-880-748-1898	Sequence 1898, Ap
40	526.5	83.2	252	US-09-880-748-988	Sequence 988, App
41	526	83.1	118	US-09-798-058-2	Sequence 2, Appl
42	525.5	83.0	123	US-10-243-265-10	Sequence 10, Appl
43	525	82.9	254	US-09-880-748-1759	Sequence 1759, Ap
44	524.5	82.9	251	US-09-880-748-955	Sequence 955, App
45	524.5	82.9	252	US-09-880-748-1394	Sequence 1394, Ap

ALIGNMENTS

RESULT 1
US-09-880-748-924 Application US/09880748
Sequence 924, Application US/09880748
Publication No. US2003005937A1
GENERAL INFORMATION:
APPLICANT: Ruden et al.
TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
FILE REFERENCE: PF523
CURRENT APPLICATION NUMBER: US/09/880,748
CURRENT FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: 60/212,210
PRIOR FILING DATE: 2000-06-15
PRIOR APPLICATION NUMBER: 60/240,816
PRIOR FILING DATE: 2000-10-17
PRIOR APPLICATION NUMBER: 60/276,248
PRIOR FILING DATE: 2001-03-16
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/293,499
PRIOR FILING DATE: 2001-05-25
NUMBER OF SEQ ID NOS: 3239
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 924
LENGTH: 247
TYPE: PRT
ORGANISM: Homo sapiens
US-09-880-748-924
Query Match 89.6%; Score 567; DB 9; Length 247;
Best Local Similarity 87.9%; Pred. No. 4, 7e-37;
Matches 109; Conservative 4; Mismatches 5; Indels 6; Gaps 1;
QY 1 QVQLVESGGGVQGRSLRLSCAASGFTFSYTHWVROAPGKGLEWVTFISYQSNKHY 60
DB 1 QVQLVESGGGVQGRSLRLSCAASGFTFSYTHWVROAPGKLEWVAVISIDGSKTY 60
QY 61 ADVYKGFYVSRDNSKNTLYLQNNSLRAEDTAIYYCAR-----TGMGLPFDYWGQGLTV 114
DB 61 ADVYKGFYVSRDNSKNTLYLQNNSLRAEDTAIYYCARPYDILTYGLTYFDYWGQGLTV 120
QY 115 TVSS 118
|||

Db 121 TVSS 124

RESULT 2

US-10-153-382-13
Sequence 13, Application US/10153382
Publication No. US20030086930A1
GENERAL INFORMATION:
APPLICANT: PFIZER PRODUCTS INC.
TITLE OF INVENTION: USES OF ANTI-CTLA-4 ANTIBODIES
FILE REFERENCE: PC23019A
CURRENT APPLICATION NUMBER: US/10/153,382
CURRENT FILING DATE: 2002-05-22
PRIOR APPLICATION NUMBER: 60/293042
PRIOR FILING DATE: 2001-05-23
NUMBER OF SEQ ID NOS: 39
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 13
LENGTH: 463
TYPE: PRT
ORGANISM: Homo sapiens
US-10-153-382-13

Query Match 89.4%; Score 566; DB 9; Length 463;
Best Local Similarity 89.8%; Pred. No. 1e-36;
Matches 106; Conservative 3; Mismatches 9; Indels 0; Gaps 0;

QY 1 QVQVLESQGGVQVQPGRSRLRLSCAASGFTSSYTMWVRQAPGKLEWTFISYDGSNKH 60
DB 20 QVQVLESQGGVQVQPGRSRLRLSCAASGFTSSYTMWVRQAPGKLEWTFISYDGSNKH 79
QY 61 ADSVKGRTVSRDNSKNTLYIQMNSLRADTAIYYCARNGWIGPPDYWGQGLTVTVSS 118
DB 80 ADSVKGRTVSRDNSKNTLYIQMNSLRADTAIYYCARAGLIGYFDYWGQGLTVTVSS 137

RESULT 3

US-09-453-234-60
Sequence 60, Application US/09453234
Publication No. US20030091995A1
GENERAL INFORMATION:
APPLICANT: Buechler, Joe
APPLICANT: Valktis, Gunars
APPLICANT: Gray, Jeff
APPLICANT: Lomborg, Nils
APPLICANT: Genpharm International, Inc.
TITLE OF INVENTION: Human Antibodies
FILE REFERENCE: 020015-000110US
CURRENT APPLICATION NUMBER: US/09/453,234
CURRENT FILING DATE: 1999-12-01
PRIOR APPLICATION NUMBER: 60/157,415
PRIOR FILING DATE: 1999-10-02
NUMBER OF SEQ ID NOS: 112
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 60
LENGTH: 225
TYPE: PRT
ORGANISM: Homo sapiens
OTHER INFORMATION: M1-5H
US-09-453-234-60

Query Match 88.4%; Score 559.5; DB 9; Length 225;
Best Local Similarity 89.8%; Pred. No. 1.6e-36;
Matches 106; Conservative 5; Mismatches 6; Indels 1; Gaps 1;

QY 1 QVQVLESQGGVQVQPGRSRLRLSCAASGFTSSYTMWVRQAPGKLEWTFISYDGSNKH 60
DB 1 QVQVLESQGGVQVQPGRSRLRLSCAASGFTSSYTMWVRQAPGKLEWTFISYDGSNKH 60
QY 61 ADSVKGRTVSRDNSKNTLYIQMNSLRADTAIYYCARNGWIGPPDYWGQGLTVTVSS 118
DB 61 ADSVKGRTVSRDNSKNTLYIQMNSLRADTAIYYCARNGWIGPPDYWGQGLTVTVSS 117

RESULT 4

US-09-453-234-92
Sequence 92, Application US/09453234
Publication No. US20030091995A1
GENERAL INFORMATION:
APPLICANT: Buechler, Joe
APPLICANT: Valktis, Gunars
APPLICANT: Gray, Jeff
APPLICANT: Lomborg, Nils
APPLICANT: Genpharm International, Inc.
TITLE OF INVENTION: Human Antibodies
FILE REFERENCE: 020015-000110US
CURRENT APPLICATION NUMBER: US/09/453,234
CURRENT FILING DATE: 1999-12-01
PRIOR APPLICATION NUMBER: 60/157,415
PRIOR FILING DATE: 1999-10-02
NUMBER OF SEQ ID NOS: 112
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 92
LENGTH: 225
TYPE: PRT
ORGANISM: Homo sapiens
OTHER INFORMATION: M2-11H
US-09-453-234-92

Query Match 88.4%; Score 559.5; DB 9; Length 225;
Best Local Similarity 89.8%; Pred. No. 1.6e-36;
Matches 106; Conservative 5; Mismatches 6; Indels 1; Gaps 1;

QY 1 QVQVLESQGGVQVQPGRSRLRLSCAASGFTSSYTMWVRQAPGKLEWTFISYDGSNKH 60
DB 1 QVQVLESQGGVQVQPGRSRLRLSCAASGFTSSYTMWVRQAPGKLEWTFISYDGSNKH 60
QY 61 ADSVKGRTVSRDNSKNTLYIQMNSLRADTAIYYCARNGWIGPPDYWGQGLTVTVSS 118
DB 61 ADSVKGRTVSRDNSKNTLYIQMNSLRADTAIYYCARNGWIGPPDYWGQGLTVTVSS 117

RESULT 5

US-09-880-748-1519
Sequence 1519, Application US/09880748
Publication No. US2003005937A1
GENERAL INFORMATION:
APPLICANT: Ruben et al.
TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
FILE REFERENCE: P5523
CURRENT APPLICATION NUMBER: US/09/880,748
CURRENT FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: 60/212,210
PRIOR FILING DATE: 2000-06-15
PRIOR APPLICATION NUMBER: 60/240,816
PRIOR FILING DATE: 2000-10-17
PRIOR APPLICATION NUMBER: 60/276,248
PRIOR FILING DATE: 2001-03-16
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/293,499
PRIOR FILING DATE: 2001-05-25
NUMBER OF SEQ ID NOS: 3239
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1519
LENGTH: 252
TYPE: PRT
ORGANISM: Homo sapiens
US-09-880-748-1519

Query Match 88.3%; Score 559; DB 9; Length 252;
Best Local Similarity 85.5%; Pred. No. 2e-36;
Matches 106; Conservative 6; Mismatches 6; Indels 6; Gaps 1;

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RESULT 9
US-10-153-382-5
; Sequence 5, Application US/10153382
; Publication No. US20030086930A1
; GENERAL INFORMATION:
; APPLICANT: PRIZER PRODUCTS INC.
; TITLE OF INVENTION: USES OF ANTI-CTLA-4 ANTIBODIES
; FILE REFERENCE: PC23019A
; CURRENT APPLICATION NUMBER: US/10/153,382
; CURRENT FILING DATE: 2002-05-22
; PRIOR APPLICATION NUMBER: 60/293042
; PRIOR FILING DATE: 2001-05-23
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 463

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TYPE: PRT
ORGANISM: Homo sapiens
US-10-153-382-5

Query Match 88.0%; Score 557; DB 9; Length 463;
Best Local Similarity 88.1%; Pred. No. 56-36;
Matches 104; Conservative 5; Mismatches 9; Indels 0; Gaps 0;

QY 1 QVQLVESGGGVQPGKSLRLSCAASGFTFSYTHMHWROAPGKLEWTFPISYGSNKHY 60
DB 20 QVQLVESGGGVQPGKSLRLSCVAGSFTFSHGHWROAPGKLEWAVIYDGRNKYY 79
QY 61 ADSVKGRTFSRDNSKNTLYIQMNSLRADTAIYYCARTGMIGPFDYWGQGLTVVSS 118
DB 80 ADSVKGRTFSRDNSKNTLYIQMNSLRADTAIYYCARTGMIGPFDYWGQGLTVVSS 137

RESULT 10
US-09-880-748-1201

Sequence 1201, Application US/09880748
Publication No. US20030059937A1
GENERAL INFORMATION:

APPLICANT: Ruben et al.
TITLE OF INVENTION: Antibodies that Immunosepecifically Bind BlyS
FILE REFERENCE: PFS23
CURRENT APPLICATION NUMBER: US/09/880,748
CURRENT FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: 60/212,210
PRIOR FILING DATE: 2000-06-15
PRIOR APPLICATION NUMBER: 60/240,816
PRIOR FILING DATE: 2000-10-17
PRIOR APPLICATION NUMBER: 60/276,248
PRIOR FILING DATE: 2001-03-16
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/293,499
PRIOR FILING DATE: 2001-05-25
NUMBER OF SEQ ID NOS: 3239
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1201
LENGTH: 252
TYPE: PRT
ORGANISM: Homo sapiens
US-09-880-748-1201

Query Match 87.5%; Score 554; DB 9; Length 252;
Best Local Similarity 84.7%; Pred. No. 4.8e-36;
Matches 105; Conservative 7; Mismatches 6; Indels 6; Gaps 1;

QY 1 QVQLVESGGGVQPGKSLRLSCAASGFTFSYTHMHWROAPGKLEWTFPISYGSNKHY 60
DB 1 QVQLVESGGGVQPGKSLRLSCAASGFTFSYTHMHWROAPGKLEWAVIYDGRNKYY 60
QY 61 ADSVKGRTFSRDNSKNTLYIQMNSLRADTAIYYCAR-----TGMIGPFDYWGQGLTV 114
DB 61 ADSVKGRTFSRDNSKNTLYIQMNSLRADTAIYYCARTGMIGPFDYWGQGLTVVSS 120
QY 115 TVSS 118
DB 121 TVSS 124

RESULT 11
US-09-453-234-106

Sequence 106, Application US/09453234
Publication No. US20030091995A1
GENERAL INFORMATION:

APPLICANT: Buechler, Joe
APPLICANT: Walkers, Gunars
APPLICANT: Gray, Jeff
APPLICANT: Lomborg, Nils
APPLICANT: Biosite Diagnostics, Inc.
APPLICANT: Genpharm International

TITLE OF INVENTION: Human Antibodies

FILE REFERENCE: 020015-000110US

CURRENT APPLICATION NUMBER: US/09/453,234

CURRENT FILING DATE: 1999-12-01

PRIOR APPLICATION NUMBER: US 60/157,415

PRIOR FILING DATE: 1999-10-02

NUMBER OF SEQ ID NOS: 112

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 106

LENGTH: 225

TYPE: PRT

ORGANISM: Homo sapiens

OTHER INFORMATION: M2-33H

US-09-453-234-106

Query Match 87.4%; Score 553.5; DB 9; Length 225;
Best Local Similarity 88.1%; Pred. No. 4.8e-36;
Matches 104; Conservative 7; Mismatches 6; Indels 1; Gaps 1;

QY 1 QVQLVESGGGVQPGKSLRLSCAASGFTFSYTHMHWROAPGKLEWTFPISYGSNKHY 60
DB 1 QVQLVESGGGVQPGKSLRLSCAASGFTFSYTHMHWROAPGKLEWTFPISYGSNKHY 60
QY 61 ADSVKGRTFSRDNSKNTLYIQMNSLRADTAIYYCARTGMIGPFDYWGQGLTVVSS 118
DB 61 ADSVKGRTFSRDNSKNTLYIQMNSLRADTAIYYCARTGMIGPFDYWGQGLTVVSS 117

RESULT 12
US-09-453-234-56

Sequence 56, Application US/09453234
Publication No. US20030091995A1
GENERAL INFORMATION:

APPLICANT: Buechler, Joe
APPLICANT: Walkers, Gunars
APPLICANT: Gray, Jeff
APPLICANT: Lomborg, Nils
APPLICANT: Biosite Diagnostics, Inc.
APPLICANT: Genpharm International
TITLE OF INVENTION: Human Antibodies
FILE REFERENCE: 020015-000110US
CURRENT APPLICATION NUMBER: US/09/453,234
CURRENT FILING DATE: 1999-12-01
PRIOR APPLICATION NUMBER: US 60/157,415
PRIOR FILING DATE: 1999-10-02
NUMBER OF SEQ ID NOS: 112
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 56
LENGTH: 225
TYPE: PRT
ORGANISM: Homo sapiens
OTHER INFORMATION: M1-3H
US-09-453-234-56

Query Match 87.1%; Score 551.5; DB 9; Length 225;
Best Local Similarity 88.9%; Pred. No. 6.8e-36;
Matches 104; Conservative 6; Mismatches 6; Indels 1; Gaps 1;

QY 2 VOLVESGGGVQPGKSLRLSCAASGFTFSYTHMHWROAPGKLEWTFPISYGSNKHY 61
DB 2 VOLVESGGGVQPGKSLRLSCAASGFTFSYTHMHWROAPGKLEWTFPISYGSNKHY 61
QY 62 DSVKGRFTFSRDNSKNTLYIQMNSLRADTAIYYCARTGMIGPFDYWGQGLTVVSS 118
DB 62 DSVKGRFTFSRDNSKNTLYIQMNSLRADTAIYYCARTGMIGPFDYWGQGLTVVSS 117

RESULT 13
US-09-453-234-110

Sequence 110, Application US/09453234
Publication No. US20030091995A1
GENERAL INFORMATION:

APPLICANT: Buechler, Joe

RESULT 15

Search completed: June 3, 2003, 08:52:53
Job time : 27.9898 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 3, 2003, 08:10:19 ; Search time 17.9215 Seconds

(without alignments)
193.728 Million cell updates/sec

Title: US-09-644-668a-19

Perfect score: 633
Sequence: 1 QVQLVESGGGVQVQGRSLRL.....TGLLGPFDYWGQGLTVTVSS 118

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

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3: /cgn2_6/ptodata/1/1aa/6A_COMB.pep:*
4: /cgn2_6/ptodata/1/1aa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/1aa/PCUTS_COMB.pep:*
6: /cgn2_6/ptodata/1/1aa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	555.5	87.8	120	1	US-07-942-245-35 Sequence 35, Appl
2	546.5	86.3	119	1	US-08-331-398A-46 Sequence 46, Appl
3	546.5	86.3	119	2	US-08-331-397B-46 Sequence 46, Appl
4	546.5	86.3	119	2	US-08-759-804A-46 Sequence 46, Appl
5	546.5	86.3	119	4	US-09-227-693-46 Sequence 46, Appl
6	535.5	84.6	125	4	US-09-240-274-9 Sequence 9, Appl
7	534.5	84.4	125	4	US-09-240-274-24 Sequence 24, Appl
8	527.5	83.3	116	1	US-08-211-202-141 Sequence 141, Appl
9	527.5	83.3	117	4	US-09-025-769B-24 Sequence 24, Appl
10	527	83.3	126	4	US-09-240-274-149 Sequence 149, Appl
11	521.5	82.4	125	4	US-09-240-274-8 Sequence 8, Appl
12	521.5	82.4	125	4	US-09-240-274-20 Sequence 20, Appl
13	521.5	82.4	125	4	US-09-240-274-21 Sequence 21, Appl
14	521.5	82.4	125	4	US-09-240-274-22 Sequence 22, Appl
15	519	82.0	126	4	US-09-240-274-10 Sequence 10, Appl
16	519	82.0	126	4	US-09-240-274-14 Sequence 14, Appl
17	514	82.0	126	4	US-09-240-274-150 Sequence 150, Appl
18	514	81.2	126	4	US-09-240-274-1 Sequence 1, Appl
19	513.5	81.1	125	4	US-09-240-274-23 Sequence 23, Appl
20	511	80.7	310	4	US-09-079-029-11 Sequence 11, Appl
21	510	80.6	126	4	US-09-240-274-152 Sequence 152, Appl
22	509	80.4	124	4	US-09-240-274-4 Sequence 4, Appl
23	508.5	80.3	113	3	US-08-974-899-6 Sequence 6, Appl
24	508	80.3	126	4	US-09-240-274-26 Sequence 26, Appl
25	508	80.3	128	4	US-09-240-274-142 Sequence 142, Appl
26	507	80.1	122	2	US-07-934-373C-21 Sequence 21, Appl
27	507	80.1	122	3	US-08-437-642B-21 Sequence 21, Appl

28	507	80.1	122	4	US-08-146-206C-21 Sequence 21, Appl
29	507	80.1	122	5	PCT-US93-07832-21 Sequence 21, Appl
30	506	79.9	141	1	US-08-259-372A-2 Sequence 2, Appl
31	506	79.9	141	1	US-08-468-671-2 Sequence 2, Appl
32	505.5	79.9	127	4	US-09-240-274-18 Sequence 18, Appl
33	504.5	79.7	123	2	US-08-665-202-30 Sequence 30, Appl
34	504	79.6	123	4	US-08-983-607-38 Sequence 38, Appl
35	503.5	79.5	117	4	US-09-157-370-1 Sequence 1, Appl
36	502	79.3	120	4	US-09-025-769B-38 Sequence 38, Appl
37	502	79.3	120	4	US-09-025-769B-63 Sequence 63, Appl
38	502	79.3	124	4	US-09-240-274-7 Sequence 7, Appl
39	502	79.3	126	4	US-09-240-274-153 Sequence 153, Appl
40	502	79.3	281	4	US-09-025-769B-178 Sequence 178, Appl
41	501.5	79.2	125	4	US-09-240-274-151 Sequence 151, Appl
42	501.5	79.2	127	4	US-09-240-274-11 Sequence 11, Appl
43	501	79.1	117	1	US-07-942-245-36 Sequence 36, Appl
44	500	79.0	124	4	US-09-240-274-2 Sequence 2, Appl
45	500	79.0	126	4	US-09-240-274-25 Sequence 25, Appl

ALIGNMENTS

RESULT 1
US-07-942-245-35
Sequence 35, Application US/07942245
Patent No. 5639641
GENERAL INFORMATION:
APPLICANT: PEDERSEN, Jan T.
APPLICANT: SEARLE, Stephen M.J.
APPLICANT: REES, Anthony R.
APPLICANT: ROGUSKA, Michael A.
APPLICANT: GUILD, Braydon C.
TITLE OF INVENTION: SURFACE RESIDUE VENERING OF RODENT
NUMBER OF SEQUENCES: 522
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sughrie, Mion, Zinn, Macpeak & Seas
STREET: 2100 Pennsylvania Avenue, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: United States
ZIP: 20037-3202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: HP 9000/700 Workstation
OPERATING SYSTEM: UNIX
SOFTWARE: In house
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/942,245
FILING DATE: 09-SEP-1992
CLASSIFICATION: 530
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 293-7060
TELEFAX: (202) 293-7860
TELEX: 6491103
INFORMATION FOR SEQ ID NO: 35:
SEQUENCE CHARACTERISTICS:
LENGTH: 120 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-07-942-245-35
Query Match 87.8%, Score 555.5, DB 1, Length 120;
Best Local Similarity 88.4%, Pred. No. 2.3e-46;
Matches 107, Conservative 3, Mismatches 6, Indels 5, Gaps 2;
QY 1 QVQLVESGGGVQVQGRSLRLCAASGFTFSYTMHWYRQAGKLEWTFISYQGNKHY 60
DB 1 QVQLVESGGGVQVQGRSLRLCAASGFTFSYTMHWYRQAGKLEWYAVSYQGNKHY 60
QY 61 ADVYKGFYVRSDNSKNTLYLQNNSLRAEDTAIYYCART---GWLGPFDYWGQGLTVTV 116

Db 61 ADVKGRFTISRDNKNTLYLQNSLRADTAIYYCA-RTGMLGPFDPWGGTTLTVSS 119

QY 117 S 117

Db 120 S 120

RESULT 2

US-08-331-398A-46
Sequence 46, Application US/08331398A
Patent No. 5608039
GENERAL INFORMATION:
APPLICANT: Pastan, Ira
APPLICANT: Willingham, Mark
APPLICANT: Fitzgerald, David
APPLICANT: Brinkmann, Ulrich
APPLICANT: Pal, Lee
TITLE OF INVENTION: Single Chain B3 Antibody Fusion Proteins
TITLE OF INVENTION: and Their Uses (as amended)
NUMBER OF SEQUENCES: 68
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew
STREET: One Market Plaza, Stewart Street Plaza
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94105-1492
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/331,398A
FILING DATE: 28-OCT-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/767,331
FILING DATE: 30-SEP-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/596,289
FILING DATE: 12-OCT-1990
ATTORNEY/AGENT INFORMATION:
NAME: Hunter, Tom
REGISTRATION NUMBER: 38,498
REFERENCE/DOCKET NUMBER: 015280-126110US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 543-9600
TELEFAX: (415) 543-5043
INFORMATION FOR SEQ ID NO: 46:
SEQUENCE CHARACTERISTICS:
LENGTH: 119 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURE:
NAME/KEY: Protein
LOCATION: 1..119
OTHER INFORMATION: /note="Human fetal immunoglobulin
OTHER INFORMATION: 56P1/CL Variable Heavy chain (V-H)"
US-08-331-398A-46

Query Match 86.3%; Score 546.5; DB 1; Length 119;
Best Local Similarity 88.2%; Pred. No. 1.7e-45;
Matches 105; Conservative 5; Mismatches 8; Indels 1; Gaps 1;

QY 1 QVQLVSSGGGVQVQPGKSLRLSCAASGFTSSITMHWVROAPGKLEWTFISYDGSNKHY 60
Db 1 QVELVESGGGVQVQPGKSLRLSCAASGFTSSITMHWVROAPGKLEWTFISYDGSNKHY 60
QY 61 ADVKGRFTISRDNKNTLYLQNSLRADTAIYYCA-RTGMLGPFDPWGGTTLTVSS 118

Db 61 ADVKGRFTISRDNKNTLYLQNSLRADTAIYYCA-CARRSARTIYFDYWGQTLTVSS 119

RESULT 3

US-08-331-397B-46
Sequence 46, Application US/08331397B
Patent No. 5981726
GENERAL INFORMATION:
APPLICANT: Pastan, Ira
APPLICANT: Benhar, Itai
TITLE OF INVENTION: Chimeric and Mutationally Stabilized Tumor-
TITLE OF INVENTION: Specific Antibody Fragments, Fusion Proteins, and Uses
TITLE OF INVENTION: Thereof
NUMBER OF SEQUENCES: 68
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew
STREET: One Market Plaza, Stewart Street Plaza
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94105-1492
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/331,397B
FILING DATE: 28-OCT-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/767,331
FILING DATE: 30-SEP-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/596,289
FILING DATE: 12-OCT-1990
ATTORNEY/AGENT INFORMATION:
NAME: Hunter, Tom
REGISTRATION NUMBER: 38,498
REFERENCE/DOCKET NUMBER: 015280-126120US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 543-9600
TELEFAX: (415) 543-5043
INFORMATION FOR SEQ ID NO: 46:
SEQUENCE CHARACTERISTICS:
LENGTH: 119 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURE:
NAME/KEY: Protein
LOCATION: 1..119
OTHER INFORMATION: /note="Human fetal immunoglobulin
OTHER INFORMATION: 56P1/CL Variable Heavy chain (V-H)"
US-08-331-397B-46

Query Match 86.3%; Score 546.5; DB 2; Length 119;
Best Local Similarity 88.2%; Pred. No. 1.7e-45;
Matches 105; Conservative 5; Mismatches 8; Indels 1; Gaps 1;

QY 1 QVQLVSSGGGVQVQPGKSLRLSCAASGFTSSITMHWVROAPGKLEWTFISYDGSNKHY 60
Db 1 QVELVESGGGVQVQPGKSLRLSCAASGFTSSITMHWVROAPGKLEWTFISYDGSNKHY 60
QY 61 ADVKGRFTISRDNKNTLYLQNSLRADTAIYYCA-RTGMLGPFDPWGGTTLTVSS 118
Db 61 ADVKGRFTISRDNKNTLYLQNSLRADTAIYYCA-CARRSARTIYFDYWGQTLTVSS 119

RESULT 4
US-08-759-804A-46

Sequence 46, Application US/08759804A
Patent No. 5990296
GENERAL INFORMATION:
APPLICANT: Pastan, Ira
APPLICANT: Millingham, Mark
APPLICANT: Fitzgerald, David J.
APPLICANT: Brinkmann, Ulrich
APPLICANT: Pai, Lee
TITLE OF INVENTION: Tumor-Specific Antibody Fragments,
TITLE OF INVENTION: Fusion Proteins, and Uses Thereof
NUMBER OF SEQUENCES: 68
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/759,804A
FILING DATE: 03-DEC-1996
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/331,398
FILING DATE: 28-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/767,331
FILING DATE: 30-SEP-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/596,289
FILING DATE: 12-OCT-1990
ATTORNEY/AGENT INFORMATION:
NAME: Weber, Ellen L.
REGISTRATION NUMBER: 32,762
REFERENCE/DOCKET NUMBER: 015280-126140US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 46:
SEQUENCE CHARACTERISTICS:
LENGTH: 119 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURE:
NAME/KEY: Protein
LOCATION: 1..119
OTHER INFORMATION: /note="Human fetal immunoglobulin
OTHER INFORMATION: 56P1 CL Variable Heavy chain (V-H)"
US-08-759-804A-46
Query Match 86.3%; Score 546.5; DB 2; Length 119;
Best Local Similarity 88.2%; Pred. No. 1.7e-45;
Matches 105; Conservative 5; Mismatches 8; Indels 1; Gaps 1;
QY 1 QVQLVSGGAVVQPGSRISRLSCAASGFTFSSTYMHVROAPGKGLVETFTSYDGSNKH 60
DB 1 QVQLVSGGAVVQPGSRISRLSCAASGFTFSSTYMHVROAPGKGLVETFTSYDGSNKH 60
QY 61 ADVSKGRTVSRDMSKNTLYIQMNSLRADPTAIYCA-RTGWLGPFDYWGQGITLVVSS 118
DB 61 ADVSKGRTVSRDMSKNTLYIQMNSLRADPTAIYCA-RTGWLGPFDYWGQGITLVVSS 118
Db 61 ADVSKGRTVSRDMSKNTLYIQMNSLRADPTAIYCA-RTGWLGPFDYWGQGITLVVSS 118
RESULT 5
US-09-227-693-46
Sequence 46, Application US/09227693

Patent No. 6287562
GENERAL INFORMATION:
APPLICANT: Pastan, Ira
APPLICANT: BENHAR, Itai
APPLICANT: PADIAN, Eduardo A.
APPLICANT: YUNG, Sun-Hee
APPLICANT: LEE, Byungkook
TITLE OF INVENTION: HUMANIZED TUMOR-SPECIFIC ANTIBODY
TITLE OF INVENTION: FRAGMENTS, FUSION PROTEINS, AND USES THEREOF
NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Kourie and Crew
STREET: Stewart Street Tower, One Market Plaza
CITY: San Francisco
STATE: California
COUNTRY: US
ZIP: 94105-1493
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/227,693
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/331,396
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/767,331
FILING DATE: 30-SEP-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/596,289
FILING DATE: 12-OCT-1990
ATTORNEY/AGENT INFORMATION:
NAME: Weber, Ellen Lauver
REGISTRATION NUMBER: 32,762
REFERENCE/DOCKET NUMBER: 15280-126-1-3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 543-9600
TELEFAX: (415) 543-5043
INFORMATION FOR SEQ ID NO: 46:
SEQUENCE CHARACTERISTICS:
LENGTH: 119 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Protein
LOCATION: 1..119
OTHER INFORMATION: /note="Human fetal immunoglobulin
OTHER INFORMATION: 56P1 CL VH region"
US-09-227-693-46
Query Match 86.3%; Score 546.5; DB 4; Length 119;
Best Local Similarity 88.2%; Pred. No. 1.7e-45;
Matches 105; Conservative 5; Mismatches 8; Indels 1; Gaps 1;
QY 1 QVQLVSGGAVVQPGSRISRLSCAASGFTFSSTYMHVROAPGKGLVETFTSYDGSNKH 60
DB 1 QVQLVSGGAVVQPGSRISRLSCAASGFTFSSTYMHVROAPGKGLVETFTSYDGSNKH 60
QY 61 ADVSKGRTVSRDMSKNTLYIQMNSLRADPTAIYCA-RTGWLGPFDYWGQGITLVVSS 118
DB 61 ADVSKGRTVSRDMSKNTLYIQMNSLRADPTAIYCA-RTGWLGPFDYWGQGITLVVSS 118
Db 61 ADVSKGRTVSRDMSKNTLYIQMNSLRADPTAIYCA-RTGWLGPFDYWGQGITLVVSS 118
RESULT 6
US-09-240-274-9
Sequence 9, Application US/09240274
GENERAL INFORMATION:

APPLICANT: Siegel, Donald L.
TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
FILE REFERENCE: 09596-42U2
CURRENT APPLICATION NUMBER: US/09/240,274
CURRENT FILING DATE: 1999-01-29
EARLIER APPLICATION NUMBER: 60/081,380
EARLIER FILING DATE: 1998-04-10
EARLIER APPLICATION NUMBER: 60/028,550
EARLIER FILING DATE: 1996-10-11
NUMBER OF SEQ ID NOS: 224
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 9
LENGTH: 125
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: anti-Rh(D) chain D03
US-09-240-274-9

Query Match 84.6%; Score 535.5; DB 4; Length 125;
Best Local Similarity 82.4%; Pred. No. 2e-44; Indels 7; Gaps 1;
Matches 103; Conservative 5; Mismatches 10;

QY 1 QVQLVDSGGGVVQPGSRSLRLSCAASGFTFSYTMHWVROAPGKGLMWTFTISYDGSNKHY 60
DB 1 EVQLDSGGGVVQPGSRSLRLSCAASGFTFSYTMHWVROAPGKGLMWTFTISYDGSNKHY 60
QY 61 ADSVKGRFTVSRNSKNTLYLQWNSLRADTAIVYCARFG-----WLGPFYWGQGL 113
DB 61 ADSVKGRFTVSRNSKNTLYLQWNSLRADTAIVYCARFEEVVGVIIMSRKPFYWGQGL 120
QY 114 VTWSS 118
DB 121 VTWSS 125

RESULT 7
US-09-240-274-24
Sequence 24, Application US/09240274
Patent No. 6255455
GENERAL INFORMATION:
APPLICANT: Siegel, Donald L.
TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
FILE REFERENCE: 09596-42U2
CURRENT APPLICATION NUMBER: US/09/240,274
CURRENT FILING DATE: 1999-01-29
EARLIER APPLICATION NUMBER: 60/081,380
EARLIER FILING DATE: 1998-04-10
EARLIER APPLICATION NUMBER: 60/028,550
EARLIER FILING DATE: 1996-10-11
NUMBER OF SEQ ID NOS: 224
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 24
LENGTH: 125
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: anti-Rh(D) chain D20
US-09-240-274-24

Query Match 84.4%; Score 534.5; DB 4; Length 125;
Best Local Similarity 81.6%; Pred. No. 2.5e-44; Indels 7; Gaps 1;
Matches 102; Conservative 6; Mismatches 10;

QY 1 QVQLVDSGGGVVQPGSRSLRLSCAASGFTFSYTMHWVROAPGKGLMWTFTISYDGSNKHY 60
DB 1 EVQLDSGGGVVQPGSRSLRLSCAASGFTFSYTMHWVROAPGKGLMWTFTISYDGSNKHY 60
QY 61 ADSVKGRFTVSRNSKNTLYLQWNSLRADTAIVYCARFG-----WLGPFYWGQGL 113
DB 61 ADSVKGRFTVSRNSKNTLYLQWNSLRADTAIVYCARFEEVVGVIIMSRKPFYWGQGL 120

QY 114 VTWSS 118
DB 121 VTWSS 125

RESULT 8
US-08-211-202-141
Sequence 141, Application US/08211202
Patent No. 5565332
GENERAL INFORMATION:
APPLICANT: HOOGENBOOM, Hendricus Reneus Jacobus Matheus
APPLICANT: BAIER, Michael
APPLICANT: JESPEERS, Laurent Stephane Anne Therese
APPLICANT: WINTER, Gregory Paul
TITLE OF INVENTION: Production of chimeric antibodies - a
NUMBER OF SEQUENCES: 144
CORRESPONDENCE ADDRESS:
ADDRESSEE: David W. Clough, Marshall O'Toole Gerstein Murray &
ADDRESS: Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
FILING DATE: 23-SEP-1992
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9120252.3
FILING DATE: 23-SEP-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9120377.8
FILING DATE: 25-SEP-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9206318.9
FILING DATE: 24-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9206372.6
FILING DATE: 24-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB92/00883
FILING DATE: 15-MAY-1992
ATTORNEY/AGENT INFORMATION:
NAME: David W. Clough
REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 28111/31960
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
TELEFAX: 312-474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 141:
SEQUENCE CHARACTERISTICS:
LENGTH: 116 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-211-202-141

Query Match 83.3%; Score 527.5; DB 1; Length 116;
Best Local Similarity 86.2%; Pred. No. 1.1e-43; Indels 5; Gaps 1;
Matches 100; Conservative 3; Mismatches 8;

QY 1 QVQLVDSGGGVVQPGSRSLRLSCAASGFTFSYTMHWVROAPGKGLMWTFTISYDGSNKHY 60
DB 1 QVQLVDSGGGVVQPGSRSLRLSCAASGFTFSYTMHWVROAPGKGLMWTFTISYDGSNKHY 60

QY 61 ADVYKGRFTVSRDNRKNTLYLQNMNSLRADTAIYYCA-----RTGWLGPFDYWGCG 111
DB 61 ADVYKGRFTISRDNKNTLYLQNMNSLRADTAIYYCAAGRYSCGSCSPFDYWGCG 116

RESULT 9
US-09-025-769B-24

Sequence 24, Application US/09025769B
Patent No. 6300064

GENERAL INFORMATION:

APPLICANT: Knappik, Achim

APPLICANT: Pack, Peter

APPLICANT: 1145, Vic

APPLICANT: Ge, Liming

APPLICANT: Moroney, Simon

APPLICANT: Plueckthun, Andreas

TITLE OF INVENTION: Protein/(Poly)peptide libraries

NUMBER OF SEQUENCES: 373

CORRESPONDENCE ADDRESS:

ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave

STREET: 1251 Avenue of the Americas

CITY: New York

STATE: New York

COUNTRY: USA

ZIP: 10021

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/025,769B

FILING DATE: 18-FEB-1998

PRIOR APPLICATION DATA:

APPLICATION NUMBER: EP 95 11 3021.0

FILING DATE: 18-AUG-1995

ATTORNEY/AGENT INFORMATION:

NAME: James F. Haley, Jr., Esq.

REGISTRATION NUMBER: 27,794

REFERENCE/DOCKET NUMBER: MORPHO/5

TELEPHONE: (212)596-9000

TELEFAX: (212)596-9090

INFORMATION FOR SEQ ID NO: 24:

SEQUENCE CHARACTERISTICS:

LENGTH: 117 amino acids

TYPE: amino acid

STRANDEDNESS:

TOPOLOGY: linear

MOLECULE TYPE: protein

US-09-025-769B-24

Query Match 83.3%; Score 527.5; DB 4; Length 117;

Best Local Similarity 85.6%; Pred. No. 1.1e-43;

Matches 101; Conservative 6; Mismatches 10; Indels 1; Gaps 1;

QY 1 QVQLVSGGAVVQPGKSLRLSCAASGFTFSYTMHWVRQAQPKGLEWVTFISYDGSNKH 60

DB 1 EVQLVESGGGVGVQPGKSLRLSCAASGFTFSYTMHWVRQAQPKGLEWVSVISYDGSNKH 60

QY 61 ADVYKGRFTVSRDNRKNTLYLQNMNSLRADTAIYYCAAGRYSCGSCSPFDYWGCG 118

DB 61 ADVYKGRFTISRDNKNTLYLQNMNSLRADTAIYYCAAGRYSCGSCSPFDYWGCG 117

RESULT 10
US-09-240-274-149

Sequence 149, Application US/09240274

Patent No. 6255455

GENERAL INFORMATION:

APPLICANT: Siegel, Donald L.

TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL

TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF

FILE REFERENCE: 09596-4202

CURRENT APPLICATION NUMBER: US/09/240,274

CURRENT FILING DATE: 1999-01-29

EARLIER APPLICATION NUMBER: 60/081,380

EARLIER FILING DATE: 1998-04-10

EARLIER APPLICATION NUMBER: 60/028,550

EARLIER FILING DATE: 1996-10-11

NUMBER OF SEQ ID NOS: 224

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 149

LENGTH: 126

TYPE: PRT

ORGANISM: Homo sapiens

FEATURE:

OTHER INFORMATION: anti-Rh(D) antibody clone SH39

US-09-240-274-149

Query Match 83.3%; Score 527; DB 4; Length 126;

Best Local Similarity 81.7%; Pred. No. 1.3e-43;

Matches 103; Conservative 5; Mismatches 10; Indels 8; Gaps 2;

QY 1 QVQLVSGGAVVQPGKSLRLSCAASGFTFSYTMHWVRQAQPKGLEWVTFISYDGSNKH 59

DB 1 EVQLVESGGGVGVQPGKSLRLSCAASGFTFSYTMHWVRQAQPKGLEWVAVIWPFGSNKH 60

QY 60 YADSVKGRFTVSRDNRKNTLYLQNMNSLRADTAIYYCAAGRYSCGSCSPFDYWGCG 112

DB 61 YADSVKGRFTISRDNKNTLYLQNMNSLRADTAIYYCAAGRYSCGSCSPFDYWGCG 120

QY 113 LVTWSS 118

DB 121 LVTWSS 126

RESULT 11
US-09-240-274-8

Sequence 8, Application US/09240274

Patent No. 6255455

GENERAL INFORMATION:

APPLICANT: Siegel, Donald L.

TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL

FILE REFERENCE: 09596-4202

CURRENT APPLICATION NUMBER: US/09/240,274

CURRENT FILING DATE: 1999-01-29

EARLIER APPLICATION NUMBER: 60/081,380

EARLIER FILING DATE: 1998-04-10

EARLIER APPLICATION NUMBER: 60/028,550

EARLIER FILING DATE: 1996-10-11

NUMBER OF SEQ ID NOS: 224

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 8

LENGTH: 125

TYPE: PRT

ORGANISM: Homo sapiens

FEATURE:

OTHER INFORMATION: anti-Rh(D) chain D01

US-09-240-274-8

Query Match 82.4%; Score 521.5; DB 4; Length 125;

Best Local Similarity 79.2%; Pred. No. 4.3e-43;

Matches 99; Conservative 10; Mismatches 9; Indels 7; Gaps 1;

QY 1 QVQLVSGGAVVQPGKSLRLSCAASGFTFSYTMHWVRQAQPKGLEWVTFISYDGSNKH 60

DB 1 EVQLVESGGGVGVQPGKSLRLSCAASGFTFSYTMHWVRQAQPKGLEWVAVIWPFGSNKH 60

QY 61 ADVYKGRFTVSRDNRKNTLYLQNMNSLRADTAIYYCAAGRYSCGSCSPFDYWGCG 113

DB 61 ADVYKGRFTISRDNKNTLYLQNMNSLRADTAIYYCAAGRYSCGSCSPFDYWGCG 120

QY 114 VTWSS 118

Db 121 VTWSS 125

RESULT 12
US-09-240-274-20
Sequence 20, Application US/09240274
Patent No. 6255455
GENERAL INFORMATION:
APPLICANT: Siegel, Donald L.
TITLE OF INVENTION: RH(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
FILE REFERENCE: 09596-4202
CURRENT FILING DATE: 1999-01-29
EARLIER APPLICATION NUMBER: 60/081,380
EARLIER FILING DATE: 1998-04-10
EARLIER APPLICATION NUMBER: 60/028,550
NUMBER OF SEQ ID NOS: 224
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 20
LENGTH: 125
TYPE: PRT
ORGANISM: Homo sapiens
OTHER INFORMATION: anti-Rh(D) chain D15
US-09-240-274-20

Query Match 82.4%; Score 521.5; DB 4; Length 125;
Best Local Similarity 79.2%; Pred. No. 4.3e-43;
Matches 99; Conservative 10; Mismatches 9; Indels 7; Gaps 1;

QY 1 QVQLVSGGAVQPGKSLRLSCAASGFTSSITMHWVQAPGKLEWVTFISYDGNKHY 60
DB 1 EVQLLESGGAVQPGKSLRLSCVSGFTFNNYGMHWVQAPGKLEWVAVIMFDGSKNKY 60

QY 61 ADSVKGRTVSRDNSKNTLYLQMSLRADTAIYYCAR-----TGMWGPPYWGQGL 113
DB 61 ADSVKGRTVSRDNSKNTLYLQMSLRADTAIYYCAR-----TGMWGPPYWGQGL 120

QY 114 VTWSS 118
DB 121 VTWSS 125

RESULT 13
US-09-240-274-21
Sequence 21, Application US/09240274
Patent No. 6255455
GENERAL INFORMATION:
APPLICANT: Siegel, Donald L.
TITLE OF INVENTION: RH(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
FILE REFERENCE: 09596-4202
CURRENT FILING DATE: 1999-01-29
EARLIER APPLICATION NUMBER: 60/081,380
EARLIER FILING DATE: 1998-04-10
EARLIER APPLICATION NUMBER: 60/028,550
NUMBER OF SEQ ID NOS: 224
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 21
LENGTH: 125
TYPE: PRT
ORGANISM: Homo sapiens
OTHER INFORMATION: anti-Rh(D) chain D16
US-09-240-274-21

Query Match 82.4%; Score 521.5; DB 4; Length 125;
Best Local Similarity 79.2%; Pred. No. 4.3e-43;
Matches 99; Conservative 10; Mismatches 9; Indels 7; Gaps 1;

Matches 99; Conservative 10; Mismatches 9; Indels 7; Gaps 1;

QY 1 QVQLVSGGAVQPGKSLRLSCAASGFTSSITMHWVQAPGKLEWVTFISYDGNKHY 60
DB 1 EVQLLESGGAVQPGKSLRLSCVSGFTFNNYGMHWVQAPGKLEWVAVIMFDGSKNKY 60

QY 61 ADSVKGRTVSRDNSKNTLYLQMSLRADTAIYYCAR-----TGMWGPPYWGQGL 113
DB 61 ADSVKGRTVSRDNSKNTLYLQMSLRADTAIYYCAR-----TGMWGPPYWGQGL 120

QY 114 VTWSS 118
DB 121 VTWSS 125

RESULT 14
US-09-240-274-22
Sequence 22, Application US/09240274
Patent No. 6255455
GENERAL INFORMATION:
APPLICANT: Siegel, Donald L.
TITLE OF INVENTION: RH(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
FILE REFERENCE: 09596-4202
CURRENT FILING DATE: 1999-01-29
EARLIER APPLICATION NUMBER: 60/081,380
EARLIER FILING DATE: 1998-04-10
EARLIER APPLICATION NUMBER: 60/028,550
NUMBER OF SEQ ID NOS: 224
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 22
LENGTH: 125
TYPE: PRT
ORGANISM: Homo sapiens
OTHER INFORMATION: anti-Rh(D) chain D17
US-09-240-274-22

Query Match 82.4%; Score 521.5; DB 4; Length 125;
Best Local Similarity 79.2%; Pred. No. 4.3e-43;
Matches 99; Conservative 10; Mismatches 9; Indels 7; Gaps 1;

QY 1 QVQLVSGGAVQPGKSLRLSCAASGFTSSITMHWVQAPGKLEWVTFISYDGNKHY 60
DB 1 EVQLLESGGAVQPGKSLRLSCVSGFTFNNYGMHWVQAPGKLEWVAVIMFDGSKNKY 60

QY 61 ADSVKGRTVSRDNSKNTLYLQMSLRADTAIYYCAR-----TGMWGPPYWGQGL 113
DB 61 ADSVKGRTVSRDNSKNTLYLQMSLRADTAIYYCAR-----TGMWGPPYWGQGL 120

QY 114 VTWSS 118
DB 121 VTWSS 125

RESULT 15
US-09-240-274-10
Sequence 10, Application US/09240274
Patent No. 6255455
GENERAL INFORMATION:
APPLICANT: Siegel, Donald L.
TITLE OF INVENTION: RH(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
FILE REFERENCE: 09596-4202
CURRENT FILING DATE: 1999-01-29
EARLIER APPLICATION NUMBER: 60/081,380
EARLIER FILING DATE: 1998-04-10
EARLIER APPLICATION NUMBER: 60/028,550
NUMBER OF SEQ ID NOS: 224

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OM protein - protein search, using sw model

Run on: June 3, 2003, 08:09:29 ; Search time 19.3549 Seconds
(Without alignments)
531.460 Million cell updates/sec

Title: US-09-644-668A-13

Sequence: 1 DIQMTQSPSSLSASVGRVT.....COQYNSYPPTFGQTKVEIK 107

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 73:.*
1: p1r1.*
2: p1r2.*
3: p1r3.*
4: p1r4.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	508	91.4	125	2 S40333	Ig kappa chain V-J
2	505	90.8	107	2 I69017	anti-HIV1 envelope
3	495	89.0	129	2 S40369	Ig kappa chain - h
4	493	88.7	117	2 B21056	Ig kappa chain pre
5	492.5	88.6	124	2 S40336	Ig kappa chain V-J
6	488	87.8	117	1 K1H011	Ig kappa chain pre
7	488	87.8	117	2 S40331	Ig kappa chain V-J
8	487	87.6	123	2 S40331	Ig kappa chain - h
9	487	87.6	125	2 S40332	Ig kappa chain V-J
10	487	87.6	131	2 S40332	Ig kappa chain V-J
11	485	87.2	117	2 S46371	Ig kappa chain V-J
12	483	86.9	128	2 S46371	Ig kappa chain V-J
13	481	86.5	132	2 S40334	Ig kappa chain var
14	480	86.3	107	2 S36264	Ig kappa chain - h
15	479.5	86.2	108	2 S30521	Ig lambda chain V
16	479	86.2	108	2 B49047	Ig kappa chain V r
17	478.5	86.1	107	2 S36275	Ig kappa chain V
18	478	86.0	108	1 K1H011	Ig kappa chain V-I
19	478	86.0	132	2 S36264	Ig kappa chain V r
20	477.5	85.9	107	2 S47183	Ig kappa chain - h
21	477	85.8	123	2 S40333	Ig kappa chain V-J
22	477	85.8	125	2 S40336	Ig kappa chain V-J
23	476	85.6	124	2 S40338	Ig kappa chain - h
24	475.5	85.5	108	2 S34007	Ig kappa chain V r
25	475	85.4	107	2 S36262	Ig kappa chain V r
26	475	85.4	127	2 S40367	Ig kappa chain V
27	474	85.3	108	1 K1H011	Ig kappa chain V-J
28	474	85.3	125	2 S40353	Ig kappa chain V-I
29	472	84.9	127	2 S11240	Ig kappa chain V r

30	471	84.7	108	1 K1H011	Ig kappa chain V-I
31	471	84.7	108	1 K1H011	Ig kappa chain V-I
32	471	84.7	129	2 S40317	Ig kappa chain - h
33	470	84.5	117	2 C21056	Ig kappa chain pre
34	470	84.5	141	2 A49134	Ig kappa chain V-I
35	469	84.4	108	1 K1H011	Ig kappa chain V-I
36	469	84.4	108	2 S36277	Ig lambda chain V
37	468	84.2	108	1 K1H011	Ig kappa chain V-I
38	467	84.0	130	2 S40368	Ig kappa chain - h
39	466	83.8	108	2 S19674	Ig kappa chain V r
40	466	83.8	110	2 P00535	Ig kappa chain V r
41	465.5	83.7	107	1 K1H011	Ig kappa chain V r
42	465	83.6	105	2 S36266	Ig kappa chain V-I
43	464	83.5	107	2 S36269	Ig lambda chain V
44	464	83.5	117	2 S21527	Ig kappa chain V
45	462	83.1	108	1 K1H011	Ig kappa chain pre

ALIGNMENTS

RESULT 1

S40333
Ig kappa chain V-J region - human
C/Species: Homo sapiens (man)
C/Date: 19-May-1994 #sequence_rev150n 26-May-1995 #text_change 21-Jan-2000
C/Accession: S40333

R/Klein, R.; Jernichen, R.; Zachau, H.G.

EUR. J. Immunol. 23, 3248-3271, 1993

A/Title: Expressed human immunoglobulin chi genes and their hypermutation.

A/Reference number: S40312; PMID:94080891; PMID:8258341

A/Accession: S40333

A/Status: preliminary; translation not shown

A/Molecule type: mRNA

A/Residues: 1-125 <K1B>

A/Cross-References: EMBL:X72443; NID:9441354; PIDN:CA51111.1; PID:9441355

C/Superfamily: Immunoglobulin V region; Immunoglobulin homology

C/Keywords: heterocyclamer; immunoglobulin

F.34-108/Domain: immunoglobulin homology <IMM>

Query Match 91.4%; Score 508; DB 2; Length 125;
Best Local Similarity 91.6%; Pred. No. 1.5e-36;
Matches 98; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

Oy 1 DIQMTQSPSSLSASVGRVTITCAASGSSSWLAWOKEKAPKSLIYAASSISQGVPS 60

Db 19 DIQMTQSPSTLSASVGRVITTCASOSISSWLAWOKEKAPKSLIYAASSISQGVPS 78

Oy 61 RFGSGSGTDFLTITISLOPEDFATYCCOQYNSYPPTFGQTKVEIK 107

Db 79 RFGSGSGTDFLTITISLOPEDFATYCCOQYNSYPPTFGQTKVEIK 125

RESULT 2

I69017
anti-HIV1 envelope protein gp120 V3 loop monoclonal antibody L chain V region - human (

C/Species: Homo sapiens (man)
C/Date: 29-May-1998 #sequence_rev150n 29-May-1998 #text_change 21-Jan-2000

C/Accession: I69017

R/Chin, L.T.; Duena, M.; Levi, M.; Hinkula, J.; Wahren, B.; Borrebaeck, C.A.

Immunol. Lett. 44, 25-30, 1995

A/Title: Molecular characterization of a human anti-HIV 1 monoclonal antibody revealed

A/Reference number: I54563; PMID:95237864; PMID:7721339

A/Accession: I69017

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: mRNA

A/Residues: 1-107 <RES>

A/Cross-References: GB:S77140; NID:9913352; PIDN:AAB34102.1; PID:9913353

A/Genes: Ig Vkapra

C/Superfamily: Immunoglobulin V region; Immunoglobulin homology

F.16-90/Domain: immunoglobulin homology <IMM>

Query Match 90.8%; Score 505; DB 2; Length 107;
 Best Local Similarity 92.5%; Pred. No. 2,4e-38;
 Matches 99; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVDGRTVITTCRASQGISWLAAYQKPKSLIYAASLSQGVPS 60
 |||
 DB 1 DIQMTQSPSSLSASVDGRTVITTCRASQGISWLAAYQKPKSLIYAASLSQGVPS 60
 |||
 QY 61 RFSGSGSGTDFTLTISLTSLQPEDPATYCCQYNSTPPTFGQGTVEIK 107
 |||
 DB 61 RFSGSGSGTDFTLTISLTSLQPEDPATYCCQYNSTPPTFGQGTVEIK 107
 |||

RESULT 3

Ig kappa chain - human
 S40369
 C/Species: Homo sapiens (man)
 C/Date: 06-Mar-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
 C/Accession: S40369
 R/Klein, R.; Jaenichen, R.; Zachau, H.G.
 Eur. J. Immunol. 23, 3248-3271, 1993
 A/Title: Expressed human immunoglobulin chi genes and their hypermutation.
 A/Reference number: S40312; PMID:94080891; PMID:8258341
 A/Accession: S40369
 A/Status: preliminary; translation not shown
 A/Molecule type: mRNA
 A/Residues: 1-129 <KLB>
 A/Cross-references: EMBL:X72479; NID:g441426; PIDN:CAA51147.1; PID:g441427
 C/Superfamily: immunoglobulin V region; immunoglobulin homology
 C/Keywords: heterotetramer; immunoglobulin
 F/37-111/Domain: immunoglobulin homology <IMM>

Query Match 89.0%; Score 495; DB 2; Length 129;
 Best Local Similarity 90.7%; Pred. No. 2,3e-37;
 Matches 97; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVDGRTVITTCRASQGISWLAAYQKPKSLIYAASLSQGVPS 60
 |||
 DB 22 DIQMTQSPSSLSASVDGRTVITTCRASQGISWLAAYQKPKSLIYAASLSQGVPS 81
 |||
 QY 61 RFSGSGSGTDFTLTISLTSLQPEDPATYCCQYNSTPPTFGQGTVEIK 107
 |||
 DB 82 RFSGSGSGTDFTLTISLTSLQPEDPATYCCQYNSTPPTFGQGTVEIK 128
 |||

RESULT 4

Ig kappa chain precursor V region (HK134) - human (fragment)
 B21056
 C/Species: Homo sapiens (man)
 C/Date: 03-Aug-1990 #sequence_revision 03-Aug-1990 #text_change 21-Jan-2000
 C/Accession: B21056
 R/Bentley, D.L.; Rabbits, T.H.
 Cell 32, 181-189, 1983
 A/Title: Evolution of immunoglobulin V genes: evidence indicating that recently duplicated
 A/Reference number: A21056; PMID:83129397; PMID:6402305
 A/Accession: B21056
 A/Status: preliminary
 A/Molecule type: DNA
 A/Residues: 1-117 <BEN>
 A/Cross-references: GB:K01323; NID:g185995; PIDN:AAA58930.1; PID:g185996
 C/Superfamily: immunoglobulin V region; immunoglobulin homology
 C/Keywords: heterotetramer; immunoglobulin
 F/38-112/Domain: immunoglobulin homology <IMM>

Query Match 88.7%; Score 493; DB 2; Length 117;
 Best Local Similarity 100.0%; Pred. No. 3,1e-37;
 Matches 95; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVDGRTVITTCRASQGISWLAAYQKPKSLIYAASLSQGVPS 60
 |||
 DB 23 DIQMTQSPSSLSASVDGRTVITTCRASQGISWLAAYQKPKSLIYAASLSQGVPS 82
 |||
 QY 61 RFSGSGSGTDFTLTISLTSLQPEDPATYCCQYNSTPPTFGQGTVEIK 107
 |||

DB 83 RFSGSGSGTDFTLTISLTSLQPEDPATYCCQYNSTPPTFGQGTVEIK 117
 |||

RESULT 5

Ig kappa chain V-J region - human
 S40336
 C/Species: Homo sapiens (man)
 C/Date: 19-May-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
 C/Accession: S40336
 R/Klein, R.; Jaenichen, R.; Zachau, H.G.
 Eur. J. Immunol. 23, 3248-3271, 1993
 A/Title: Expressed human immunoglobulin chi genes and their hypermutation.
 A/Reference number: S40312; PMID:94080891; PMID:8258341
 A/Accession: S40336
 A/Status: preliminary; translation not shown
 A/Molecule type: mRNA
 A/Residues: 1-124 <KLB>
 A/Cross-references: EMBL:X72446; NID:g441360; PIDN:CAA5114.1; PID:g441361
 C/Superfamily: immunoglobulin V region; immunoglobulin homology
 C/Keywords: heterotetramer; immunoglobulin
 F/31-105/Domain: immunoglobulin homology <IMM>

Query Match 88.6%; Score 492.5; DB 2; Length 124;
 Best Local Similarity 89.8%; Pred. No. 3,7e-37;
 Matches 97; Conservative 6; Mismatches 4; Indels 1; Gaps 1;

QY 1 DIQMTQSPSSLSASVDGRTVITTCRASQGISWLAAYQKPKSLIYAASLSQGVPS 60
 |||
 DB 16 DIQMTQSPSSLSASVDGRTVITTCRASQGISWLAAYQKPKSLIYAASLSQGVPS 75
 |||
 QY 61 RFSGSGSGTDFTLTISLTSLQPEDPATYCCQYNSTPPTFGQGTVEIK 107
 |||
 DB 76 RFSGSGSGTDFTLTISLTSLQPEDPATYCCQYNSTPPTFGQGTVEIK 123
 |||

RESULT 6

Ig kappa chain precursor V-I region (HK101) - human
 K1H011
 C/Species: Homo sapiens (man)
 C/Date: 31-Mar-1981 #sequence_revision 31-Mar-1981 #text_change 24-Sep-1999
 C/Accession: A01881; A21056
 R/Bentley, D.L.; Rabbits, T.H.
 Nature 288, 730-733, 1980
 A/Title: Human immunoglobulin variable region genes - DNA sequences of two V-kappa
 A/Reference number: A93241; PMID:81098966; PMID:6779204
 A/Accession: A01881
 A/Molecule type: DNA
 A/Residues: 1-117 <BEN1>
 A/Cross-references: GB:V00558; GB:J00244; GB:J00246; NID:g33176; PIDN:CAA23824.1; PID:V00558
 A/Note: the sequence was determined from the germline gene
 R/Bentley, D.L.; Rabbits, T.H.
 Cell 32, 181-189, 1983
 A/Title: Evolution of immunoglobulin V genes: evidence indicating that recently dupl
 A/Reference number: A21056; PMID:83129397; PMID:6402305
 A/Accession: A21056
 A/Molecule type: DNA
 A/Residues: 1-117 <BEN2>
 A/Cross-references: GB:K01322; NID:g185993; PIDN:AAA58930.1; PID:g185994
 C/Genetics:
 A/Status: preliminary
 A/Map position: 2p12-2p12
 A/Intron: 19/1
 C/Complex: An immunoglobulin heterotetramer subunit consists of two identical light
 chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate int
 C/Superfamily: immunoglobulin V region; immunoglobulin homology
 C/Keywords: heterotetramer
 F/1-22/Domain: signal sequence #status predicted <SIG>
 F/23-117/Product: Ig kappa chain V-I region (HK101) #status predicted <MAT>
 F/38-112/Domain: immunoglobulin homology <IMM>
 F/45-110/Disulfide bonds: #status predicted

```
Query Match      67.8%; Score 488; DB 1; Length 117;
Best Local Similarity 98.9%; Pred. No. 8.8e-37;
Matches 94; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 DIOMTQSPSSLSASVGRVITTCRASQGISISWLAAYQOKPEKAPKSLIYAASLSQGVPS 60
Db 23 DIOMTQSPSSLSASVGRVITTCRASQGISISWLAAYQOKPEKAPKSLIYAASLSQGVPS 82

OY 61 RFGSGSGTDFTLTISLQPEDPATYCCQYNSYPPTFGGTKEIK 95
Db 83 RFGSGSGTDFTLTISLQPEDPATYCCQYNSYP 117

RESULT 7
S46376
Ig kappa chain V-J region (T33-14) - human (fragment)
C/Species: Homo sapiens (man)
C/Date: 27-Jan-1995 #sequence_revision 01-Sep-1995 #text_change 21-Jan-2000
C/Accession: S46376; S38649
R/Bensimon, C.; Chastagner, P.; Zouali, M.
EMBO J. 13, 2951-2962, 1994
A/Title: Human lupus anti-DNA autoantibodies undergo essentially primary V(chI) gene ree
A/Reference number: S46369; MUID:94313975; PMID:8039491
A/Accession: S46376
A/Molecule type: mRNA
A/Residues: 1-117 <KLE>
A/Cross-references: EMBL:Z27177; NID:9415969; PIDN:CA51701.1; PID:9415970
C/Superfamily: Immunoglobulin V region; Immunoglobulin homology
C/Keywords: heterotetramer; Immunoglobulin
F/25-99/Domain: Immunoglobulin homology <IMM>

Query Match      87.8%; Score 488; DB 2; Length 117;
Best Local Similarity 88.8%; Pred. No. 8.8e-37;
Matches 95; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

OY 1 DIOMTQSPSSLSASVGRVITTCRASQGISISWLAAYQOKPEKAPKSLIYAASLSQGVPS 60
Db 10 DIOMTQSPSSLSASVGRVITTCRASQDISWLAAYQOKPEKAPKSLIYAASLSQGVPL 69

OY 61 RFGSGSGTDFTLTISLQPEDPATYCCQYNSYPPTFGGTKEIK 107
Db 70 RFGSGSGTDFTLTISLQPEDPATYCCQYNSYPPTFGGTKEIK 116

RESULT 8
S40331
Ig kappa chain - human
C/Species: Homo sapiens (man)
C/Date: 06-Mar-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C/Accession: S40331
R/Klein, R.; Jaenichen, R.; Zachau, H.G.
Eur. J. Immunol. 23, 3248-3271, 1993
A/Title: Expressed human immunoglobulin chi genes and their hypermutation.
A/Reference number: S40312; MUID:94080891; PMID:8258341
A/Accession: S40331
A/Molecule type: mRNA
A/Status: preliminary; translation not shown
A/Residues: 1-123 <KLE>
A/Cross-references: EMBL:X72441; NID:9441350; PIDN:CA51109.1; PID:9441351
C/Superfamily: Immunoglobulin V region; Immunoglobulin homology
C/Keywords: heterotetramer; Immunoglobulin
F/32-106/Domain: Immunoglobulin homology <IMM>

Query Match      87.6%; Score 487; DB 2; Length 123;
Best Local Similarity 91.6%; Pred. No. 1.1e-36;
Matches 98; Conservative 1; Mismatches 8; Indels 0; Gaps 0;

OY 1 DIOMTQSPSSLSASVGRVITTCRASQGISISWLAAYQOKPEKAPKSLIYAASLSQGVPS 60
Db 17 DIOMTQSPSSLSASVGRVITTCRASQGISISWLAAYQOKPEKAPKSLIYAASLSQGVPS 76

OY 61 RFGSGSGTDFTLTISLQPEDPATYCCQYNSYPPTFGGTKEIK 107
Db 61 RFGSGSGTDFTLTISLQPEDPATYCCQYNSYPPTFGGTKEIK 107
```

```
Db 77 RFGSGSGTDFTLTISLQPEDPATYCCQYNSYPPTFGGTKEIK 123

RESULT 9
S40349
Ig kappa chain V-J region - human
C/Species: Homo sapiens (man)
C/Date: 19-May-1994 #sequence_revision 21-Jul-1995 #text_change 21-Jan-2000
C/Accession: S40349
R/Klein, R.; Jaenichen, R.; Zachau, H.G.
Eur. J. Immunol. 23, 3248-3271, 1993
A/Title: Expressed human immunoglobulin chi genes and their hypermutation.
A/Reference number: S40312; MUID:94080891; PMID:8258341
A/Accession: S40349
A/Molecule type: mRNA
A/Status: preliminary; translation not shown
A/Residues: 1-125 <KLE>
A/Cross-references: EMBL:X72459; NID:9441386; PIDN:CA51127.1; PID:9441387
C/Superfamily: Immunoglobulin V region; Immunoglobulin homology
C/Keywords: heterotetramer; Immunoglobulin
F/33-107/Domain: Immunoglobulin homology <IMM>

Query Match      87.6%; Score 487; DB 2; Length 125;
Best Local Similarity 90.6%; Pred. No. 1.2e-36;
Matches 96; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

OY 2 DIOMTQSPSSLSASVGRVITTCRASQGISISWLAAYQOKPEKAPKSLIYAASLSQGVPSR 61
Db 19 DIOMTQSPSSLSASVGRVITTCRASQGISISWLAAYQOKPEKAPKSLIYAASLSQGVPSR 78

OY 62 RFGSGSGTDFTLTISLQPEDPATYCCQYNSYPPTFGGTKEIK 107
Db 79 RFGSGSGTDFTLTISLQPEDPATYCCQYNSYPPTFGGTKEIK 124

RESULT 10
S40352
Ig kappa chain V-J-C region - human
C/Species: Homo sapiens (man)
C/Date: 19-May-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C/Accession: S40352
R/Klein, R.; Jaenichen, R.; Zachau, H.G.
Eur. J. Immunol. 23, 3248-3271, 1993
A/Title: Expressed human immunoglobulin chi genes and their hypermutation.
A/Reference number: S40312; MUID:94080891; PMID:8258341
A/Accession: S40352
A/Molecule type: mRNA
A/Status: preliminary; translation not shown
A/Residues: 1-131 <KLE>
A/Cross-references: EMBL:X72462; NID:9441392; PIDN:CA51130.1; PID:9441393
C/Superfamily: Immunoglobulin V region; Immunoglobulin homology
C/Keywords: heterotetramer; Immunoglobulin
F/36-110/Domain: Immunoglobulin homology <IMM>

Query Match      87.6%; Score 487; DB 2; Length 131;
Best Local Similarity 88.8%; Pred. No. 1.2e-36;
Matches 95; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

OY 1 DIOMTQSPSSLSASVGRVITTCRASQGISISWLAAYQOKPEKAPKSLIYAASLSQGVPS 60
Db 21 DIOMTQSPSSLSASVGRVITTCRASQGISISWLAAYQOKPEKAPKSLIYAASLSQGVPS 80

OY 61 RFGSGSGTDFTLTISLQPEDPATYCCQYNSYPPTFGGTKEIK 107
Db 81 RFGSGSGTDFTLTISLQPEDPATYCCQYNSYPPTFGGTKEIK 127

RESULT 11
S46371
Ig kappa chain V-J region (T24-3) - human (fragment)
C/Species: Homo sapiens (man)
C/Date: 27-Jan-1995 #sequence_revision 01-Sep-1995 #text_change 21-Jan-2000
C/Accession: S46371; S38645
```

R.Bensimon, C.; Chaetagner, P.; Zouali, M.
EMBO J. 13, 2951-2962, 1994
A>Title: Human lupus anti-DNA autoantibodies undergo essentially primary V(chi) gene recombination
A/Reference number: S46371
A/Accession: S46371
A/Molecule type: mRNA
A/Residues: 1-117 <BEN>
A/Cross-references: EMBL:Z27172; NID:G415959; PIDN:CAA81696.1; PID:G415960
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin
F/23-97/Domain: immunoglobulin homology <IMM>

Query Match 87.2%; Score 485; DB 2; Length 117;
Best Local Similarity 86.2%; Pred. No. 1.6e-36;
Matches 94; Conservative 8; Mismatches 5; Indels 2; Gaps 1;

QY 1 DIOMTQSPSSLSASVGDRTVITTCRASQGISWLAAYQOKPEKAPKSLIYAASLSQGVPS 60
DB 8 DIOMTQSPSSLSASVGDRTVITTCRASRSISWLAAYQOKPEKAPKSLIYAASLSQGVPS 67
QY 61 RFGSGSGTDFLTITSSLOPEDPATYCCQVNSYPTFGQGTKEIK 107
DB 68 RFGSGSGTDFLTITSSLOPEDPATYCCQVNSYPTFGQGTKEIK 116

RESULT 12

IG light chain variable region (VJ) - human
C/Species: Homo sapiens (man)
C/Date: 07-May-1995 #sequence_revision 21-Jul-1995 #text_change 21-Jan-2000
A/Accession: S46372
R.Bensimon, C.; Chaetagner, P.; Zouali, M.
EMBO J. 13, 2951-2962, 1994
A>Title: Human lupus anti-DNA autoantibodies undergo essentially primary V(chi) gene recombination
A/Reference number: S46372
A/Accession: S46372
A/Molecule type: mRNA
A/Residues: 1-128 <BEN>
A/Cross-references: EMBL:Z27173
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: immunoglobulin
F/36-110/Domain: immunoglobulin homology <IMM>

Query Match 86.9%; Score 483; DB 2; Length 128;
Best Local Similarity 89.6%; Pred. No. 2.7e-36;
Matches 95; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

QY 2 IOMTQSPSSLSASVGDRTVITTCRASQGISWLAAYQOKPEKAPKSLIYAASLSQGVPS 61
DB 22 IITQSPSSLSASVGDRTVITTCRASGISWLAAYQOKPEKAPKSLIYAASLSQGVPS 81
QY 62 RFGSGSGTDFLTITSSLOPEDPATYCCQVNSYPTFGQGTKEIK 107
DB 82 RFGSGSGTDFLTITSSLOPEDPATYCCQVNSYPTFGQGTKEIK 127

RESULT 13

IG kappa chain - human
C/Species: Homo sapiens (man)
C/Date: 06-Mar-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
A/Accession: S40334
R.Klein, R.; Jaenichen, R.; Zachau, H.G.
Eur. J. Immunol. 23, 3248-3271, 1993
A>Title: Expressed human immunoglobulin chi genes and their hypermutation.
A/Reference number: S40334; MUID:94080891; PMID:8258341
A/Accession: S40334
A/Status: preliminary
A/Status: preliminary; translation not shown
A/Molecule type: mRNA
A/Residues: 1-132 <KLB>
A/Cross-references: EMBL:X72444
C/Superfamily: immunoglobulin V region; immunoglobulin homology

Query Match 86.2%; Score 479.5; DB 2; Length 108;
Best Local Similarity 87.9%; Pred. No. 4.6e-36;
Matches 94; Conservative 6; Mismatches 6; Indels 1; Gaps 1;

C/Keywords: heterotetramer; immunoglobulin
F/37-111/Domain: immunoglobulin homology <IMM>

Query Match 86.5%; Score 481; DB 2; Length 132;
Best Local Similarity 86.0%; Pred. No. 4.2e-36;
Matches 92; Conservative 9; Mismatches 6; Indels 0; Gaps 0;

QY 1 DIOMTQSPSSLSASVGDRTVITTCRASQGISWLAAYQOKPEKAPKSLIYAASLSQGVPS 60
DB 22 DIOMTQSPSSLSASVGDRTVITTCRASQGISWLAAYQOKPEKAPKSLIYAASLSQGVPS 81
QY 61 RFGSGSGTDFLTITSSLOPEDPATYCCQVNSYPTFGQGTKEIK 107
DB 82 RFGSGSGTDFLTITSSLOPEDPATYCCQVNSYPTFGQGTKEIK 128

RESULT 14

IG lambda chain V region (clone alpha-CEA-8A) - human (fragment)
C/Species: Homo sapiens (man)
C/Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 21-Jan-2000
A/Accession: S36264
R.Grieffels, A.D.; Malmqvist, M.; Marks, J.D.; Bye, J.M.; Embleton, M.J.; McCafferty, J.
EMBO J. 12, 725-734, 1993
A>Title: Human anti-self antibodies with high specificity from phage display library
A/Reference number: S36256; MUID:93178448; PMID:7679990
A/Accession: S36264
A/Status: preliminary; nucleic acid sequence not shown
A/Molecule type: mRNA
A/Residues: 1-107 <GRI>
A/Cross-references: EMBL:Z18645; NID:G33426; PIDN:CAA79297.1; PID:G939919
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin
F/16-90/Domain: immunoglobulin homology <IMM>

Query Match 86.3%; Score 480; DB 2; Length 107;
Best Local Similarity 87.9%; Pred. No. 4.1e-36;
Matches 94; Conservative 6; Mismatches 7; Indels 0; Gaps 0;

QY 1 DIOMTQSPSSLSASVGDRTVITTCRASQGISWLAAYQOKPEKAPKSLIYAASLSQGVPS 60
DB 1 EIVLTQSPSSLSASVGDRTVITTCRASQGISWLAAYQOKPEKAPKSLIYAASLSQGVPS 60
QY 61 RFGSGSGTDFLTITSSLOPEDPATYCCQVNSYPTFGQGTKEIK 107
DB 61 RFGSGSGTDFLTITSSLOPEDPATYCCQVNSYPTFGQGTKEIK 107

RESULT 15

IG kappa chain V region - human
C/Species: Homo sapiens (man)
C/Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 21-Jan-2000
A/Accession: S30521
R.Mariette, X.
submitted to the EMBL Data Library, October 1992
A/Reference number: S30520
A/Accession: S30521
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-108 <MAR>
A/Cross-references: EMBL:Z18327
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin
F/16-90/Domain: immunoglobulin homology <IMM>

Query Match 86.2%; Score 479.5; DB 2; Length 108;
Best Local Similarity 87.9%; Pred. No. 4.6e-36;
Matches 94; Conservative 6; Mismatches 6; Indels 1; Gaps 1;

QY 1 DIOMTQSPSSLSASVGDRTVITTCRASQGISWLAAYQOKPEKAPKSLIYAASLSQGVPS 60
DB 1 DIOMTQSPSSLSASVGDRTVITTCRASQGISWLAAYQOKPEKAPKSLIYAASLSQGVPS 60

QY 61 RPSGSGSTDFLTITISSLOPEDPATYCCOONSYP-TRGQTKVBI 106
Db 61 RPSGSGSGTEFTLTITISSLOPEDPATYCCOONSYPYTFGQTKLEI 107

Search completed: June 3, 2003, 08:22:38
Job time : 19.3549 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 3, 2003, 08:02:44 ; Search time 9.86007 seconds

(without alignments)
450.095 Million cell updates/sec

Title: US-09-644-668a-13

Perfect score: 556

Sequence: 1 DIQMTQSPSSLSASVGDRVT.....CQYNSYPPTFGQTKVEIK 107

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	488	87.8	117	KV1I_HUMAN	P01601 homo sapien
2	478	86.0	108	KV1V_HUMAN	P04430 homo sapien
3	474	85.3	108	KV1G_HUMAN	P01599 homo sapien
4	471	84.7	108	KV1F_HUMAN	P01598 homo sapien
5	471	84.7	108	KV1L_HUMAN	P01604 homo sapien
6	469	84.4	108	KV1R_HUMAN	P01610 homo sapien
7	468	84.2	108	KV1H_HUMAN	P01600 homo sapien
8	465.5	83.7	107	KV1D_HUMAN	P01596 homo sapien
9	462	83.1	108	KV1S_HUMAN	P01605 homo sapien
10	455	81.8	129	KV1S_HUMAN	P01611 homo sapien
11	451	81.1	129	KV1M_HUMAN	P04431 homo sapien
12	448	80.6	117	KV1J_HUMAN	P01602 homo sapien
13	445	80.0	108	KV1B_HUMAN	P01594 homo sapien
14	442	79.5	108	KV1A_HUMAN	P01593 homo sapien
15	442	79.5	108	KV1K_HUMAN	P01603 homo sapien
16	440	79.1	108	KV1Y_HUMAN	P01607 homo sapien
17	439	79.0	108	KV1Y_HUMAN	P01603 homo sapien
18	438	78.8	108	KV1N_HUMAN	P01608 homo sapien
19	437	78.6	108	KV1E_HUMAN	P01608 homo sapien
20	434	78.1	108	KV1E_HUMAN	P01597 homo sapien
21	429	77.2	108	KV1Q_HUMAN	P01609 homo sapien
22	426	76.6	108	KV1C_HUMAN	P01595 homo sapien
23	421	75.7	129	KV1X_HUMAN	P04432 homo sapien
24	408.5	73.5	109	KV1F_HUMAN	P01624 homo sapien
25	405	72.8	112	KV1T_HUMAN	P01613 homo sapien
26	404.5	72.8	109	KV1T_HUMAN	P01612 homo sapien
27	402	72.3	108	KV1J_HUMAN	P01643 mus musculu
28	400.5	72.0	109	KV1D_HUMAN	P01622 mus musculu
29	399.5	71.9	129	KV1L_HUMAN	P01613 mus musculu
30	396.5	71.3	109	KV1B_HUMAN	P01620 mus musculu
31	396	71.2	108	KV1E_HUMAN	P01644 mus musculu
32	395.5	71.1	129	KV1H_HUMAN	P04207 mus musculu
33	394.5	71.0	129	KV1M_HUMAN	P01613 mus musculu

34	391	70.3	108	1	KV1E_MOUSE	P01645 mus musculu
35	391	70.3	108	1	KV1D_MOUSE	P01648 mus musculu
36	390.5	70.2	109	1	KV1E_HUMAN	P01623 mus musculu
37	386	69.4	108	1	KV1M_MOUSE	P01646 mus musculu
38	386	69.4	134	1	KV1C_HUMAN	P06314 mus musculu
39	384	69.1	108	1	KV1N_MOUSE	P01647 mus musculu
40	384	69.1	128	1	KV1E_MOUSE	P01637 mus musculu
41	383	68.9	108	1	KV1D_MOUSE	P01636 mus musculu
42	382	68.7	108	1	KV1S_MOUSE	P01652 mus musculu
43	381	68.5	114	1	KV1A_HUMAN	P01625 mus musculu
44	381	68.5	149	1	KV1A_MOUSE	P01633 mus musculu
45	380	68.3	108	1	KV1P_MOUSE	P01649 mus musculu

ALIGNMENTS

RESULT 1
KV1I_HUMAN STANDARD, PRT, 117 AA.
AC P01601;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-I region HK101 precursor (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_Taxid=9606;
RN (1)
RP SEQUENCE FROM N.A.
RX MEDLINE=81098966; PubMed=6779204;
RA Bentley D.L., Rabbits T.H.;
RT "Human immunoglobulin variable region genes -- DNA sequences of two V
kappa genes and a pseudogene".
RT Nature 288:730-733(1980).
RN (2)
RP SEQUENCE FROM N.A.
RX MEDLINE=83129397; PubMed=6402305;
RA Bentley D.L., Rabbits T.H.;
RT "Evolution of immunoglobulin V genes: evidence indicating that
recently duplicated human V kappa sequences have diverged by gene
conversion".
RT Cell 32:181-189(1983).
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CC
EMBL; K01322; AA58930.1; -
EMBL; K01324; AA58932.1; -
EMBL; V00558; CAA23824.1; -
DR PIR; A01881; K1HVL1.
DR PIR; A21056; A21056.
DR HSSP; P01607; IRR1.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF00047; IG_1.
DR SMART; SM00406; IG_1.
KW Immunoglobulin V region, signal.
FT SIGNAL
FT CHAIN
FT 1
FT 22
FT 23
FT 23
FT 45
FT 46
FT 56
FT 71
FT 72
FT 78
FT 79
FT 110
FT 111
FT >117
FT 110
FT DISULFID 45
FT 110
IG KAPPA CHAIN V-I REGION HK101.
FRAMEWORK-1.
COMPLEMENTARITY-DETERMINING-1.
FRAMEWORK-2.
COMPLEMENTARITY-DETERMINING-2.
FRAMEWORK-3.
COMPLEMENTARITY-DETERMINING-3.
BY SIMILARITY.

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FT   NON TER      117      117
SQ   SEQUENCE      117 AA; 12799 MW; D7D0FP3718CFE587 CRC64;
Query Match
Best Local Similarity 87.8%; Score 488; DB 1; Length 117;
Matches 94; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGDRTVITTCRASQGISWLAHYQOKPEKAPKSLIYAASLSGVS 60
    |||
DB 23 DIQMTQSPSSLSASVGDRTVITTCRASQGISWLAHYQOKPEKAPKSLIYAASLSGVS 82
    |||

QY 61 RFGSGSGTDPFTLTISLQPEDPATYYCCQYNSYP 95
    |||
DB 83 RFGSGSGTDPFTLTISLQPEDPATYYCCQYNSYP 117
    |||

RESULT 2
KVYV_HUMAN STANDARD; PRT; 108 AA.
AC P04430;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DR 15-JUL-1999 (Rel. 38, Last annotation update)
DS Ig kappa chain V-I region BAN.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
ON NCBI_TaxId=9606;
RX MEDLINE=66174817; PubMed=3083240;
RA Dwyer F.E., O'Connor T.P., Benson M.D.;
RT "Polymorphism in a kappa I primary (AL) amyloid protein (BAN).";
RL Mol. Immunol. 23:73-78(1986).
DR PIR; A01878; KIHUEN.
DR HSSP; P80362; 1MTL.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; IgV_1.
DR SMART; SM00406; IgV_1.
KW Immunoglobulin V region; Amyloid.
FT DOMAIN 1 23 FRAMEWORK-1.
FT DOMAIN 2 34 FRAMEWORK-2.
FT DOMAIN 3 49 FRAMEWORK-3.
FT DOMAIN 4 56 FRAMEWORK-4.
FT DOMAIN 5 57 FRAMEWORK-5.
FT DOMAIN 6 58 FRAMEWORK-6.
FT DOMAIN 7 59 FRAMEWORK-7.
FT DOMAIN 8 60 FRAMEWORK-8.
FT DISULFID 98 107 FRAMEWORK-4.
FT DISULFID 108 108 BY SIMILARITY.
SQ SEQUENCE 108 AA; 11840 MW; CD3FD944F836FD37 CRC64;

Query Match
Best Local Similarity 86.0%; Score 478; DB 1; Length 108;
Matches 91; Conservative 9; Mismatches 7; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGDRTVITTCRASQGISWLAHYQOKPEKAPKSLIYAASLSGVS 60
    |||
DB 1 DIQMTQSPSSLSASVGDRTVITTCRASQGISWLAHYQOKPEKAPKSLIYAASLSGVS 60
    |||

QY 61 RFGSGSGTDPFTLTISLQPEDPATYYCCQYNSYP 107
    |||
DB 61 RFGSGSGTDPFTLTISLQPEDPATYYCCQYNSYP 107
    |||

RESULT 3
KVYV_HUMAN STANDARD; PRT; 108 AA.
AC P01599;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DR 15-JUL-1999 (Rel. 38, Last annotation update)
DS Ig kappa chain V-I region GAL.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
ON NCBI_TaxId=9606;
RX MEDLINE=71064027; PubMed=4923144;
RA Gell W.E., Edelman G.M.;
RT "The covalent structure of a human gamma G-immunoglobulin. X.
RT Intrachain disulfide bonds.";
RT Biochemistry 9:3188-3196(1970).
CC -1- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.

```

```

OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
ON NCBI_TaxId=9606;
RX MEDLINE=75059122; PubMed=4215718;
RA Laue C.J., Watanabe S., Hilschmann N.;
RT "The primary structure of a monoclonal IgM-immunoglobulin
RT (macroglobulin Gal.), I. The amino acid sequence of the L-chain of
RT kappa-type, subgroup I.";
RT Hoppe-Sayler's Z. Physiol. Chem. 354:1503-1504(1973).
CC -1- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A WALDENSTROM'S
CC MACROGLOBULIN.
DR PIR; A01867; KIHUEN.
DR HSSP; P01607; IRET.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; IgV_1.
DR SMART; SM00406; IgV_1.
KW Immunoglobulin V region.
FT DOMAIN 1 23 FRAMEWORK-1.
FT DOMAIN 2 34 FRAMEWORK-2.
FT DOMAIN 3 49 FRAMEWORK-3.
FT DOMAIN 4 56 FRAMEWORK-4.
FT DOMAIN 5 57 FRAMEWORK-5.
FT DOMAIN 6 58 FRAMEWORK-6.
FT DOMAIN 7 59 FRAMEWORK-7.
FT DOMAIN 8 60 FRAMEWORK-8.
FT DISULFID 98 107 FRAMEWORK-4.
FT DISULFID 108 108 BY SIMILARITY.
SQ SEQUENCE 108 AA; 11814 MW; C1AD3CB0F60DF73 CRC64;

Query Match
Best Local Similarity 85.3%; Score 474; DB 1; Length 108;
Matches 93; Conservative 5; Mismatches 9; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGDRTVITTCRASQGISWLAHYQOKPEKAPKSLIYAASLSGVS 60
    |||
DB 1 DIQMTQSPSSLSASVGDRTVITTCRASQGISWLAHYQOKPEKAPKSLIYAASLSGVS 60
    |||

QY 61 RFGSGSGTDPFTLTISLQPEDPATYYCCQYNSYP 107
    |||
DB 61 RFGSGSGTDPFTLTISLQPEDPATYYCCQYNSYP 107
    |||

RESULT 4
KVYF_HUMAN STANDARD; PRT; 108 AA.
AC P01598;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DR 15-JUL-1999 (Rel. 38, Last annotation update)
DS Ig kappa chain V-I region EU.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
ON NCBI_TaxId=9606;
RX MEDLINE=71064023; PubMed=5489770;
RA Gottlieb P.D., Cunningham B.A., Rutishauser U., Edelman G.M.;
RT "The covalent structure of a human gamma G-immunoglobulin. VI. Amino
RT acid sequence of the light chain.";
RT Biochemistry 9:3155-3161(1970).
CC -1- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.

```

CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN.
 DR PIR; A01866; K1HHEU.
 DR HSSP; P01607; 1RE1.
 DR InterPro; IPR003006; IG_MHC.
 DR InterPro; IPR003596; IG_V.
 DR Pfam; PF00047; 1G; 1.
 DR SMART; SM00406; IGV; 1.
 DR Immunoglobulin V region.
 FT DOMAIN 1 23
 FT DOMAIN 24 34
 FT DOMAIN 35 49
 FT DOMAIN 50 56
 FT DOMAIN 57 88
 FT DOMAIN 89 97
 FT DOMAIN 98 107
 FT DISULFID 23 88
 FT NON TER 108 108
 SQ SEQUENCE 108 AA; 11788 MW; 9CD294F2AD8823 CRC64;
 Query Match 84.7%; Score 471; DB 1; Length 108;
 Best Local Similarity 84.1%; Pred. No. 5.1e-42;
 Matches 90; Conservative 8; Mismatches 9; Indels 0; Gaps 0;
 QY 1 DIQMTQSPSSISASVGDRTVITTCRASQGISWLAAYQOKPEKAPSLIYAASLSQGVPS 60
 1 DIQMTQSPSTLSASVGDRTVITTCRASQGISWLAAYQOKPEKAPSLIYAASLSQGVPS 60
 DB 61 RFSSGSGSTDEFTLTITSLQPEDPATYTCQOYNSYPPTFGCGTKVEIK 107
 61 RFSSGSGSTDEFTLTITSLQPEDPATYTCQOYNSYDMSKMFQGTKEVK 107
 RESULT 5
 KVLH HUMAN STANDARD; PRT; 108 AA.
 ID KVLH HUMAN
 AC P01604;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Ig kappa chain V-I region Kue.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 NC NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=79237924; PubMed=112021;
 RA Eulitz M., Kley H.-P., Zeltner H.-J.;
 RT "The primary structure of the Bence-Jones protein Kue. The amino acid
 sequence of the variable part of a human L-chain of the kappa-type.";
 HL Hoppe-Seyler's Z. Physiol. Chem. 360:725-734(1979).
 CC -1- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
 CC -1- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.
 DR PIR; A01870; K1HUKU.
 DR HSSP; P01607; 1RE1.
 DR InterPro; IPR003006; IG_MHC.
 DR InterPro; IPR003596; IG_V.
 DR Pfam; PF00047; 1G; 1.
 DR SMART; SM00406; IGV; 1.
 DR Immunoglobulin V region; Bence-Jones protein.
 FT DOMAIN 1 23
 FT DOMAIN 24 34
 FT DOMAIN 35 49
 FT DOMAIN 50 56
 FT DOMAIN 57 88
 FT DOMAIN 89 97
 FT DOMAIN 98 107
 FT DISULFID 23 88
 FT NON TER 108 108
 SQ SEQUENCE 108 AA; 12127 MW; 906679A5D90E4E98 CRC64;
 Query Match 84.7%; Score 471; DB 1; Length 108;
 Best Local Similarity 82.2%; Pred. No. 5.1e-42;

Matches 88; Conservative 11; Mismatches 8; Indels 0; Gaps 0;
 QY 1 DIQMTQSPSSISASVGDRTVITTCRASQGISWLAAYQOKPEKAPSLIYAASLSQGVPS 60
 1 DIQMTQSPSTLSASVGDRTVITTCRASQGISWLAAYQOKPEKAPSLIYAASLSQGVPS 60
 DB 61 RFSSGSGSTDEFTLTITSLQPEDPATYTCQOYNSYPPTFGCGTKVEIK 107
 61 RFSSGSGSTDEFTLTITSLQPEDPATYTCQOYNSYRPPYTFGQTKVDIK 107
 RESULT 6
 KVLH HUMAN STANDARD; PRT; 108 AA.
 ID KVLH HUMAN
 AC P01610;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Ig kappa chain V-I region WEA.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 NC NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=83273707; PubMed=6410398;
 RA Goni F., Frangione B.;
 RT "Amino acid sequence of the Fv region of a human monoclonal IgM
 (protein WEA) with antibody activity against 3,4-pyruvylated
 galactose in Klebsiella polysaccharides K30 and K3.";
 HL Proc. Natl. Acad. Sci. U.S.A. 80:4837-4841(1983).
 CC -1- MISCELLANEOUS: THIS CHAIN WAS OBTAINED FROM A MONOCLONAL ANTIBODY
 AGAINST 3,4-PYRUVYLATED GALACTOSE AND ISOLATED FROM A PATIENT WITH
 WALDENSTROM'S MACROGLOBULINEMIA.
 CC PIR; A01876; K1HUME.
 DR HSSP; P80362; 1MTL.
 DR InterPro; IPR003006; IG_MHC.
 DR InterPro; IPR003596; IG_V.
 DR Pfam; PF00047; 1G; 1.
 DR SMART; SM00406; IGV; 1.
 DR Immunoglobulin V region; Monoclonal antibody.
 FT DOMAIN 1 23
 FT DOMAIN 24 34
 FT DOMAIN 35 49
 FT DOMAIN 50 56
 FT DOMAIN 57 88
 FT DOMAIN 89 97
 FT DOMAIN 98 107
 FT DISULFID 23 88
 FT NON TER 108 108
 SQ SEQUENCE 108 AA; 11840 MW; 9249B61F0945618C CRC64;
 Query Match 84.4%; Score 469; DB 1; Length 108;
 Best Local Similarity 85.0%; Pred. No. 8.1e-42;
 Matches 91; Conservative 7; Mismatches 9; Indels 0; Gaps 0;
 QY 1 DIQMTQSPSSISASVGDRTVITTCRASQGISWLAAYQOKPEKAPSLIYAASLSQGVPS 60
 1 DIQMTQSPSTLSASVGDRTVITTCRASQGISWLAAYQOKPEKAPSLIYAASLSQGVPS 60
 DB 61 RFSSGSGSTDEFTLTITSLQPEDPATYTCQOYNSYPPTFGCGTKVEIK 107
 61 RFSSGSGSTDEFTLTITSLQPEDPATYTCQOYNSYDMSKMFQGTKEVK 107
 RESULT 7
 KVLH HUMAN STANDARD; PRT; 108 AA.
 ID KVLH HUMAN
 AC P01600;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Ig kappa chain V-I region Hau.

OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 NX NCBI_Taxid=9606;
 RN (1)
 RP MEDLINE=71032830; PubMed=4097974;
 RA Watanabe S., Hlischmann N.,
 RT "The primary structure of a monoclonal kappa-type immunoglobulin L-
 chain of subgroup I (Bence-Jones Protein Hau) : subdivision within
 subgroups."
 RL Hope-Seyler's Z. Physiol. Chem. 351:1291-1295(1970).
 CC -1- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
 CC -1- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.
 DR PIR; A01868; K1HMU.
 DR HSSP; P80362; 1WTU.
 DR InterPro; IPR003006; IG_MHC.
 DR Pfam; PF00047; IG_1.
 DR SMART; SM00406; IG_1.
 SQ SEQUENCE 108 AA; 11671 MW; 08D3A6160D8D0618 CRC64;
 Query Match 84.2%; Score 468; DB 1; Length 108;
 Best Local Similarity 86.9%; Pred. No. 1e-41;
 Matches 93; Conservative 5; Mismatches 9; Indels 0; Gaps 0;
 QY 1 DIOMTQSPSSLSASVGDRTVITCRASQGISWLAHYQOKPEKAPSLIYAASLSQGVPS 60
 DB 1 DIOMTQSPSSLSASVGDRTVITCRASQGISWLAHYQOKPEKAPSLIYAASLSQGVPS 60
 QY 61 RFSGSGSGTDFLTITISLOPEDFATYCCQYNSYPPTFGGTVEIK 107
 DB 61 RFSGSGSGTDFLTITISLOPEDFATYCCQYNSYPPTFGGTVEIK 107
 RESULT 8
 KVID_HUMAN STANDARD; PRT; 107 AA.
 AC P01586;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Ig kappa chain V-I region CAR.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 NX NCBI_Taxid=9606;
 RN (1)
 RP MEDLINE=75075135; PubMed=4216454;
 RA Milestein C.P., Deverson B.V.;
 RT "Primary structure of kappa light chain from a human myeloma
 RT protein."
 RL Eur. J. Biochem. 49:377-391(1974).
 CC -1- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (1,2)
 CC MARKER.
 CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN.
 DR PIR; A01864; K1HUR.
 DR HSSP; P80362; 1WTU.
 DR InterPro; IPR003006; IG_MHC.
 DR Pfam; PF00047; IG_1.
 DR SMART; SM00406; IG_1.

KM Immunoglobulin V region; Glycoprotein.
 FT CAROHD 28 28 N-LINKED (GLCNAC. .).
 FT NON TER 107 107
 SQ SEQUENCE 107 AA; 11703 MW; E1BF0DF9844C346 CRC64;
 Query Match 83.7%; Score 465.5; DB 1; Length 107;
 Best Local Similarity 84.1%; Pred. No. 1.9e-41;
 Matches 90; Conservative 9; Mismatches 7; Indels 1; Gaps 1;
 QY 1 DIOMTQSPSSLSASVGDRTVITCRASQGISWLAHYQOKPEKAPSLIYAASLSQGVPS 60
 DB 1 DIOMTQSPSSLSASVGDRTVITCRASQGISWLAHYQOKPEKAPSLIYAASLSQGVPS 60
 QY 61 RFSGSGSGTDFLTITISLOPEDFATYCCQYNSYPPTFGGTVEIK 107
 DB 61 RFSGSGSGTDFLTITISLOPEDFATYCCQYNSYPPTFGGTVEIK 107
 RESULT 9
 KVID_HUMAN STANDARD; PRT; 108 AA.
 AC P01605;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Ig kappa chain V-I region IAY.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 NX NCBI_Taxid=9606;
 RN (1)
 RP MEDLINE=77038198; PubMed=824717;
 RA Capra J.D., Klapper D.G.;
 RT "Complete amino acid sequence of the variable domains of two human
 RT IgM anti-gamma globulins (Lay/Pom) with shared idiotypic
 RT specificities."
 RL Scand. J. Immunol. 5:677-684(1976).
 CC -1- MISCELLANEOUS: THE SECOND AND THIRD. HYPERVARIABLE REGIONS OF THIS
 CC CHAIN ARE IDENTICAL WITH THOSE OF THE HUMAN POM V-III KAPPA CHAIN,
 CC WITH WHICH IT SHARES CERTAIN IDIOTYPIC DETERMINANTS.
 CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGM WITH ANTI-GAMMA
 CC GLOBULIN ACTIVITY.
 DR PIR; A01871; K1HULY.
 DR HSSP; P01607; 1REI.
 DR InterPro; IPR003006; IG_MHC.
 DR Pfam; PF00047; IG_1.
 DR SMART; SM00406; IG_1.
 KW Immunoglobulin V region.
 FT DOMAIN 1 23
 FT DOMAIN 2 34
 FT DOMAIN 3 49
 FT DOMAIN 4 56
 FT DOMAIN 5 57
 FT DOMAIN 6 88
 FT DOMAIN 7 97
 FT DOMAIN 8 107
 FT DISULFID 23 88
 FT NON TER 108 108
 SQ SEQUENCE 108 AA; 11834 MW; 739993A95431434A CRC64;
 Query Match 83.1%; Score 462; DB 1; Length 108;
 Best Local Similarity 80.4%; Pred. No. 4.3e-41;
 Matches 86; Conservative 11; Mismatches 10; Indels 0; Gaps 0;
 QY 1 DIOMTQSPSSLSASVGDRTVITCRASQGISWLAHYQOKPEKAPSLIYAASLSQGVPS 60
 DB 1 DIOMTQSPSSLSASVGDRTVITCRASQGISWLAHYQOKPEKAPSLIYAASLSQGVPS 60
 QY 61 RFSGSGSGTDFLTITISLOPEDFATYCCQYNSYPPTFGGTVEIK 107
 DB 61 RFSGSGSGTDFLTITISLOPEDFATYCCQYNSYPPTFGGTVEIK 107

RESULT 10
KV1S_HUMAN STANDARD; PRT; 108 AA.
AC P01611;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-I region Wes.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
NCBI_TaxID=9606;
[1]
RP SEQUENCE.
RX MEDLINE=81092279; PubMed=6778806;
RA Kretzlin H., Yang C., Krusche J.U., Hilschmann N.;
RT "Preparative separation of the tryptic hydrolyate of a protein by
RT high-pressure liquid chromatography. The primary structure of a
RT monoclonal L-chain of K-type, subgroup I (Bence-Jones Protein
Wes)";
RI Hoppe-Seyler's Z. Physiol. Chem. 361:1591-1598 (1980).
CC -1- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
CC -1- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.
DR PIR: A01877; K1HUMS.
DR HSSP: P80362; 1MTL.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; Ig; 1.
DR SMART; SM00406; IG; 1.
KW Immunoglobulin V region; Bence-Jones protein.
FT DOMAIN 1 23
FT DOMAIN 24 34
FT DOMAIN 35 49
FT DOMAIN 50 56
FT DOMAIN 57 88
FT DOMAIN 89 97
FT DOMAIN 98 107
FT DISULFID 23 88
FT NON TER 108 108
SQ SEQUENCE 108 AA; 11608 MW; 782B14A649A60E45 CRC64;
Query Match 81.8%; Score 455; DB 1; Length 108;
Best Local Similarity 83.2%; Pred. No. 2.3e-40;
Matches 89; Conservative 8; Mismatches 10; Indels 0; Gaps 0;
QY 1 DIOMTQSSSSASVSGDRVTITTCRASQGISISWLMVYQOKPEKAPSLIYAASSLSQGVPS 60
DB 1 DIOMTQSSSSASVSGDRVTITTCRASQGISISWLMVYQOKPEKAPSLIYAASSLSQGVPS 60
QY 61 RFSGSGSGTDFTLTITSSIQPEDPATYVYCOQVNSYPTFGQGTVEIK 107
DB 61 RFSGSGSGTDFTLTITSSIQPEDPATYVYCOQVNSYPTFGQGTVEIK 107
QY 61 RFSGSGSGTDFTLTITSSIQPEDPATYVYCOQVNSYPTFGQGTVEIK 107
DB 61 RFSGSGSGTDFTLTITSSIQPEDPATYVYCOQVNSYPTFGQGTVEIK 107
RESULT 11
KV1W_HUMAN STANDARD; PRT; 129 AA.
AC P04431;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-I region Walker precursor.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
NCBI_TaxID=9606;
[1]
RP SEQUENCE FROM N.A.
RX MEDLINE=85014148; PubMed=6091049;
RA Klobbeck H.G., Combricato G., Zachau H.G.;
RT "Immunoglobulin genes of the kappa light chain type from two human
RT lymphoid cell lines are closely related.";

RL Nucleic Acids Res. 12:6995-7006 (1984).
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; X00965; CAA25477.1; ALT_TERM.
DR PIR: A01883; K1HUMK.
DR HSSP: P01607; 1PRT.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IG; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 22
FT CHAIN 23 129
FT DOMAIN 23 45
FT DOMAIN 46 56
FT DOMAIN 57 71
FT DOMAIN 72 78
FT DOMAIN 79 110
FT DOMAIN 111 119
FT DOMAIN 120 129
FT DISULFID 45 110
FT NON TER 129 129
SQ SEQUENCE 129 AA; 14069 MW; F941FA07D4AF2F9 CRC64;
Query Match 81.1%; Score 451; DB 1; Length 129;
Best Local Similarity 86.0%; Pred. No. 7.3e-40;
Matches 92; Conservative 4; Mismatches 11; Indels 0; Gaps 0;
QY 1 DIOMTQSSSSASVSGDRVTITTCRASQGISISWLMVYQOKPEKAPSLIYAASSLSQGVPS 60
DB 23 DIOMTQSSSSASVSGDRVTITTCRASQGISISWLMVYQOKPEKAPSLIYAASSLSQGVPS 82
QY 61 RFSGSGSGTDFTLTITSSIQPEDPATYVYCOQVNSYPTFGQGTVEIK 107
DB 61 RFSGSGSGTDFTLTITSSIQPEDPATYVYCOQVNSYPTFGQGTVEIK 107
QY 83 RFSGSGSGTDFTLTITSSIQPEDPATYVYCOQVNSYPTFGQGTVEIK 129
DB 83 RFSGSGSGTDFTLTITSSIQPEDPATYVYCOQVNSYPTFGQGTVEIK 129
RESULT 12
KV1J_HUMAN STANDARD; PRT; 117 AA.
AC P01602;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-I region HK102 precursor (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
NCBI_TaxID=9606;
[1]
RP SEQUENCE FROM N.A.
RX MEDLINE=81098966; PubMed=6779204;
RA Bentley D.L., Rabbits T.H.;
RT "Human immunoglobulin variable region genes -- DNA sequences of two V
RT kappa genes and a pseudogene.";
RL Nature 288:730-733 (1980).
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CC
CC EMBL; J00245; AAA59087.1; -

DR EMBL: Z00001; CAA77292.1; -
 DR PIR: A01882; K1H12.
 DR HSSP: P01607; 1RRI.
 DR Genew: H0NC5741; IGK1-5.
 DR InterPro: IPR003006; IG_MHC.
 DR InterPro: IPR003596; IG_V.
 DR Pfam: PF00047; 1g.1.
 DR SMART: SMO0406; 1g.1.
 DR Immunoglobulin V region; signal.
 KM SIGNAL 1 22
 FT CHAIN 1 22
 FT DOMAIN 23 >117 IG KAPPA CHAIN V-I REGION HK102.
 FT DOMAIN 23 45 FRAMEWORK-1.
 FT DOMAIN 46 56 COMPLEMENTARITY-DETERMINING-1.
 FT DOMAIN 57 71 FRAMEWORK-2.
 FT DOMAIN 72 78 COMPLEMENTARITY-DETERMINING-2.
 FT DOMAIN 79 110 FRAMEWORK-3.
 FT DOMAIN 111 >117 COMPLEMENTARITY-DETERMINING-3.
 FT DISULFID 45 110 BY SIMILARITY.
 FT NON TER 117 117
 SQ SEQUENCE 117 AA; 12768 MW; ADIDF3A40AFLA49B CRC64;
 Query Match 80.6%; Score 448; DB 1; Length 117;
 Best Local Similarity 91.5%; Pred. No. 1.3e-39;
 Matches 86; Conservative 4; Mismatches 4; Indels 0; Gaps 0;
 QY 1 DIOMTQSPSSLSASVGDRTVITTCRASQGISWLAHYQOKPEKPKSLIYAASLSQGVPS 60
 DB 23 DIOMTQSPSSLSASVGDRTVITTCRASQGISWLAHYQOKPEKPKSLIYAASLSQGVPS 82
 QY 61 RFGSGSGTDFTLTISLQPEDPATYCCQYNSTPPTFGQTKVEIK 107
 DB 83 RFGSGSGTDFTLTISLQPEDPATYCCQYNSTPPTFGQTKVEIK 116
 Db 83 RFGSGSGTDFTLTISLQPEDPATYCCQYNSTPPTFGQTKVEIK 116
 RESULT 13
 KX1B_HUMAN STANDARD; PRT; 108 AA.
 ID P01594;
 AC P01594;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Ig kappa chain V-I region AG.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_Taxid=9606;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=72189444; PubMed=5028201;
 RA Schiechl H., Hilschmann N.;
 RT "Rule of antibody structure. The primary structure of a monoclonal
 immunoglobulin L-chain of the kappa-type, subgroup I (Bence-Jones
 protein Au).";
 RL Hoppe-Seyler's Z. Physiol. Chem. 353:345-370(1972).
 RN [2]
 RP X-RAY CRYSTALLOGRAPHY.
 RX MEDLINE=77022433; PubMed=1234024;
 RA Fehlhämmer H., Schiffer M., Epp O., Colman P.M., Tattman E.E.,
 RA Schwager P., Steigemann W., Schramm H.J.;
 RT "The structure determination of the variable portion of the
 Bence-Jones protein Au.";
 RL Biophys. Struct. Mech. 1:139-146(1975).
 CC -1- MISCELLANEOUS: THE STRUCTURE OF THE V REGION WAS DETERMINED BY
 MOLECULAR REPLACEMENT METHODS USING THE KNOWN STRUCTURE OF THE V
 REGION OF THE KAPPA CHAIN REI.
 CC -1- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
 CC -1- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.
 DR HSSP: P01607; 1RRI.
 DR InterPro: IPR003006; IG_MHC.
 DR InterPro: IPR003596; IG_V.
 DR Pfam: PF00047; 1g.1.
 DR SMART: SMO0406; 1g.1.

KM Immunoglobulin V region; Bence-Jones protein.
 FT DOMAIN 1 23 FRAMEWORK-1.
 FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING-1.
 FT DOMAIN 35 49 FRAMEWORK-2.
 FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING-2.
 FT DOMAIN 57 88 FRAMEWORK-3.
 FT DOMAIN 89 97 COMPLEMENTARITY-DETERMINING-3.
 FT DOMAIN 98 107 FRAMEWORK-4.
 FT DISULFID 23 88 BY SIMILARITY.
 FT NON TER 108 108
 SQ SEQUENCE 108 AA; 11939 MW; E801187EE6F6B9 CRC64;
 Query Match 80.0%; Score 445; DB 1; Length 108;
 Best Local Similarity 82.2%; Pred. No. 2.5e-39;
 Matches 88; Conservative 5; Mismatches 14; Indels 0; Gaps 0;
 QY 1 DIOMTQSPSSLSASVGDRTVITTCRASQGISWLAHYQOKPEKPKSLIYAASLSQGVPS 60
 DB 1 DIOMTQSPSSLSASVGDRTVITTCRASQGISWLAHYQOKPEKPKSLIYAASLSQGVPS 60
 QY 61 RFGSGSGTDFTLTISLQPEDPATYCCQYNSTPPTFGQTKVEIK 107
 DB 61 RFGSGSGTDFTLTISLQPEDPATYCCQYNSTPPTFGQTKVEIK 107
 Db 61 RFGSGSGTDFTLTISLQPEDPATYCCQYNSTPPTFGQTKVEIK 107
 RESULT 14
 KX1A_HUMAN STANDARD; PRT; 108 AA.
 ID P01593;
 AC P01593;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Ig kappa chain V-I region AG.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_Taxid=9606;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=69234734; PubMed=4893682;
 RA Titani K., Shinoda T., Putnam F.W.;
 RT "The amino acid sequence of a kappa type Bence-Jones protein. 3. The
 complete sequence and the location of the disulfide bridges.";
 RL J. Biol. Chem. 244:3550-3560(1969).
 CC -1- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
 CC -1- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.
 DR HSSP: P01607; 1RRI.
 DR InterPro: IPR003006; IG_MHC.
 DR InterPro: IPR003596; IG_V.
 DR Pfam: PF00047; 1g.1.
 DR SMART: SMO0406; 1g.1.
 KM Immunoglobulin V region; Bence-Jones protein.
 FT DOMAIN 1 23 FRAMEWORK-1.
 FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING-1.
 FT DOMAIN 35 49 FRAMEWORK-2.
 FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING-2.
 FT DOMAIN 57 88 FRAMEWORK-3.
 FT DOMAIN 89 97 COMPLEMENTARITY-DETERMINING-3.
 FT DISULFID 23 88
 FT NON TER 108 108
 SQ SEQUENCE 108 AA; 11992 MW; E3B38246C18F0CAF CRC64;
 Query Match 79.5%; Score 442; DB 1; Length 108;
 Best Local Similarity 79.4%; Pred. No. 5e-39;
 Matches 85; Conservative 10; Mismatches 12; Indels 0; Gaps 0;
 QY 1 DIOMTQSPSSLSASVGDRTVITTCRASQGISWLAHYQOKPEKPKSLIYAASLSQGVPS 60
 DB 1 DIOMTQSPSSLSASVGDRTVITTCRASQGISWLAHYQOKPEKPKSLIYAASLSQGVPS 60
 QY 61 RFGSGSGTDFTLTISLQPEDPATYCCQYNSTPPTFGQTKVEIK 107
 Db 61 RFGSGSGTDFTLTISLQPEDPATYCCQYNSTPPTFGQTKVEIK 107

Db 61 RFGSGSGTDFTTTISGLQPEDIATYCCQYDTLPRTFGGKTKL 107

RESULT 15

KV10 HUMAN STANDARD; PRT; 108 AA.

ID KV10 HUMAN

AC P01607;

DT 21-JUL-1986 (Rel. 01, Created)

DT 21-JUL-1986 (Rel. 01, Last sequence update)

DT 15-JUL-1999 (Rel. 38, Last annotation update)

DE IG kappa chain V-I region Rel.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

OX NCBI_TaxID=9606;

[1]

RP SEQUENCE.

RA MEDLINE=76023758; PubMed=809329;

RA Palm W., Hilschmann N.;

RT "The primary structure of a crystalline monoclonal immunoglobulin kappa-type L-chain, subgroup I (Bence-Jones protein Rel); isolation and characterization of the tryptic peptides; the complete amino acid sequence of the protein; a contribution to the elucidation of the three-dimensional structure of antibodies, in particular their combining site.";

RT Hoppe-Seyler's Z. Physiol. Chem. 356:167-191 (1975).

RL [2]

RN X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).

RX MEDLINE=76039968; PubMed=1182131;

RA Epp O., Iatman E.E., Schiffer M., Huber R., Palm W.;

RT "The molecular structure of a dimer composed of the variable portions of the Bence-Jones protein Rel refined at 2.0-A resolution.";

RT Biochemistry 14:4943-4952 (1975).

CC -1- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (1,2) MARKER.

CC -1- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.

DR PIR; A01873; KIHURE.

DR PDB; 1REI; 17-FEB-84.

DR InterPro; IPR003006; IG_MHC.

DR InterPro; IPR003596; IG_V.

DR Pfam; PF00047; IG; 1.

DR SMART; SM00406; IGv; 1.

DR Immunoglobulin V region; Bence-Jones protein; 3D-structure.

FT DOMAIN 1 23 FRAMEWORK-1.

FT DOMAIN 24 34 FRAMEWORK-2.

FT DOMAIN 35 49 FRAMEWORK-3.

FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING-1.

FT DOMAIN 57 88 COMPLEMENTARITY-DETERMINING-2.

FT DOMAIN 89 97 FRAMEWORK-3.

FT DOMAIN 98 107 COMPLEMENTARITY-DETERMINING-3.

FT DISULFID 23 88 FRAMEWORK-4.

FT STRAND 4 7

FT STRAND 10 13

FT TURN 15 16

FT STRAND 19 25

FT TURN 30 31

FT STRAND 33 38

FT TURN 40 41

FT STRAND 45 49

FT TURN 50 52

FT STRAND 53 54

FT TURN 56 57

FT TURN 60 61

FT STRAND 62 67

FT TURN 68 69

FT STRAND 70 75

FT HELIX 80 82

FT STRAND 85 90

FT STRAND 98 98

FT STRAND 102 106

FT NON TER 108 108

SEQUENCE 108 AA; 11902 MM; 9E8143E1188BCE2A CRC64;

Query Match 79.5%; Score 442; DB 1; Length 108;

Best Local Similarity 81.1%; Pred. No. Se-39;

Matches 86; Conservative 7; Mismatches 13; Indels 0; Gaps 0;

QY 1 DIOMTQSPSSLSASVGDVTTITCRASQGISSWLAWYQOKPEKAPSLITYAASLSQGVPS 60

DB 1 DIOMTQSPSSLSASVGDVTTITCRASQGISSWLAWYQOKPEKAPSLITYAASLSQGVPS 60

QY 61 RFGSGSGTDFTTTISGLQPEDIATYCCQYDTLPRTFGGKTKL 106

DB 61 RFGSGSGTDFTTTISGLQPEDIATYCCQYDTLPRTFGGKTKL 106

Search completed: June 3, 2003, 08:15:44

Job time : 10.8601 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 3, 2003, 08:07:54 / Search time 53.3174 Seconds

(without alignments)
413.506 Million cell updates/sec

Title: US-09-644-668a-13

Sequence: 1 DQWTPSSLSASVGRVT.....COQNSVPTFGQKVEIK 107

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL 21:*

- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mhc:*
- 8: sp_organelle:*
- 9: sp_plant:*
- 10: sp_plant:*
- 11: sp_rhodent:*
- 12: sp_virus:*
- 13: sp_vertebrate:*
- 14: sp_unclassified:*
- 15: sp_virus:*
- 16: sp_bacteriap:*
- 17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	492	88.5	108	4	Q9UL70
2	476	85.6	108	4	Q9UL79
3	469	84.4	108	4	Q9UL77
4	464.5	83.5	107	4	Q96SA9
5	439.5	79.0	107	4	Q9UL81
6	412	74.1	107	4	Q96PF6
7	406	73.0	116	4	Q96PF6
8	403	72.5	233	11	Q91WS9
9	394.5	71.0	109	4	Q9UL83
10	394	70.9	108	4	Q9UL83
11	392	70.5	107	11	Q9UL84
12	391	70.3	214	11	Q9UL84
13	389	70.0	108	11	Q9UL84
14	386.5	69.5	109	4	Q9UL78
15	383	68.9	234	11	Q9UL78
16	383	68.9	234	11	Q9UL78

17	382	68.7	109	11	Q920B6	Q920B6 mus musculus
18	374	67.3	298	11	Q9QYF0	Q9QYF0 mus musculus
19	364	65.5	127	11	Q925S9	Q925S9 mus musculus
20	363.5	65.4	109	4	Q9UL86	Q9UL86 homo sapien
21	354	63.7	111	11	Q920B9	Q920B9 mus musculus
22	340.5	61.2	134	11	Q9VDD0	Q9VDD0 mus musculus
23	338.5	60.9	241	11	Q921A6	Q921A6 mus musculus
24	333.5	60.0	106	5	Q9U410	Q9U410 schistosoma
25	332	59.7	107	11	Q9ER29	Q9ER29 mus musculus
26	326.5	58.7	235	11	Q91W12	Q91W12 mus musculus
27	326	58.6	99	11	Q9UL74	Q9UL74 mus musculus
28	322.5	58.0	238	11	Q9VC16	Q9VC16 mus musculus
29	318.5	57.3	238	11	Q99W37	Q99W37 mus musculus
30	316	56.8	97	11	Q9UL76	Q9UL76 mus musculus
31	310	55.8	101	11	Q9UL78	Q9UL78 mus musculus
32	309	55.6	103	11	Q9UL80	Q9UL80 mus musculus
33	308.5	55.5	239	4	Q9TCD0	Q9TCD0 homo sapien
34	306	55.0	114	4	Q9UL80	Q9UL80 homo sapien
35	301	54.1	109	6	Q9N0M5	Q9N0M5 oryctolagus
36	298.5	53.7	239	11	Q9VC55	Q9VC55 mus musculus
37	285	51.3	234	11	Q8R028	Q8R028 mus musculus
38	284.5	51.2	104	11	Q9UL82	Q9UL82 mus musculus
39	236.5	42.5	237	4	Q8WTU6	Q8WTU6 homo sapien
40	235.5	42.4	237	4	Q8WTU6	Q8WTU6 homo sapien
41	228.5	40.6	233	4	Q8TBC9	Q8TBC9 homo sapien
42	223.5	40.2	236	4	Q96B61	Q96B61 homo sapien
43	221.5	39.8	112	4	Q96JD1	Q96JD1 homo sapien
44	219	39.4	218	11	Q925S1	Q925S1 mus musculus
45	215.5	38.6	107	4	Q9NSD6	Q9NSD6 homo sapien

ALIGNMENTS

RESULT 1

ID Q9UL70 PRELIMINARY; PRT; 108 AA.

AC Q9UL70;

DT 01-MAY-2000 (TREMBLrel. 13, Created)

DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)

DE Myosin-reactive immunoglobulin light chain variable region (Fragment).

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

NCBI_TaxID:9606;

SEQUENCE FROM N.A.

MEDLINE=98277139; PubMed=9614934;

Wu X., Liu B., Van der Merwe P.L., Kalle N.N., Berney S.M., Young D.C.;

"Myosin-reactive autoantibodies in rheumatic carditis and normal fetus";

Clin. Immunol. Immunopathol. 87:184-192(1998).

EMBL; AF035044; AAD56280.1; -

HSSP; P01607; IREI.

InterPro; IPR003006; IG_MHC.

InterPro; IPR003596; IG_V.

Pfam; PF00047; Ig; 1.

SMART; SM00406; IGV; 1.

NON_TER 1

NON_TER 1

SEQUENCE 108 AA; 11633 MW; B7BEDC3E41FCCA37 CRC64;

Query Match 88.5%; Score 492; DB 4; Length 108;

Best Local Similarity 89.7%; Pred. No. 5.1e-45;

Matches 96; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

Qy 1 DQWTPSSLSASVGRVITTCASAGISSWLAWYQKPKKSIYAASTQSVPS 60

Db 1 DQWTPSSLSASVGRVITTCASAGISSWLAWYQKPKKSIYAASTQSVPS 60

Qy 61 RFGSGSGTDFLTITSSLOPEDFATYCCQYNSYPFGGTVEIK 107
 Db 61 RFGSGSGTDFLTITSSLOPEDFATYCCQYNSAPRTFGGTVEIK 107

RESULT 2

Q9UL79 PRELIMINARY; PRT; 108 AA.

AC Q9UL79
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE Myosin-reactive immunoglobulin light chain variable region (Fragment).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID=9606;
 RN 1)

RP SEQUENCE FROM N.A.

RX MEDLINE=98277139; PubMed=9614934;
 RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
 RA Young D.C.;
 RT "Myosin-reactive autoantibodies in rheumatic carditis and normal fetus.";
 RL Clin. Immunol. Immunopathol. 87:184-192(1998).

DR HSP; P01607; IRET.
 DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR003596; Ig_V.
 DR Pfam; PF00047; Ig; 1.
 DR SMART; SM00406; Ig; 1.
 FT NON TER 1
 FT NON TER 108
 SQ SEQUENCE 108 AA; 11787 MW; DB5845F19724FB4E CRC64;

Query Match 85.6%; Score 476; DB 4; Length 108;
 Best Local Similarity 86.9%; Pred. No. 2, 6e-43;
 Matches 93; Conservative 5; Mismatches 9; Indels 0; Gaps 0;

Qy 1 DIOMTQSPSSLSASVGDRTVITCRASQISSWLAWYQOKPEKAPKSLIYAASSLSQGVPS 60
 Db 1 DIOMTQSPSSLSASVGDRTVITCRASQISSWLAWYQOKPEKAPKSLIYAASSLSQGVPS 60
 Qy 61 RFGSGSGTDFLTITSSLOPEDFATYCCQYNSYPFGGTVEIK 107
 Db 61 RFGSGSGTDFLTITSSLOPEDFATYCCQYNSYPFGGTVEIK 107

RESULT 3

Q9UL77 PRELIMINARY; PRT; 108 AA.

AC Q9UL77
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE Myosin-reactive immunoglobulin light chain variable region (Fragment).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID=9606;
 RN 1)
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98277139; PubMed=9614934;
 RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
 RA Young D.C.;
 RT "Myosin-reactive autoantibodies in rheumatic carditis and normal fetus.";
 RL Clin. Immunol. Immunopathol. 87:184-192(1998).
 DR EMBL; AF035037; AAD56273.1; -.
 DR HSP; P01607; IRET.
 DR InterPro; IPR003006; Ig_MHC.

DR InterPro; IPR003596; Ig_V.
 DR Pfam; PF00047; Ig; 1.
 DR SMART; SM00406; Ig; 1.
 FT NON TER 1
 FT NON TER 108
 SQ SEQUENCE 108 AA; 11738 MW; C06681716C4D16F3 CRC64;

Query Match 84.4%; Score 469; DB 4; Length 108;
 Best Local Similarity 88.8%; Pred. No. 1, 5e-42;
 Matches 95; Conservative 2; Mismatches 10; Indels 0; Gaps 0;

Qy 1 DIOMTQSPSSLSASVGDRTVITCRASQISSWLAWYQOKPEKAPKSLIYAASSLSQGVPS 60
 Db 1 DIOMTQSPSSLSASVGDRTVITCRASQISSWLAWYQOKPEKAPKSLIYAASSLSQGVPS 60
 Qy 61 RFGSGSGTDFLTITSSLOPEDFATYCCQYNSYPFGGTVEIK 107
 Db 61 RFGSGSGTDFLTITSSLOPEDFATYCCQYNSYPFGGTVEIK 107

RESULT 4

Q96SA9 PRELIMINARY; PRT; 107 AA.

AC Q96SA9
 DT 01-DEC-2001 (TREMBLrel. 19, Created)
 DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
 DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
 DE Anti-streptococcal/anti-myosin immunoglobulin kappa light chain variable region (Fragment).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID=9606;
 RN 1)
 RP SEQUENCE FROM N.A.

RX MEDLINE=98375893; PubMed=9712075;
 RA Adderson E.B., Shikhan A.R., Ward K.E., Cunningham M.W.;
 RT "Molecular analysis of polyclonal monoclonal antibodies from rheumatic carditis: human anti-N-acetylglucosamine/anti-myosin antibody V region genes.";
 RL J. Immunol. 161:2020-2031(1998).
 DR EMBL; U96396; AAB68785.1; -.
 DR InterPro; IPR003006; Ig_MHC.
 DR Pfam; PF00047; Ig; 1.
 FT NON TER 1
 FT NON TER 107
 SQ SEQUENCE 107 AA; 11520 MW; 4BB43B9C5B577F16 CRC64;

Query Match 83.5%; Score 464.5; DB 4; Length 107;
 Best Local Similarity 89.8%; Pred. No. 4, 4e-42;
 Matches 97; Conservative 1; Mismatches 7; Indels 3; Gaps 2;

Qy 1 DIOMTQSPSSLSASVGDRTVITCRASQISSWLAWYQOKPEKAPKSLIYAASSLSQGVPS 60
 Db 1 DIOMTQSPSSLSASVGDRTVITCRASQISSWLAWYQOKPEKAPKSLIYAASSLSQGVPS 60
 Qy 61 RFGSGSGTDFLTITSSLOPEDFATYCCQYNSYPFGGTVEIK 107
 Db 61 RFGSGSGTDFLTITSSLOPEDFATYCCQYNSYPFGGTVEIK 106

RESULT 5

Q9UL81 PRELIMINARY; PRT; 107 AA.

AC Q9UL81
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE Myosin-reactive immunoglobulin light chain variable region (Fragment).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

```
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berny S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035033; AAD56269.1; -.
DR HSSP; P01607; IREI.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; Ig_1.
DR SMART; SM00406; IgV; 1.
FT NON_TER 1
FT NON_TER 107
SQ SEQUENCE 107 AA; 11501 MW; 070549FDE0754748 CRC64;

Query Match
Best Local Similarity 79.0%; Score 439.5; DB 4; Length 107;
Matches 91; Conservative 4; Mismatches 10; Indels 3; Gaps 2;

OY 1 DIOMTQSSSLASVGDRTVITTCRASQGISWLAWYQOKPEKAPKSLIYAASSLSQGVPS 60
DB 1 DIOMTQSSSLASVGDRTVITTCRASQGISWLAWYQOKPEKAPKSLIYAASSLSQGVPS 60
OY 61 RFSSGSGTDFTLTITSLQPEDPATYTCQOYNSYPP-FTFGGCTKYEIK 107
DB 61 RFSSGSGTDFTLTITSLQPEDPATYTCQOYNSYPP-FTFGGCTKYEIK 106

RESULT 6
OY 08R062 PRELIMINARY; PRT; 234 AA.
AC 08R062;
DT 01-JUN-2002 (TREMblrel. 21, Created)
DT 01-JUN-2002 (TREMblrel. 21, Last sequence update)
DT 01-JUN-2002 (TREMblrel. 21, Last annotation update)
DE Hypothetical 25.9 kDa protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
CX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=COLON;
RA Strauberg R.;
RL Submitted (Apr-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC027418; AAH27418.1; -.
KW Hypothetical protein.
SQ SEQUENCE 234 AA; 25857 MW; 4EB08C81426AEAB1 CRC64;

Query Match
Best Local Similarity 74.1%; Score 412; DB 11; Length 234;
Matches 79; Conservative 13; Mismatches 15; Indels 0; Gaps 0;

OY 1 DIOMTQSSSLASVGDRTVITTCRASQGISWLAWYQOKPEKAPKSLIYAASSLSQGVPS 60
DB 21 DIOMTQSSSLASVGDRTVITTCRASQGISWLAWYQOKPEKAPKSLIYAASSLSQGVPS 80
OY 61 RFSSGSGTDFTLTITSLQPEDPATYTCQOYNSYPP-FTFGGCTKYEIK 107
DB 81 RFSSGSGTDFTLTITSLQPEDPATYTCQOYNSYPP-FTFGGCTKYEIK 127

RESULT 7
OY 096PF6 PRELIMINARY; PRT; 116 AA.
AC 096PF6;
DT 01-DEC-2001 (TREMblrel. 19, Created)
DT 01-DEC-2001 (TREMblrel. 19, Last sequence update)
DT 01-MAR-2002 (TREMblrel. 20, Last annotation update)
```

```
DE Kappa 1 light chain variable region (Fragment).
GN SDRK1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21361171; PubMed=11468171;
RA Comenzo R.L., Zhang Y., Martinez C., Osman K., Herrera G.A.;
RT "The tropism of organ involvement in primary systemic amyloidosis:
RT contributions of Ig V(L) germ line gene use and clonal plasma cell
RT burden";
RL Blood 98:714-720(2001).
DR EMBL; AF361758; AAK51465.1; -.
DR InterPro; IPR003006; IG_MHC.
DR Pfam; PF00047; Ig_1.
FT NON_TER 1
FT NON_TER 116
SQ SEQUENCE 116 AA; 12735 MW; E796FC2217BFCF57 CRC64;

Query Match
Best Local Similarity 73.0%; Score 406; DB 4; Length 116;
Matches 79; Conservative 11; Mismatches 17; Indels 0; Gaps 0;

OY 1 DIOMTQSSSLASVGDRTVITTCRASQGISWLAWYQOKPEKAPKSLIYAASSLSQGVPS 60
DB 1 DIOMTQSSSLASVGDRTVITTCRASQGISWLAWYQOKPEKAPKSLIYAASSLSQGVPS 60
OY 61 RFSSGSGTDFTLTITSLQPEDPATYTCQOYNSYPP-FTFGGCTKYEIK 107
DB 61 RFSSGSGTDFTLTITSLQPEDPATYTCQOYNSYPP-FTFGGCTKYEIK 107

RESULT 8
OY 091WS9 PRELIMINARY; PRT; 233 AA.
AC 091WS9;
DT 01-DEC-2001 (TREMblrel. 19, Created)
DT 01-DEC-2001 (TREMblrel. 19, Last sequence update)
DT 01-MAR-2002 (TREMblrel. 20, Last annotation update)
DE Hypothetical 25.8 kDa protein (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
CX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=COLON;
RA Strauberg R.;
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC013486; AAH13486.1; -.
DR InterPro; IPR003006; IG_MHC.
DR Pfam; PF00047; Ig_2.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW Hypothetical protein.
FT NON_TER 1
SQ SEQUENCE 233 AA; 25781 MW; B1C184DA149A16EB CRC64;

Query Match
Best Local Similarity 72.9%; Score 403; DB 11; Length 233;
Matches 78; Conservative 12; Mismatches 17; Indels 0; Gaps 0;

OY 1 DIOMTQSSSLASVGDRTVITTCRASQGISWLAWYQOKPEKAPKSLIYAASSLSQGVPS 60
DB 20 DIOMTQSSSLASVGDRTVITTCRASQGISWLAWYQOKPEKAPKSLIYAASSLSQGVPS 79
OY 61 RFSSGSGTDFTLTITSLQPEDPATYTCQOYNSYPP-FTFGGCTKYEIK 107
DB 80 RFSSGSGTDFTLTITSLQPEDPATYTCQOYNSYPP-FTFGGCTKYEIK 126

RESULT 9
```

Q9UL85
ID Q9UL85 PRELIMINARY; PRT; 109 AA.
AC Q9UL85;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Myosin-reactive immunoglobulin kappa chain variable region (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berny S.M., Young D.C.,
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal fetus".
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR HSBP; P80362; IWTU.
DR InterPro; IPR003006; IG_MHC.
DR Pfam; PF00047; IG_1.
DR SMART; SM00406; IG_1.
FT NON_TER 1
FT 109
SQ SEQUENCE 109 AA; 11761 MW; FBIE43E7CAFAACC CRC64;

Query Match 71.0%; Score 394.5; DB 4; Length 109;
Best Local Similarity 71.3%; Pred. No. 1.3e-34;
Matches 77; Conservative 15; Mismatches 15; Indels 1; Gaps 1;

QY 1 DIQMTQSPSSLSASVGRVTITCRASQGISISMLAWYQOKPEKAPKSLIYAASLSQGVPS 60
DB 1 EIVMTQSPATLSVSPERATLSCWASQGISISMLAWYQOKPEKAPKSLIYAASLSQGVPS 60
QY 61 RFSSGSGSTDTLTITSSLOPEDFATYCCQVNSYPTFGQGTKEIK 107
DB 61 RFSSGSGSTDTLTITSSLOPEDFATYCCQVNSYPTFGQGTKEIK 107

RESULT 10
Q9UL83
ID Q9UL83 PRELIMINARY; PRT; 108 AA.
AC Q9UL83;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Myosin-reactive immunoglobulin light chain variable region (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berny S.M., Young D.C.,
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal fetus".
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR HSBP; P80362; IWTU.
DR InterPro; IPR003006; IG_MHC.
DR Pfam; PF00047; IG_1.
DR SMART; SM00406; IG_1.
FT NON_TER 1
FT 108
SQ SEQUENCE 108 AA; 11834 MW; 9F9C5A92EBA9EEA CRC64;

Query Match 70.9%; Score 394; DB 4; Length 108;
Best Local Similarity 69.2%; Pred. No. 1.5e-34;
Matches 74; Conservative 17; Mismatches 16; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGRVTITCRASQGISISMLAWYQOKPEKAPKSLIYAASLSQGVPS 60
DB 1 EIVMTQSPATLSVSPERATLSCWASQGISISMLAWYQOKPEKAPKSLIYAASLSQGVPS 60
QY 61 RFSSGSGSTDTLTITSSLOPEDFATYCCQVNSYPTFGQGTKEIK 107
DB 61 RFSSGSGSTDTLTITSSLOPEDFATYCCQVNSYPTFGQGTKEIK 107

RESULT 11
Q9UL84
ID Q9UL84 PRELIMINARY; PRT; 107 AA.
AC Q9UL84;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Anti-myosin immunoglobulin light chain variable region (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=BALB/C;
RX MEDLINE=20448942; PubMed=10992488;
RA Malkiel S., Liao L., Cunningham M.W., Diamond B.,
RT "T-cell-dependent antibody response to the dominant epitope of streptococcal polysaccharide, N-acetyl-glucosamine, is cross-reactive with cardiac myosin".
RL Infect. Immun. 68:5803-5808 (2000).
DR EMBL; AF206022; AAF69320.1; --
DR HSBP; P80362; IWTU.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF00047; IG_1.
DR SMART; SM00406; IG_1.
FT NON_TER 1
FT 107
SQ SEQUENCE 107 AA; 11648 MW; ACF9B1253ACA1E5D CRC64;

Query Match 70.5%; Score 392; DB 11; Length 107;
Best Local Similarity 71.0%; Pred. No. 2.4e-34;
Matches 76; Conservative 11; Mismatches 20; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGRVTITCRASQGISISMLAWYQOKPEKAPKSLIYAASLSQGVPS 60
DB 1 DIQMTQSPSSLSASVGRVTITCRASQGISISMLAWYQOKPEKAPKSLIYAASLSQGVPS 60
QY 61 RFSSGSGSTDTLTITSSLOPEDFATYCCQVNSYPTFGQGTKEIK 107
DB 61 RFSSGSGSTDTLTITSSLOPEDFATYCCQVNSYPTFGQGTKEIK 107

RESULT 12
Q9RLAS
ID Q9RLAS PRELIMINARY; PRT; 214 AA.
AC Q9RLAS;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Kappa light chain of Mab7 (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.

RA Wilde K.G., Yu X., Ekramoddoullah A.K.M., Misra S.;
 RT "Cloning of cDNAs encoding for anti-white pine blister rust monoclonal
 antibody (mab 7, its light and heavy chains) and construction of a
 single chain antibody (scfv).";
 RL Submitted (May-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF152371; AAD40242.1; -
 DR HSSP; P01679; 2FBJ.
 DR InterPro; IPR003600; IG_1ike.
 DR InterPro; IPR003006; IG_MHC.
 DR InterPro; IPR003596; IG_V.
 DR Pfam; PF00047; IG_2.
 DR SMART; SM00406; IGV; 1.
 DR SMART; SM00410; IG_1ike; 1.
 DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
 FT NON_TER 1 1
 FT NON_TER 214 214
 SQ SEQUENCE 214 AA; 23922 MW; 52BA205FDE395E2A CRC64;
 Query Match 70.3%; Score 391; DB 11; Length 214;
 Best Local Similarity 68.2%; Pred. No. 7.4e-34;
 Matches 73; Conservative 18; Mismatches 16; Indels 0; Gaps 0;
 QY 1 DIQMTQSPSSLSASVGRVTITCRASQGISWLAWYQOKPEKAPKSLIYAASLSQGVPS 60
 DB 1 DIQLTQSPSSWYASLGERVTITCKASQDINSYLSWFOQKRGKSPKTLIRANLVGVPS 60
 QY 61 RFGSGSGGTDFTLTISLSLOPEDPATYYCCQYNSYPPTFGGKVEIK 107
 DB 61 RFGSGSGGQDYSILTSLSEYEDMGVYCIQYDEFPPTFGSGTLEIK 107
 RESULT 13
 QSVIJO PRELIMINARY; PRT; 108 AA.
 ID QSVIJO;
 AC QSVIJO;
 DT 01-MAR-2002 (TrEMBLrel. 20, Created)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 DE Anti-DNA light chain (Fragment).
 GN VK19.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 CX NCB1_Taxid=10090;
 RN NCB1_Taxid=10090;
 RP SEQUENCE FROM N.A.
 RC STRAIN=C3H/HEJ-LPR/LPR;
 RX MEDLINE=96409289; PubMed=8814271;
 RL Wloch M.K., Alexander A.L., Pippen A.M., Pisetsky D.S., Gilkeson G.S.;
 RT "Differences in V kappa gene utilization and VH CDR3 sequence among
 anti-DNA from C3H-1pr mice and lupus mice with nephritis";
 DR Eur. J. Immunol. 26:2225-2233(1996).
 DR EMBL; U59155; AAB02917.1; -
 DR InterPro; IPR003599; IG_1.
 DR InterPro; IPR003006; IG_MHC.
 DR InterPro; IPR003596; IG_V.
 DR Pfam; PF00047; IG_1.
 DR SMART; SM00409; IGV; 1.
 DR SMART; SM00406; IGV; 1.
 FT NON_TER 1 1
 FT NON_TER 108 108
 SQ SEQUENCE 108 AA; 11859 MW; 68506D75613DBEBC CRC64;
 Query Match 70.0%; Score 389; DB 11; Length 108;
 Best Local Similarity 68.2%; Pred. No. 5e-34;
 Matches 73; Conservative 17; Mismatches 17; Indels 0; Gaps 0;
 QY 1 DIQMTQSPSSLSASVGRVTITCRASQGISWLAWYQOKPEKAPKSLIYAASLSQGVPS 60
 DB 1 DIQMTQSPSSLSASVGRVTITCRASQGISWLAWYQOKPEKAPKSLIYAASLSQGVPS 60
 QY 61 RFGSGSGGTDFTLTISLSLOPEDPATYYCCQYNSYPPTFGGKVEIK 107
 DB 61 RFGSGSGGTDFTLTISLSLOPEDPATYYCCQYNSYPPTFGGKVEIK 107

DB 61 RFGSGSGGTDFTLTISNVQSEDLAFYCCQYNSYPPTFGGKVEIK 107
 RESULT 14
 QSVL78 PRELIMINARY; PRT; 109 AA.
 ID QSVL78;
 AC QSVL78;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE Myosin-reactive immunoglobulin light chain variable region
 DE (Fragment).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 CX NCB1_Taxid=9606;
 RN NCB1_Taxid=9606;
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98277139; PubMed=9614934;
 RA Wu X., Liu B., Van der Werf P.L., Kalle N.N., Berney S.M.,
 RA Young D.C.;
 RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
 fetus";
 RL Clin. Immunol. Immunopathol. 87:184-192(1998).
 DR EMBL; AF035036; AAD56272.1; -
 DR HSSP; P80362; 1MTL.
 DR InterPro; IPR003006; IG_MHC.
 DR InterPro; IPR003596; IG_V.
 DR Pfam; PF00047; IGV; 1.
 DR SMART; SM00406; IGV; 1.
 FT NON_TER 1 1
 FT NON_TER 109 109
 SQ SEQUENCE 109 AA; 11646 MW; 5F675C52BC7BE197 CRC64;
 Query Match 69.5%; Score 386.5; DB 4; Length 109;
 Best Local Similarity 69.4%; Pred. No. 9.4e-34;
 Matches 75; Conservative 13; Mismatches 19; Indels 1; Gaps 1;
 QY 1 DIQMTQSPSSLSASVGRVTITCRASQGI-SSWLAWYQOKPEKAPKSLIYAASLSQGVPS 59
 DB 1 EIVLTQSPGTLISLGERATISCRASQSVSSYLAWYQOKPEQARLLIYGSSSRATGIP 60
 QY 60 SRFSGSGGTDFTLTISLSLOPEDPATYYCCQYNSYPPTFGGKVEIK 107
 DB 61 DRFGSGSGGTDFTLTISRLEPEDCAVYCCQYGGSSPLTFGGGKVEIK 108
 RESULT 15
 QSVF8 PRELIMINARY; PRT; 234 AA.
 ID QSVF8;
 AC QSVF8;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
 DE Hypothetical 25.9 kDa protein.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 CX NCB1_Taxid=10090;
 RN NCB1_Taxid=10090;
 RP SEQUENCE FROM N.A.
 RC TISSUE=COLON;
 RA Strausberg R.;
 RL Submitted (Oct-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC015292; AAH15292.1; -
 DR InterPro; IPR003006; IG_MHC.
 DR InterPro; IPR003596; IG_V.
 DR Pfam; PF00047; IG_2.
 DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
 DR PROSITE; PS00962; RIBOSOMAL_S2_1; UNKNOWN_1.
 KW Hypothetical protein.
 SQ SEQUENCE 234 AA; 25929 MW; B0D0B0E6EB7812D2 CRC64;

Tue Jun 3 08:12:16 2003

us-09-644-668a-13.rsp

Page 6

	Query March	68.9%	Score 383,	DB 11,	Length 234;
	Besst Local Similarity	70.1%;	Pred. No. 5.9e-33;		
	Matches	75; Conservative	14; Mismatches	18; Indels	0; Gaps
Oy	1	DIDMTQSSSASVAGDRVTITCRASQISIMLWYOOKPEKAPSLTYAASSLOSCTPS	60		
		: : :			
Dd	21	DIDMTQTSSASALGDRVTISCRASQISINILMWYOOKPGGTVALITYYSRLYLGPS	80		
		: : :			
Oy	61	RFSGGSGTDFLTITSSLOPEDFAATYYCOQNSYPPTFGQGTKEIK	107		
		: : : :			
Dd	81	RFSGGSGGTDTLTSSLNLEDIATYFCQGQNTPTFTGSGSTKLGVK	127.		
		: : :			

Search completed: June 3, 2003, 08:20:45
Job time : 54.3174 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: June 3, 2003, 08:02:14 ; Search time 48,2048 Seconds

(without alignments)
295.776 Million cell updates/sec

Title: US-09-644-668a-13

Perfect score: 556

Sequence: 1 DIQMTQSSSSASVGDRTV.....CQQVNSYPTFGQKVEIK 107

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

A.GeneSeq.101002:*

- 1: /SID2/gcgdata/geneSeq/geneSeq-emb1/AA1980.DAT:*
- 2: /SID2/gcgdata/geneSeq/geneSeq-emb1/AA1981.DAT:*
- 3: /SID2/gcgdata/geneSeq/geneSeq-emb1/AA1982.DAT:*
- 4: /SID2/gcgdata/geneSeq/geneSeq-emb1/AA1983.DAT:*
- 5: /SID2/gcgdata/geneSeq/geneSeq-emb1/AA1984.DAT:*
- 6: /SID2/gcgdata/geneSeq/geneSeq-emb1/AA1985.DAT:*
- 7: /SID2/gcgdata/geneSeq/geneSeq-emb1/AA1986.DAT:*
- 8: /SID2/gcgdata/geneSeq/geneSeq-emb1/AA1987.DAT:*
- 9: /SID2/gcgdata/geneSeq/geneSeq-emb1/AA1988.DAT:*
- 10: /SID2/gcgdata/geneSeq/geneSeq-emb1/AA1989.DAT:*
- 11: /SID2/gcgdata/geneSeq/geneSeq-emb1/AA1990.DAT:*
- 12: /SID2/gcgdata/geneSeq/geneSeq-emb1/AA1991.DAT:*
- 13: /SID2/gcgdata/geneSeq/geneSeq-emb1/AA1992.DAT:*
- 14: /SID2/gcgdata/geneSeq/geneSeq-emb1/AA1993.DAT:*
- 15: /SID2/gcgdata/geneSeq/geneSeq-emb1/AA1994.DAT:*
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- 21: /SID2/gcgdata/geneSeq/geneSeq-emb1/AA2000.DAT:*
- 22: /SID2/gcgdata/geneSeq/geneSeq-emb1/AA2001.DAT:*
- 23: /SID2/gcgdata/geneSeq/geneSeq-emb1/AA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	556	100.0	107	22	AA67511
2	543	97.7	107	22	AA672880
3	538	96.8	107	22	AA672882
4	538	96.8	107	22	AA682890
5	538	96.8	107	22	AA682890
6	537	96.6	108	23	AAU76522
7	531	95.5	224	22	AA675040
8	527	94.8	224	22	AA675044
9	509	91.5	109	18	AA67543
10	508	91.4	124	21	AA67523

11	507	91.2	107	22	AA655571
12	507	91.2	224	22	AA675043
13	505	90.8	109	14	AA640956
14	505	90.8	130	21	AA656737
15	503	90.5	107	22	AA662087
16	503	90.5	107	22	AA660400
17	503	90.5	107	22	AA661585
18	503	90.5	108	19	AA670622
19	503	90.5	108	21	AA682345
20	503	90.5	109	23	AA661191
21	503	90.5	109	23	AAU74544
22	503	90.5	244	23	ABP45870
23	501	90.1	164	20	AA674317
24	499	88.7	214	20	AA608600
25	498	88.6	109	15	AA647041
26	496	89.2	107	14	AA630770
27	495	89.0	107	23	AB607237
28	495	89.0	126	20	AA608701
29	495	89.0	126	20	AA617492
30	495	89.0	126	21	AA683645
31	495	89.0	126	23	AB604943
32	495	89.0	126	23	AAU10768
33	494	88.8	236	23	AAU74297
34	494	88.8	241	23	AAU90948
35	493	88.7	108	18	AA618895
36	493	88.7	109	14	AA630764
37	493	88.7	117	14	AA638651
38	493	88.7	117	15	AA662931
39	493	88.7	117	17	AA603949
40	493	88.7	117	18	AA641147
41	493	88.7	117	19	AA662185
42	493	88.7	117	20	AA640432
43	493	88.7	239	23	AAU90905
44	493	88.7	240	22	AA646000
45	492.5	88.6	108	22	AA612062

ALIGNMENTS

RESULT 1	AA67511	standard; peptide; 107 AA.
ID	AA67511	
AC	AA67511	
XX		
DT	29-MAY-2001	(first entry)
XX		
DE		Light chain variable region of anti-CTLA-4 antibody 1E2.
XX		
KW		Complementarily determining region; CDR; immune response; antibody;
KW		Cytotoxic T lymphocyte associated antigen-4; CTLA-4; B7 ligand; cancer;
KW		autoimmune disease; infectious disease; inflammation; allergy;
KW		rheumatoid arthritis; myasthenia gravis; lupus erythematosus;
KW		multiple sclerosis; insulin-dependent diabetes mellitus; inflammation;
XX		transplant rejection; graft versus host disease.
XX		
OS		Homo sapiens.
XX		
FT	Key	Location/Qualifiers
FT	Region	24..34
FT	/note= "CDR1"	
FT	Region	50..66
FT	/note= "CDR2"	
FT	Region	89..97
FT	/note= "CDR3"	
XX		
XX		WO200114424-A2.
XX		01-MAR-2001.
XX		24-AUG-2000; 2000WO-US23356.
XX		

Amino acid sequenc
TR0005 Humab kappa
Human germ-line ge
Amino acid sequenc
Human VI consensus
Consensus human 11
Human variable 11g
Human consensus fr
Human consensus se
Human anti-VEGF an
Human subgroup 11g
Human Bly5 binding
IGC antibody 2.6.1
UP1127855 Seq ID
Sequence of the co
Consensus humanise
Acti-IL-4 and IL-1
Human consensus 11
Consensus light ch
Conserved light ch
Human CD28 synchab
Amino acid sequenc
Acti-human Altim m
Insulin/insulin-11
CD4-specific anti b
Consensus humanise
Human V-kappa 4r65
Human V-kappa 4r65
DNA fragment vK65
Human vKappa65.15
Human DNA vKappa65
Amino acid sequenc
Insulin/insulin-11
Human MTC-1 scFv c
Human anti-tissue

PR 24-AUG-1999; 99US-0150452.
XX (MEDA-) MEDAREX INC.
PA Korman AJ, Halk EL, Lomberg N;
XX WPI; 2001-202933/20.
DR
XX
PT Novel human sequence antibody that binds to human cytotoxic T
PT lymphocyte associated antigen-4, useful for inducing, augmenting or
PT prolonging immune response to antigen or for suppressing immune
PT response in patient
XX
PS Claim 27; Fig 7; 127pp; English.
XX
XX The present sequence represents the light chain variable region of
CC human antibody 1E2. This antibody specifically binds to human
CC cytotoxic T lymphocyte associated antigen-4 (CTLA-4). Such antibodies
CC are used in methods for inducing, augmenting or prolonging an immune
CC response to an antigen in a patient, where the antibodies block
CC binding of human CTLA-4 to human B7 ligands. The antibodies are
CC also useful for treating autoimmune disease in a subject caused or
CC exacerbated by increased activity of T cells and for treating prostate
CC cancer, melanoma or epithelial cancer. A polyvalent or polyclonal
CC antibody preparation comprising two antibodies of the invention are
CC useful for suppressing a immune response in a patient. They are used for
CC treating cancer, infectious diseases and promoting beneficial autoimmune
CC reactions for the treatment of diseases with inflammatory or allergic
CC components. The polyvalent or polyclonal preparations are useful for
CC treating autoimmune diseases such as rheumatoid arthritis, myasthenia
CC gravis and lupus erythematosus, multiple sclerosis, insulin-dependent
CC diabetes mellitus, transplant rejection, and inflammation, graft versus
CC host disease.
XX
SQ Sequence 107 AA;
XX
Query Match 100.0%; Score 556; DB 22; Length 107;
Best Local Similarity 100.0%; Pred. No. 1.8e-35;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 DIQMTPSSLSASVGDVTTTCRASQGISWLAHYQKPEKAPKSLIYAASLSGCVS 60
DB 1 DIQMTPSSLSASVGDVTTTCRASQGISWLAHYQKPEKAPKSLIYAASLSGCVS 60
QY 61 RFGSGSGTDFTLTISLQPEDFATYYCOQVNSYPTFGQGTVEIK 107
DB 61 RFGSGSGTDFTLTISLQPEDFATYYCOQVNSYPTFGQGTVEIK 107
RESULT 2
AAB72880
ID AAB72880 standard; Protein; 107 AA.
XX
AC AAB72880;
XX
DT 10-MAY-2001 (first entry)
XX
XX Human anti-HER2/neu antibody 3-F2 light chain.
XX
XX Human; HER2; neu; erbB2; oncogene; cancer; antibody; immunotherapy;
XX 3-F2; 1-D2; 2-E8; growth factor receptor.
XX
OS Homo sapiens.
XX
XX WO200109187-A2.
XX
PD 08-FEB-2001.
XX
PF 25-JUL-2000; 2000WO-US20272.
XX
PR 29-JUL-1999; 99US-0146313.
PR 10-MAR-2000; 2000US-0186539.
XX

PA (MEDA-) MEDAREX INC.
XX
XX Keler T, Deo Y;
XX
DR WPI; 2001-168698/17.
DR N-PSDB; AAF75586.
XX
XX
PT New human monoclonal antibody that specifically binds to growth factor
PT receptor HER2/neu, for treating, preventing or diagnosing diseases
PT characterized by aberrant HER2/neu expression e.g. cancers
XX
PS Disclosure; Page 104-105; 113pp; English.
XX
XX The present invention provides the protein and coding sequences for human
CC monoclonal antibodies which bind specifically to the HER2/neu growth
CC factor receptor (also known as erbB2). These are designated 3-F2, 1-D2
CC and 2-E8. They can be used in the immunotherapy-based treatment and
CC prognosis of cancers, particularly adenocarcinomas such as salivary
CC gland, stomach, kidney, mammary gland, lung and squamous cell carcinomas,
CC and ovarian cancer. The present sequence is part of an antibody of the
CC invention.
XX
SQ Sequence 107 AA;
XX
Query Match 97.7%; Score 543; DB 22; Length 107;
Best Local Similarity 98.1%; Pred. No. 1.7e-34;
Matches 105; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 DIQMTPSSLSASVGDVTTTCRASQGISWLAHYQKPEKAPKSLIYAASLSGCVS 60
DB 1 DIQMTPSSLSASVGDVTTTCRASQGISWLAHYQKPEKAPKSLIYAASLSGCVS 60
QY 61 RFGSGSGTDFTLTISLQPEDFATYYCOQVNSYPTFGQGTVEIK 107
DB 61 RFGSGSGTDFTLTISLQPEDFATYYCOQVNSYPTFGQGTVEIK 107
RESULT 3
AAB72882
ID AAB72882 standard; Protein; 107 AA.
XX
AC AAB72882;
XX
DT 10-MAY-2001 (first entry)
XX
XX Human anti-HER2/neu antibody 1-D2 light chain.
XX
XX Human; HER2; neu; erbB2; oncogene; cancer; antibody; immunotherapy;
XX 3-F2; 1-D2; 2-E8; growth factor receptor.
XX
OS Homo sapiens.
XX
XX WO200109187-A2.
XX
PD 08-FEB-2001.
XX
PF 25-JUL-2000; 2000WO-US20272.
XX
PR 29-JUL-1999; 99US-0146313.
PR 10-MAR-2000; 2000US-0186539.
XX
XX (MEDA-) MEDAREX INC.
XX
XX Keler T, Deo Y;
XX
DR WPI; 2001-168698/17.
DR N-PSDB; AAF75588.
XX
XX
PT New human monoclonal antibody that specifically binds to growth factor
PT receptor HER2/neu, for treating, preventing or diagnosing diseases
PT characterized by aberrant HER2/neu expression e.g. cancers
XX
PS Disclosure; Page 107; 113pp; English.

XX The present invention provides the protein and coding sequences for human
 CC monoclonal antibodies which bind specifically to the HER2/neu growth
 CC factor receptor (also known as erbB2). These are designated 3-F2, 1-D2
 CC and 2-B8. They can be used in the immunotherapy-based treatment and
 CC prognosis of cancers, particularly adenocarcinomas such as salivary
 CC gland, stomach, kidney, mammary gland, lung and squamous cell carcinomas,
 CC and ovarian cancer. The present sequence is part of an antibody of the
 CC invention.

XX Sequence 107 AA:

XX Query Match 96.8%; Score 538; DB 22; Length 107;
 XX Best Local Similarity 97.2%; Pred. No. 4.2e-34;
 XX Matches 104; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 DIQMTGSPSSISASVGDRTTTCRASQGISWLMWYQKPEKAKSLIYAASLSQGVPS 60
 DB 1 DIQMTGSPSSISASVGDRTTTCRASQGISWLMWYQKPEKAKSLIYAASLSQGVPS 60
 OY 61 RFGSGSGTDFLTITSSLOPEDPATYCCOQNSYPTFGGKTKEIK 107
 DB 61 RFGSGSGTDFLTITSSLOPEDPATYCCOQNSYPTFGGKTKEIK 107

RESULT 4

AA82890 standard; Protein; 107 AA.

XX AAB82890;
 XX 26-NOV-2001 (first entry)

DE Anti-human CD154 antibody ABR793 light chain variable region.
 XX CD154; gp39; CD40-L; antibody; ABR793; transplant rejection;
 XX autoimmune disease; inflammation; atherosclerosis;
 KM Alzheimer's disease; antiinflammatory; antiarteriosclerotic;
 XX immunosuppressive; therapy.

XX Mus musculus.

XX Key Location/Qualifiers
 FT 1..23
 FT /label= FR1
 FT /note= "framework region 1"

FT Region 24..34
 FT /label= CDR1
 FT /note= "complementarity determining region 1"

FT Region 35..49
 FT /label= FR2
 FT /note= "framework region 2"

FT Region 50..56
 FT /label= CDR2
 FT /note= "complementarity determining region 2"

FT Region 57..88
 FT /label= FR3
 FT /note= "framework region 1"

FT Region 89..97
 FT /label= CDR3
 FT /note= "complementarity determining region 3"

FT Region 98..107
 FT /label= FR4
 FT /note= "framework region 4"

XX MO200168860-A1.

XX 20-SEP-2001.

XX 14-MAR-2001; 2001WO-EP02875.

XX 16-MAR-2000; 2000GB-0006398.

XX

PA (NOVS) NOVARTIS AG.
 PA (NOVS) NOVARTIS-ERFINDUNGEN VERM GES MBH.

PI Di Padova FE, Schuler W;

DR WPI; 2001-590062/66.

DR N-PsDB; AAH26789.

XX CD154 binding molecule, in particular antibody to human CD154 for use
 PT in treatment, prevention of autoimmune, inflammatory diseases,
 PT atherosclerosis, Alzheimer's disease and prevention of transplant
 PT rejection

PS Claim 4; Page 32; 37pp; English.

XX The present sequence is that of the light chain variable region
 CC (VL) of mouse anti-human CD154 monoclonal antibody ABR793. The
 CC antibody is produced by hybridoma 207.2, which was obtained by
 CC fusing spleen cells from mice immunised with a soluble human CD154
 CC recombinant protein with murine P1-O myeloma cells. The invention
 CC provides a CD154 binding molecule, in particular an antibody to
 CC human CD154, in which the VH region has the complementarity
 CC determining regions CDR1, CDR2 and CDR3 of ABR793 VH and the VL
 CC region has the CDR1, CDR2 and CDR3 of ABR793 VL. The CD154 binding
 CC molecule is especially a human antibody in which the VH and VL
 CC domains are essentially those of ABR793, with the constant parts of
 CC human heavy and light chains. DNA constructs and expression vectors
 CC are also claimed. The CD154 binding molecules are useful in
 CC inhibition of an immune response mediated by CD154-positive cell
 CC interactions with CD40-positive cells, in the treatment and/or
 CC prevention of diseases, disorders or conditions where CD154
 CC modulation and/or interference with or inhibition of the CD154:CD40
 CC interactions is therapeutically beneficial, prevention of
 CC macrophage-associated inflammatory processes and in the treatment of
 CC diseases where suppression of antibody responses to antigens is
 CC desirable (claimed). The CD154 binding molecules are useful for
 CC prevention of cell, tissue or organ graft rejection, in the prevention
 CC and treatment of autoimmune or inflammatory diseases, atherosclerosis
 CC or Alzheimer's disease, and also for inhibiting B cell proliferation
 CC and differentiation, T cell responses, induction or modulation of T
 CC or B cell tolerance or inhibition of the growth of tumour cells
 CC expressing CD154 antigen. Such conditions include autoimmune and
 CC non-autoimmune disorders, in particular: Addison's disease, Celiac
 CC sprue, glomerulonephritis, Grave's disease, Hashimoto's thyroiditis,
 CC haemolytic disease of the newborn, keratitis, multiple sclerosis,
 CC polymyositis, psoriasis, rheumatic fever, rheumatoid arthritis,
 CC sarcoidosis, syphilis, tuberculosis, ulcerative colitis,
 CC HIV infection, leukaemia or lymphoma.

XX Sequence 107 AA:

XX Query Match 96.8%; Score 538; DB 22; Length 107;
 XX Best Local Similarity 98.1%; Pred. No. 4.2e-34;
 XX Matches 105; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 DIQMTGSPSSISASVGDRTTTCRASQGISWLMWYQKPEKAKSLIYAASLSQGVPS 60
 DB 1 DIQMTGSPSSISASVGDRTTTCRASQGISWLMWYQKPEKAKSLIYAASLSQGVPS 60
 OY 61 RFGSGSGTDFLTITSSLOPEDPATYCCOQNSYPTFGGKTKEIK 107
 DB 61 RFGSGSGTDFLTITSSLOPEDPATYCCOQNSYPTFGGKTKEIK 107

RESULT 5

AA48004 standard; protein; 107 AA.

XX AA48004;

XX 08-MAR-2002 (first entry)

DE Human monoclonal antibody B11 variable light chain protein.

KV	Human; monoclonal antibody; B1; antigen binding portion; dendritic cell;
KW	mannose receptor; growth cytolysis; pathogen; virus; bacterium;
KX	autoimmune disease; inflammatory disorder; rheumatoid arthritis;
KY	multiple sclerosis; diabetes mellitus; immunomodulatory;
KZ	antiinflammatory; antirheumatic; antiarthritic; neuroprotective;
LX	antidiabetic; antianemic; endocrine; dermatological; antihypoid;
LY	uropathic; ophthalmological; muscular.
MX	
NY	Homo sapiens.
OZ	
PX	WO200185798-A2.
PN	
PD	15-NOV-2001.
PP	
PF	08-MAY-2001; 2001WO-US15114.
PG	
PH	08-MAY-2000; 2000US-203126P.
PI	07-SEP-2000; 2000US-230739P.
PJ	
PK	(MEDA-) MEDAREX INC.
PL	
PM	Deo YM, Keler T;
PN	
PO	MP1; 2002-089788/12.
PP	N-PEDB; ABA06023.
PQ	
PR	New human monoclonal antibodies specific for dendritic cells, useful
PS	for inhibiting growth or inducing cytolysis of a dendritic cell and
PT	treating or preventing a dendritic cell mediated disease, e.g.,
PU	autoimmune disorders -
PV	
PW	Example 2; Fig 13; 95pp; English.
PX	
PY	The invention relates to human monoclonal antibodies or their antigen
PZ	binding portions that specifically bind to dendritic cells and has one or
QA	more of the following characteristics:
QB	(a) a binding affinity constant to a dendritic cell of at least about
QC	10 ⁶ to the power 7 M-1;
QD	(b) the ability to opsonise a dendritic cell;
QE	(c) the ability to internalise after binding to dendritic cells; or
QF	(d) the ability to activate dendritic cells.
QG	The isolated human monoclonal antibody or its antigen binding portion
QH	may also have any of the following characteristics:
QI	(a) mediates cytolysis of dendritic cells in the presence of human
QJ	effector cells; or
QK	(b) inhibits growth of dendritic cells.
QL	(c) The antibodies or its antigen binding portion, binds to and blocks the
QM	human mannose receptor on dendritic cells. The antibodies have
QN	immunomodulatory, antiinflammatory, antirheumatic, antiarthritic,
QO	neuroprotective, antidiabetic, antianemic, endocrine, dermatological,
QP	corticosteroid, uropathic, ophthalmological and muscular activity. The
QQ	antibodies or their antigen-binding fragments are useful for inhibiting
QR	growth of a dendritic cell, inducing cytolysis of a dendritic cell,
QS	treating or preventing a dendritic cell mediated disease, detecting the
QT	presence of a dendritic cell, targeting an antigen to a dendritic cell
QU	and preventing binding of a pathogen (a virus or a bacterium) to human
QV	mannose receptor on dendritic cells. In particular, the antibodies may be
QW	used to treat, autoimmune disease, graft versus host disease, immune
QX	system or inflammatory disorders (e.g. rheumatoid arthritis), multiple
QY	sclerosis, diabetes mellitus, myasthenia gravis, pernicious anaemia,
QZ	Addison's disease, lupus erythematosus, Reiter's syndrome and Graves
RA	disease. The present sequence is that of the human monoclonal antibody
RB	B1 variable light chain, useful to the invention.
RC	
RD	
RE	
RF	
RG	
RH	
RI	
RJ	
RK	
RL	
RM	
RN	
RO	
RP	
RQ	
RR	
RS	
RT	
RU	
RV	
RW	
RX	
RY	
RZ	
SA	
SB	
SC	
SD	
SE	
SF	
SG	
SH	
SI	
SJ	
SK	
SL	
SM	
SN	
SO	
SP	
SQ	
SR	
SS	
ST	
SV	
SW	
SX	
SY	
SZ	
TA	
TB	
TC	
TD	
TE	
TF	
TF	
TH	
TI	
TJ	
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UQ	
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UX	
UY	
UZ	
VX	
VY	
VZ	
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WX	
WY	
WZ	
XA	
XB	
XC	
XD	
XE	
XE	
XF	
XG	
XH	
XI	
XI	
XJ	
XK	
XL	
XM	
XN	
XO	
XP	
XQ	
XR	
XS	
XT	
YT	</

[illegible]

```

RESULT 7
ID AAB75040 standard; Protein; 224 AA.
XX
AC AAB75040;
XX
DT 19-JUL-2001 (first entry)
XX
DE TRO005 Humab kappa chain protein sequence JELK.
XX
KW Human; antibody; immunoglobulin; interleukin 8; IL8; immunogen;
human antibody phage display library; immunisation; transgenic animal.
OS Homo sapiens.
XX Synthetic.
PN WO200125492-A1.
PD 12-APR-2001.
PF 02-OCT-2000; 2000MO-US27237.
PR 02-OCT-1999; 99US-0157415.
PR 01-DEC-1999; 99US-0453234.
PA (BIOS-) BIOSITE DIAGNOSTICS INC.
PI (GENP-) GENPHARM INT SUBSIDIARY OF MEDAREX INC.
PI Buechler J, Valkirs G, Gray J, Lonberg N;
DR MPI; 2001-335567/35.
PT Producing a human antibody phage display library comprises providing a
transgenic animal whose genome comprises human immunoglobulin genes and
isolating nucleic acids encoding antibody chains from lymphatic cells -
Example 37; Page 121-122; 161pp; English.
PS
XX
CC The present invention describes a method (M1) for producing a human
antibody phage display library (I), comprising: (1) providing a nonhuman
transgenic animal (II) whose genome comprises human immunoglobulin genes
(2) isolating nucleic acids encoding human antibody chains (III) from
lymphatic cells; and (3) forming a library of display packages whose
members comprise a nucleic acid encoding (III) which is displayed from
the package. The method is used for producing a human antibody display
library; e.g., a Rab phage display library. The display method may be
used to screen nucleic acids encoding antibody chains obtained from
immunised nonhuman transgenic animals, and from this a population of
antibodies may be prepared. Production of a human monoclonal antibodies
display library using this method means there is no need to immunise
humans with antigens, and the difficulties faced with immortalising B
cells are avoided. AAH2958 to AAH3006 and AAB74994 to AAB75056
represent sequences used in the exemplification of the present invention.
XX
SQ Sequence 224 AA;
Query Match 95.5%; Score 531; DB 22; Length 224;
Best Local Similarity 96.3%; Pred. No. 2,9e-33;
Matches 103; Conservative 2; Mismatches 2; Indels 0; Gaps 0
QY 1 DIOMTSPSSLSASVDRVTITTCRAQGSIISLAWYOQKEKAPKSLITYAASSLOSQVPS 60
DB 1 NIQMTPSSLSASVGDRTVITTRASQGISWLAWOQKEKAPKSLITYAASSLOSQVPS 60
QY 61 RSSGSGSGTDFTLTSSLOPEDPATYYCOQYNSYPPTFGGTIVEIK 107
DB 61 RSSGSGSGTDFTLTSSLOPEDPATYYCOQYNSYPPTFGGTIVDK 107

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XX AA075044;
AC
XX
XX 19-JUL-2001 (first entry)
XX
XX TR0005 HuMab kappa chain protein sequence 359K.
DE
XX
XX Human; antibody; immunoglobulin; interleukin 8; IL8; immunogen;
KW human antibody phage display library; immunisation; transgenic animal.
XX
XX Homo sapiens.
OS Synthetic.
XX
XX MO200125492-A1.
XX
XX 12-APR-2001.
XX
XX 02-OCT-2000; 2000MO-US27237.
XX
XX PF
XX
XX 02-OCT-1999; 99US-0157415.
XX
XX PR 01-DEC-1999; 99US-0453234.
XX
XX PA (BIOS-) BIOSITE DIAGNOSTICS INC.
XX (GENP-) GENPHARM INT SUBSIDIARY OF MEDAREX INC.
XX
XX Buechler J, Walkiers G, Gray J, Lonberg N;
XX
XX WPI; 2001-335567/35.
XX
XX
XX Producing a human antibody phage display library comprises providing a
XX transgenic animal whose genome comprises human immunoglobulin genes and
XX isolating nucleic acids encoding antibody chains from lymphatic cells -
XX
XX Example 37; Page 121-122; 161pp; English.
XX
XX The present invention describes a method (M1) for producing a human
XX antibody phage display library (I), comprising: (1) providing a nonhuman
XX transgenic animal (II) whose genome comprises human immunoglobulin genes;
XX (2) isolating nucleic acids encoding human antibody chains (III) from
XX lymphatic cells; and (3) forming a library of display packages whose
XX members comprise a nucleic acid encoding (III) which is displayed from
XX the package. The method is used for producing a human antibody display
XX library, e.g., a Fab phage display library. The display method may be
XX used to screen nucleic acids encoding antibody chains obtained from
XX immunised nonhuman transgenic animals, and from this a population of
XX antibodies may be prepared. Production of a human monoclonal antibodies
XX display library using this method means there is no need to immunise
XX humans with antigens, and the difficulties faced with immortalising B
XX cells are avoided. AAH9998 to AAH3006 and AA074994 to AA075056
XX represent sequences used in the exemplification of the present invention.
XX
XX Sequence 224 AA;
XX
XX Query Match 94.8%; Score 527; DB 22; Length 224;
XX Best Local Similarity 94.4%; Pred. No. 5.8e-33;
XX Matches 101; Conservative 4; Mismatches 2; Indels 0; Gaps 0;
XX
XX 1 DIGNTPSSISASVDPGRVTTTCASGIGISWLMYQCKEKPASLIIYASSLSQSGVPS 60
XX ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
XX 1 ELVWTQSPSSISASVGRVITTCASGIGISWLMYQCKEKPASLIIYASSLSQSGVPS 60
XX
XX RFSGSGSGTDFTLTITSSLOPEDFATYCCQVNSYVPTFGQGTKEIK 107
XX ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
XX 61 RFSGSGSGTDFTLTITSSLOPEDFATYCCQVNSYVPTFGQGTKEIK 107
XX
XX ID AA07543 standard; Protein: 109 AA.
XX
XX AA07543;
XX
XX 22-JAN-1998 (first entry)
XX

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XX Human Ab light chain variable region V-kappa-1 consensus.
DB XX
XX Human, antibody, preparation, library, V-kappa-1, variable region,
KM light chain, consensus.
XX
XX Homo sapiens.
OS
XX MO9708320-AL.
PN
XX
XX 06-MAR-1997.
PD
XX 19-AUG-1996; 96WO-EP03647.
PF
XX 18-AUG-1995; 95EP-0113021.
PR
XX (MORP-) MORPHOSYS GES PROTEINOPTIMERUNG MBH.
PA
XX Ge L, Ilag V, Knapik A, Moroney S, Pack P, Plueckthun A,
PI WPI; 1997-179277/16.
XX
XX N-PSDB; AA187938.
DR
XX Preparation of human derived antibody gene library - using synthetic
PT consensus sequences, and signal consensus antibody gene as universal
PT framework for highly diverse antibody libraries
XX
XX Example 1; Fig 3A, 436pp; English.
PS
XX The present sequence is the human antibody light chain
CC variable region synthetic kappa sequence V-kappa-1, used in the
CC preparation of a human derived antibody gene library.
XX
XX Sequence 109 AA;
SQ
Query Match 91.5%; Score 509; DB 18; Length 109;
Best Local Similarity 93.5%; Pred. No. 6.9e-32;
Matches 100; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
QY 1 DIQMTQSPSSLSASVDGRTTITCRASQGISWLAAYQOKPKSLIYAASLSQGVPS 60
DB 1 DIQMTQSPSSLSASVDGRTTITCRASQGISWLAAYQOKPKSLIYAASLSQGVPS 60
QY 61 RFGSGSGTDFLTITSSLOPEDFATYCCQVNSYPTFGQTKVEIK 107
DB 61 RFGSGSGTDFLTITSSLOPEDFATYCCQVNSYPTFGQTKVEIK 107
RESULT 10
AAYS6723
ID AAYS6723 standard; protein; 124 AA.
XX
XX AAYS6723;
AC
XX
XX 15-FEB-2000 (first entry)
DT
XX
XX Amino acid sequence of chimpanzee V kappa cDNA clone 46-11.
DB
XX Complementarity determining region; antibody; primate; immunogenicity;
KM Old world ape; Old world monkey; antigen-binding affinity.
XX
XX Pan troglodytes.
OS
XX MO9555369-AL.
PN
XX
XX 04-NOV-1999.
PD
XX
XX 28-APR-1999; 99WO-US09131.
PF
XX 28-APR-1998; 98US-0083367.
PR
XX (SMK) SMITHKLINE BEECHAM CORP.
PA
XX
XX

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PI Taylor AH;
XX
XX WPI; 2000-023265/02.
DR
XX N-PSDB; AA239326.
DR
XX
XX Antibodies containing donor complementarity determining regions and
PT non-human primate acceptor frameworks, having reduced immunogenicity in
PT humans -
XX
XX Example 2; Page 66; 123pp; English.
PS
XX
XX The invention provides an antibody (Ab) comprising donor CDRs
CC (complementarity determining regions) derived from a non-human antigen-
CC specific donor antibody, and an acceptor framework from a non-human
CC primate. The Abs are prepared by grafting CDRs from a non-human antigen-
CC specific donor antibody onto homologous Old World ape or monkey acceptor
CC frameworks. The Abs have reduced immunogenicity and are better tolerated
CC in humans (because of the close similarity between the human and primate
CC proteins), but retain the full antigen-binding affinity of the donor
CC antibody.
XX
XX Sequence 124 AA;
SQ
Query Match 91.4%; Score 508; DB 21; Length 124;
Best Local Similarity 90.7%; Pred. No. 9.3e-32;
Matches 97; Conservative 6; Mismatches 4; Indels 0; Gaps 0;
QY 1 DIQMTQSPSSLSASVDGRTTITCRASQGISWLAAYQOKPKSLIYAASLSQGVPS 60
DB 18 DIQMTQSPSSLSASVDGRTTITCRASQGISWLAAYQOKPKSLIYAASLSQGVPS 77
QY 61 RFGSGSGTDFLTITSSLOPEDFATYCCQVNSYPTFGQTKVEIK 107
DB 78 RFGSGSGTDFLTITSSLOPEDFATYCCQVNSYPTFGQTKVEIK 124
RESULT 11
AAG65571
ID AAG65571 standard; protein; 107 AA.
XX
XX AAG65571;
AC
XX
XX 30-NOV-2001 (first entry)
DT
XX
XX Amino acid sequence of protein seg Id No. 96.
DB
XX Gene library; immunoglobulin; antibody library; human.
XX
XX Homo sapiens.
OS
XX
XX WO200162907-AL.
PN
XX
XX 30-AUG-2001.
PD
XX
XX 22-FEB-2001; 2001WO-JP01298.
PF
XX
XX 22-FEB-2000; 2000JP-0050543.
PR
XX
XX (MEDI-) MEDICAL & BIOLOGICAL LAB CO LTD.
PA
XX
XX Kurosawa Y, Akahori Y, Iba Y, Morino K, Shinohara M, Takahashi M;
PI Okuno Y, Shiraki K;
XX
XX WPI; 2001-565420/63.
DR
XX N-PSDB; AA47735.
DR
XX
XX Producing gene libraries and antibody libraries, involves selecting a
PT light chain that binds to a heavy chain product to produce a functional
PT region, and producing a gene library of the light chain variable
PT regions -
XX
XX Examples; p 172; 181pp; Japanese.
XX

```

CC The invention relates to producing gene libraries, comprising
 CC immunoglobulin light and heavy variable region. The method involves
 CC selecting light chain that binds with the heavy chain product to produce
 CC a functional conformation, producing a gene library comprising a
 CC collection of these light chain variable genes, and combining with gene
 CC library of heavy chain variable genes. The method is used for production
 CC of gene and antibody libraries.

XX Sequence 107 AA;

Query Match 91.2%; Score 507; DB 22; Length 107;

Best Local Similarity 92.5%; Pred. No. 9, 7e-32;
 Matches 99; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 1 DIQMTSPSSLSASVGDRTITTCRASOGISSWLAWYQKPEKAPKSLIYAASSLSGVS 60
 DB 1 DIQMTSPSSLSASVGDRTITTCRASOGISSWLAWYQKPEKAPKSLIYAASSLSGVS 60

QY 61 RFSGSGSGTDFLTITSSLOPEDFATYCCQVNSYPTFGQTKVEIK 107
 DB 61 RFSGSGSGTDFLTITSSLOPEDFATYCCQVNSYPTFGQTKVEIK 107

RESULT 12

AA875043 standard; Protein; 224 AA.

AA875043;

19-JUL-2001 (first entry)

TR0005 Humab kappa chain protein sequence 388K.

Human; antibody; immunoglobulin; interleukin 8; IL8; immunogen;
 human antibody phage display library; immunisation; transgenic animal.

Homo sapiens.
 Synthetic.

WO200125492-A1.

12-APR-2001.

02-OCT-2000; 2000WO-US27237.

02-OCT-1999; 99US-0157415.

01-DEC-1999; 99US-0453234.

(BIOS-) BIOSITE DIAGNOSTICS INC.
 (GENP-) GENPHARM INT SUBSIDIARY OF MEDAREX INC.

Buechler J, Valikire G, Gray J, Lonberg N;

WPI; 2001-335567/35.

Producing a human antibody phage display library comprises providing a
 transgenic animal whose genome comprises human immunoglobulin genes and
 isolating nucleic acids encoding antibody chains from lymphatic cells -

Example 37; Page 121-122; 161pp; English.

CC The present invention describes a method (M1) for producing a human
 CC antibody phage display library (I), comprising: (1) providing a nonhuman
 CC transgenic animal (II) whose genome comprises human immunoglobulin genes;
 CC (2) isolating nucleic acids encoding human antibody chains (III) from
 CC lymphatic cells; and (3) forming a library of display packages whose
 CC members comprise a nucleic acid encoding (III) which is displayed from
 CC the package. The method is used for producing a human antibody display
 CC library, e.g., a Fab phage display library. The display method may be
 CC used to screen nucleic acids encoding antibody chains obtained from
 CC immunised nonhuman transgenic animals, and from this a population of
 CC antibodies may be prepared. Production of a human monoclonal antibodies
 CC display library using this method means there is no need to immunise

CC humans with antigens, and the difficulties faced with immortalising B
 CC cells are avoided. AA82958 to AA83006 and AA87494 to AA875056
 CC represent sequences used in the exemplification of the present invention.

XX Sequence 224 AA;

Query Match 91.2%; Score 507; DB 22; Length 224;

Best Local Similarity 94.3%; Pred. No. 1, 9e-31;
 Matches 100; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 2 IQMTSPSSLSASVGDRTITTCRASOGISSWLAWYQKPEKAPKSLIYAASSLSGVS 61
 DB 2 IQMTSPSSLSASVGDRTITTCRASOGISSWLAWYQKPEKAPKSLIYAASSLSGVS 61

QY 62 RFSGSGSGTDFLTITSSLOPEDFATYCCQVNSYPTFGQTKVEIK 107
 DB 62 RFSGSGSGTDFLTITSSLOPEDFATYCCQVNSYPTFGQTKVEIK 107

RESULT 13

AA840956 standard; Protein; 109 AA.

AA840956;

25-FEB-1994 (first entry)

Human germ-line gene HK137 antibody light (kappa) chain.

humanised antibody; human germ-line; light chain; variable region;
 framework region; reshaped antibody; CDR-grafted antibody;
 complementary determining region; immuno silent.

Homo sapiens.

Location/Qualifiers

1..23 /label= FR1

24..34 /note= "framework region"

35..49 /label= CDR1

50..56 /label= FR2

57..88 /label= CDR2

89..97 /label= FR3

98..109 /label= CDR3

110..120 /label= FR4

121..131 /note= "framework region"

WO9317105-A.

02-SEP-1993.

19-FEB-1993; 93WO-GB00363.

19-FEB-1992; 92GB-0003459.

(SCOT-) SCOTGEN LTD.

Carr FU, Harris WJ, Winter GP;

WPI; 1993-288411/36.

New altered antibodies with reduced immune responses - have
 germ-line aminoacid residues replacing somatically mutated
 residues

CC (light kappa subgroup I).

XX Sequence 107 AA;

Query Match 90.5%; Score 503; DB 22; Length 107;
 Best Local Similarity 92.5%; Pred. No. 2e-31;
 Matches 99; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 1 DIOMTQSPSSLSASVGDRTTICRASOGISWLAWYQOKPEKAPKSLIYAAASSLGVP 60
 |||||||
 Db 1 DIOMTQSPSSLSASVGDRTTICRASOGISWLAWYQOKPEKAPKSLIYAAASSLGVP 60

QY 61 RPSGSGSGTDFTLTITSSLOPEDFATYYCQYNSYPTFGQTKVEIK 107
 |||||||
 Db 61 RPSGSGSGTDFTLTITSSLOPEDFATYYCQYNSYPTFGQTKVEIK 107

Search completed: June 3, 2003, 08:14:45
 Job time : 50.2048 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: June 3, 2003, 08:21:07 ; Search time 25.3805 Seconds

(without alignments)
426.742 Million cell updates/sec

Title: US-09-644-668a-13

Perfect score: 556
Sequence: 1 DIQMTQSSSSASASVGDVVT.....COQVNSYPPTFGQGTKEIK 107

Scoring table:
BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 383519 seqs, 101223594 residues

Total number of hits satisfying chosen parameters: 383519

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

Published Applications AA.*
1: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
4: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
6: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
7: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep.*
8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
9: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
10: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep.*
11: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
12: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep.*
13: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
14: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	538	96.8	107	US-10-035-637-2	Sequence 2, Appl1
2	509	91.5	108	US-10-125-687-8	Sequence 8, Appl1
3	509	91.5	108	US-10-025-687-8	Sequence 8, Appl1
4	503	90.5	107	US-10-268-501-5	Sequence 5, Appl1
5	503	90.5	108	US-09-056-160B-12	Sequence 12, Appl1
6	503	90.5	109	US-09-811-123-6	Sequence 6, Appl1
7	503	90.5	244	US-09-880-748-1881	Sequence 1881, Ap
8	494	88.8	236	US-09-859-053-10	Sequence 30, Appl1
9	490.5	88.2	109	US-09-798-058-4	Sequence 4, Appl1
10	488	87.8	95	US-10-194-975-62	Sequence 62, Appl1
11	488	87.8	107	US-09-801-185A-1	Sequence 1, Appl1
12	487	87.6	107	US-09-801-185A-9	Sequence 9, Appl1
13	487	87.6	240	US-09-968-561A-2	Sequence 2, Appl1
14	487	87.6	240	US-09-192-854-2	Sequence 2, Appl1
15	487	87.6	244	US-09-880-748-82	Sequence 82, Appl1
16	487	87.6	244	US-09-880-748-261	Sequence 261, App
17	485	87.2	107	US-10-073-644C-4	Sequence 4, Appl1
18	485	87.2	214	US-10-153-382-19	Sequence 19, Appl1
19	484	87.1	111	US-09-920-171-7	Sequence 7, Appl1

20	484	87.1	263	9	US-09-956-086-3	Sequence 3, Appl1
21	484	87.1	263	9	US-09-956-087-3	Sequence 3, Appl1
22	484	87.1	283	10	US-09-985-442-6	Sequence 6, Appl1
23	484	87.1	283	10	US-09-983-580-6	Sequence 6, Appl1
24	483	86.9	244	9	US-09-880-748-164	Sequence 164, App
25	482.5	86.8	106	9	US-10-040-244-17	Sequence 17, Appl
26	482	86.7	244	9	US-09-880-748-280	Sequence 280, App
27	479	86.2	107	9	US-10-143-437-25	Sequence 25, Appl
28	479	86.2	107	10	US-09-863-693-25	Sequence 25, Appl
29	479	86.2	237	9	US-09-880-748-1906	Sequence 1906, Ap
30	479	86.2	237	9	US-09-880-748-2003	Sequence 2003, Ap
31	479	86.2	237	9	US-09-880-748-2005	Sequence 2005, Ap
32	479	86.2	237	9	US-09-880-748-2017	Sequence 2017, Ap
33	479	86.2	237	9	US-09-880-748-2019	Sequence 2019, Ap
34	479	86.2	237	9	US-09-880-748-2020	Sequence 2020, Ap
35	479	86.2	237	9	US-09-880-748-2027	Sequence 2027, Ap
36	479	86.2	237	9	US-09-880-748-2028	Sequence 2028, Ap
37	479	86.2	237	9	US-09-880-748-2040	Sequence 2040, Ap
38	479	86.2	237	9	US-09-880-748-2043	Sequence 2043, Ap
39	479	86.2	237	9	US-09-880-748-2104	Sequence 2104, Ap
40	479	86.2	237	9	US-09-880-748-2114	Sequence 2114, Ap
41	479	86.2	239	9	US-09-880-748-1882	Sequence 1882, Ap
42	479	86.2	239	9	US-09-880-748-1922	Sequence 1922, Ap
43	479	86.2	239	9	US-10-151-882-23	Sequence 23, Appl
44	479	86.2	241	9	US-09-880-748-1889	Sequence 1889, Ap
45	479	86.2	241	9	US-09-880-748-1901	Sequence 1901, Ap

ALIGNMENTS

RESULT 1
US-10-035-637-2
Sequence 2, Application US/10035637
Publication No. US2003003167A1
GENERAL INFORMATION:
APPLICANT: Keler, Tibor
TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO DENDRITIC
FILE REFERENCE: MXI-166CP
CURRENT APPLICATION NUMBER: US/10/035,637
CURRENT FILING DATE: 2001-11-07
PRIOR APPLICATION NUMBER: 09/851,614
PRIOR FILING DATE: 2001-03-08
PRIOR APPLICATION NUMBER: USSN 60/203,126
PRIOR FILING DATE: 2000-05-08
PRIOR APPLICATION NUMBER: USSN 60/230,739
NUMBER OF SEQ ID NOS: 9
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 2
LENGTH: 107
TYPE: PRT
ORGANISM: Homo sapiens
US-10-035-637-2
Query Match
Best Local Similarity 96.8% Score 538; DB 9; Length 107;
Matches 104; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 DIQMTQSSSSASASVGDVVTITCRASQGISGSIWAWQOKPEKAPKSLITYAASSLQSGVPS 60
DB 1 DIQMTQSSSSASASVGDVVTITCRASQGISGSIWAWQOKPEKAPKSLITYAASSLQSGVPS 60
QY 61 RFGSGSGTDFTLTITSLQPEDFATYYCOQVNSYPPTFGQGTKEIK 107
DB 61 RFGSGSGTDFTLTITSLQPEDFATYYCOQVNSYPPTFGQGTKEIK 107
RESULT 2
US-10-125-687-8
Sequence 8, Application US/10125687

Publication No. US20030054407A1
GENERAL INFORMATION:
APPLICANT: Luo, Peter
TITLE OF INVENTION: STRUCTURE-BASED CONSTRUCTION OF HUMAN ANTIBODY LIBRARY
FILE REFERENCE: 26050-705
CURRENT APPLICATION NUMBER: US/10/125,687
CURRENT FILING DATE: 2002-04-17
NUMBER OF SEQ ID NOS: 28
SOFTWARE: Patent in version 3.1
SEQ ID NO 8
LENGTH: 108
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Human consensus antibody light chain variable region
US-10-125-687-8

Query Match 91.5%; Score 509; DB 9; Length 108;
Best Local Similarity 93.5%; Pred. No. 5,4e-30;
Matches 100; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVDGRTITCRASQGISSTLAWYQOKPKSLIYAASSLSGSPS 60
DB 1 DIQMTQSPSSLSASVDGRTITCRASQGISSTLAWYQOKPKSLIYAASSLSGSPS 60
QY 61 RFGSGSGTDFLTITSLQPEDFATYYCCQVNSYPTFGQTKVEIK 107
DB 61 RFGSGSGTDFLTITSLQPEDFATYYCCQVNSYPTFGQTKVEIK 107

RESULT 3
US-10-025-687-8
Sequence 8, Application US/10025687
Patent No. US2002014225A1
GENERAL INFORMATION:
APPLICANT: Luo, Peter
TITLE OF INVENTION: STRUCTURE-BASED CONSTRUCTION OF HUMAN ANTIBODY LIBRARY
FILE REFERENCE: 26050-705
CURRENT APPLICATION NUMBER: US/10/025,687
CURRENT FILING DATE: 2002-04-17
NUMBER OF SEQ ID NOS: 28
SOFTWARE: Patent in version 3.1
SEQ ID NO 8
LENGTH: 108
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Human consensus antibody light chain variable region
US-10-025-687-8

Query Match 91.5%; Score 509; DB 12; Length 108;
Best Local Similarity 93.5%; Pred. No. 5,4e-30;
Matches 100; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVDGRTITCRASQGISSTLAWYQOKPKSLIYAASSLSGSPS 60
DB 1 DIQMTQSPSSLSASVDGRTITCRASQGISSTLAWYQOKPKSLIYAASSLSGSPS 60
QY 61 RFGSGSGTDFLTITSLQPEDFATYYCCQVNSYPTFGQTKVEIK 107
DB 61 RFGSGSGTDFLTITSLQPEDFATYYCCQVNSYPTFGQTKVEIK 107

RESULT 4
US-10-268-501-5
Sequence 5, Application US/10268501
Publication No. US20030086924A1
GENERAL INFORMATION:
APPLICANT: Sliwkowski, Mark X.
TITLE OF INVENTION: Treatment with Anti-ErbB2 Antibodies
FILE REFERENCE: P1467R2P1
CURRENT APPLICATION NUMBER: US/10/268,501
CURRENT FILING DATE: 2002-10-10

PRIOR APPLICATION NUMBER: US 09/602,812
PRIOR FILING DATE: 2000-06-23
PRIOR APPLICATION NUMBER: US 60/141,316
PRIOR FILING DATE: 1999-06-25
NUMBER OF SEQ ID NOS: 13
SEQ ID NO 5
LENGTH: 107
TYPE: PRT
ORGANISM: Artificial sequence
FEATURE:
OTHER INFORMATION: light chain consensus sequence
US-10-268-501-5

Query Match 90.5%; Score 503; DB 9; Length 107;
Best Local Similarity 92.5%; Pred. No. 1,4e-29;
Matches 99; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVDGRTITCRASQGISSTLAWYQOKPKSLIYAASSLSGSPS 60
DB 1 DIQMTQSPSSLSASVDGRTITCRASQGISSTLAWYQOKPKSLIYAASSLSGSPS 60
QY 61 RFGSGSGTDFLTITSLQPEDFATYYCCQVNSYPTFGQTKVEIK 107
DB 61 RFGSGSGTDFLTITSLQPEDFATYYCCQVNSYPTFGQTKVEIK 107

RESULT 5
US-09-056-160B-12
Sequence 12, Application US/09056160B
Patent No. US20020032315A1
GENERAL INFORMATION:

APPLICANT: Baca, Manuel
APPLICANT: Wells, James A.
APPLICANT: Presta, Leonard G.
APPLICANT: Lowman, Henry B.
APPLICANT: Chen, Yvonne M.
TITLE OF INVENTION: ANTI-VEGF ANTIBODIES
NUMBER OF SEQUENCES: 131
CORRESPONDENCE ADDRESS:
ADDRESS: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA

ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/056,160B
FILING DATE: 06-Apr-1998
CLASSIFICATION: 424

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/054,856
FILING DATE: 06-AUG-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hasak, Janet E.
REGISTRATION NUMBER: 28,616
REFERENCE/DOCKET NUMBER: P1093R2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1896
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 108 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-09-056-160B-12

Query Match 90.5%; Score 503; DB 10; Length 108;
Best Local Similarity 92.5%; Pred. No. 1,4e-29;

	Matches	99, Conservative	3, Mismatches	5, Indels	0, Gaps	0, Nucleotide
Qy	1	DIOMTOSPSLSASVAGDE	RVTTITTCRASGSISSW	LMAYQOKPEKAPKSLI	YLAASSLSQGPS	60
		1	DIQMTGSSSSLSASVAG	DERVTTITTCRASGSI	SWLMAYQOKPEKAPK	SLIYLAASSLSQGPS
Dd	1	DIQMTGSSSSLSASVAG	DERVTTITTCRASGSI	SWLMAYQOKPEKAPK	SLIYLAASSLSQGPS	60
Qy	61	RFSSGGSGTDFTLTIT	SLSDPEDFATYYCOO	NSVPTTGCGKVKIK		107
Dd	61	RFSSGGSGTDFTLTIT	SLSDPEDFATYYCOO	NSLPTTGCGKVKIK		107

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RESULT 6
US-09-811-123-6
/ Sequence 6, Application US/09811123
/ Patient No. US20020001587A1
GENERAL INFORMATION:
APPLICANT: Sharon Erickson
APPLICANT: Ralph Schwall
APPLICANT: Mark Sliwowski
TITLE OF INVENTION: METHODS OF TREATMENT USING ANTI-EPDB
TITLE OF INVENTION: ANTIBODY-WAYMANSINOID CONJUGATES
FILE REFERENCE: GENENT.073A2
CURRENT APPLICATION NUMBER: US/09/811,123
CURRENT FILING DATE: 2001-03-16
PRIOR APPLICATION NUMBER: 60/238,347
PRIOR FILING DATE: 2000-10-05
PRIOR APPLICATION NUMBER: 09/602,530
PRIOR FILING DATE: 2000-06-23
NUMBER OF SEQ ID NOS: 11
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 6
LENGTH: 109
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Humanized Antibody Sequence
US-09-811-123-6

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Query Match	90.5%: Score 503; DB 10;	Length 109;
Best Local Similarity	92.5%: Pred. No. 1.5e-29;	
Matches	99; Conservative 3; Mismatches 25;	Indels 0; Gaps 0;
QY	1 DIQWTSPPSSIASVGDVRVITTCRASQGISMLAWYQOQKPEKAPSLIYAASSLSQGVPS	60
	:::	
Db	1 DIQWTSPPSSIASVGDVRVITTCRASQGISNRYLAWYQOQKPGAPLTLIYAASSLSQGVPS	60
QY	61 RFSQSGSGDTFTLTISLQPEDFATYCYCOQNSYPTPRGQGGKKEIK	107
Db	61 RFSQSGSGDTFTLTISLQPEDFATYCYCOQNSLPMWTGGQGGKKEIK	107

US-09-880-748-1881
 RESULT 7
 , Sequence 1881, Application US/09880748
 , Publication No. US2003005937A1
 , GENERAL INFORMATION:
 , APPLICANT: Ruben et al.
 , TITLE OF INVENTION: Antibodies that Immunospecifically Bind BlyS
 , FILE REFERENCE: p5523
 , CURRENT APPLICATION NUMBER: US/09/880,748
 , CURRENT FILING DATE: 2001-06-15
 , PRIOR APPLICATION NUMBER: 60/212,210
 , PRIOR FILING DATE: 2000-06-15
 , PRIOR APPLICATION NUMBER: 60/240,816
 , PRIOR FILING DATE: 2000-10-17
 , PRIOR APPLICATION NUMBER: 60/276,248
 , PRIOR FILING DATE: 2001-03-16
 , PRIOR APPLICATION NUMBER: 60/277,379
 , PRIOR FILING DATE: 2001-03-21
 , PRIOR APPLICATION NUMBER: 60/299,499
 , PRIOR FILING DATE: 2001-05-25
 , NUMBER OF SEQ ID NOS: 3239
 , SOFTWARE: PatentIn Ver. 2.0

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; SEQ ID NO 1881
; LENGTH: 244
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-1881

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Query Match	90.5%	Score 503	DB 9	length 244
Best Local Similarity	92.5%	Pred. No.	3e-29	
Matches 99	Conservative	2	Mismatches 6	Indels 0
				Gaps 0

QY 1 DIQHTQPSLSLSVGEVRVITTCRAQGISLMTAAWQOKPEKAPKSLIAASLSQGVPS 60
Db 137 DIWVGQPSFLSLASVGEVRVITTCRAQGISLMTAAWQOKPEKAPKSLIAASLSQGVPS 19
QY 61 RFSSSGSGTDFLLISLQPEDPATYCCQXNSPPTFQGGTVEIK 107
Db 197 RFSSSGSGTDFLLISLQPEDPATYCCQXNSPPTFQGGTVEIK 243

RESULT 8
 US-09-859-053-30
 Sequence 30. Application US/09859053
 Patent No. US20020102658A1
 GENERAL INFORMATION:
 APPLICANT: Teuji, Takashi
 APPLICANT: Tezuka, Katsunari
 APPLICANT: Hori, No. US20020102658A1uaki
 TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODY AGAINST A
 TITLE OF INVENTION: COSTIMULATORY SIGNAL TRANSDUCTION MOLECULE AILIM AND
 TITLE OF INVENTION: PHARMACEUTICAL USE THEREOF
 FILE REFERENCE: 06501-079001
 CURRENT APPLICATION NUMBER: US/09/859, 053
 CURRENT FILING DATE: 2001-05-16
 PRIOR APPLICATION NUMBER: JP 2001-99508
 PRIOR FILING DATE: 2001-03-30
 PRIOR APPLICATION NUMBER: JP 2000-147116
 PRIOR FILING DATE: 2000-05-18
 NUMBER OF SEQ ID NOS: 43
 SOFTWARE: FastSeq for Windows Version 4.0
 SEQ ID NO 30
 LENGTH: 236
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-09-859-053-30

[illegible]

RESULT 9
US-09-798-058-4
Sequence 4, Application US/09798058
Patent No. US20020098523A1
GENERAL INFORMATION:
APPLICANT: Vaughan, Tristram John
APPLICANT: Wilton, Alison Jane
APPLICANT: Smith, Stephen
TITLE OF INVENTION: Main, Sarah Helen
FILE REFERENCE: 84632-000100
CURRENT APPLICATION NUMBER: US/09/798,058
CURRENT FILING DATE: 2001-08-29
PRIOR APPLICATION NUMBER: US 60/187,246
PRIOR FILING DATE: 2000-03-03

NUMBER OF SEQ ID NOS: 20
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 4
LENGTH: 109
TYPE: PRT
ORGANISM: Homo sapiens
US-09-798-058-4

Query Match 88.2% Score 490.5; DB 10; Length 109;
Best Local Similarity 89.8%; Pred. No. 1.1e-28;
Matches 97; Conservative 5; Mismatches 5; Indels 1; Gaps 1;

QY 1 DIQMTQSPSSLSASVGRVITTCRASQGISSTLAWYQOKPEKAPKSLIYAASLSQGVPS 60
DB 1 DIQMTQSPSSVSAVSDRVTITCRASQDISSTLAWYQOKPEKAPKSLIYAASLSQGVPS 60
QY 61 RFSGSGSGTDFTLTITSSLOPEDFATYYCOQYNSYP-TRGQGTKEIK 107
DB 61 RFSGSGSGTDFTLTITSSLOPEDFATYYCOQYNSYFPIITGQGTKEIK 108

RESULT 10

US-10-194-975-62
Sequence 62, Application US/10194975
Publication No. US20030039649A1
GENERAL INFORMATION:
APPLICANT: Foote, Jefferson
TITLE OF INVENTION: Super Humanized Antibodies
FILE REFERENCE: 501231.01
CURRENT APPLICATION NUMBER: US/10/194,975
CURRENT FILING DATE: 2002-10-10
PRIOR APPLICATION NUMBER: US 60/305,111
PRIOR FILING DATE: 2001-07-12
NUMBER OF SEQ ID NOS: 122
SOFTWARE: Patentin version 3.1
SEQ ID NO 62
LENGTH: 95
TYPE: PRT
ORGANISM: Homo sapiens
US-10-194-975-62

Query Match 87.8% Score 488; DB 9; Length 95;
Best Local Similarity 98.9%; Pred. No. 1.5e-28;
Matches 94; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGRVITTCRASQGISSTLAWYQOKPEKAPKSLIYAASLSQGVPS 60
DB 1 DIQMTQSPSSLSASVGRVITTCRASQGISSTLAWYQOKPEKAPKSLIYAASLSQGVPS 60
QY 61 RFSGSGSGTDFTLTITSSLOPEDFATYYCOQYNSYP 95
DB 61 RFSGSGSGTDFTLTITSSLOPEDFATYYCOQYNSYP 95

RESULT 11

US-09-801-185A-1
Sequence 1, Application US/09801185A
Publication No. US20030092059A1
GENERAL INFORMATION:
APPLICANT: BASF Aktiengesellschaft
TITLE OF INVENTION: Human Antibodies that Bind Human TNFalpha
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 28 State Street
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/801,185A
FILING DATE: 07-Mar-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/599,226
FILING DATE: 09-FEB-1996
APPLICATION NUMBER: US 60/031,476
FILING DATE: 25-NOV-1996
APPLICATION NUMBER: US 09/125,098
FILING DATE: 07-AUG-1998

ATTORNEY/AGENT INFORMATION:
NAME: DeConli, Giulio A., Jr.
REGISTRATION NUMBER: 31,503
REFERENCE/DOCKET NUMBER: BBI-043CPUSCN
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)227-5941

INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 107 amino acids
TOPOLOGY: linear
TYPE: amino acid

MOLECULE TYPE: peptide
FRAGMENT TYPE: internal
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-801-185A-1

Query Match 87.8% Score 488; DB 9; Length 107;
Best Local Similarity 89.7%; Pred. No. 1.7e-28;
Matches 96; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGRVITTCRASQGISSTLAWYQOKPEKAPKSLIYAASLSQGVPS 60
DB 1 DIQMTQSPSSLSASVGRVITTCRASQGISSTLAWYQOKPEKAPKSLIYAASLSQGVPS 60
QY 61 RFSGSGSGTDFTLTITSSLOPEDFATYYCOQYNSYPTFGQGTKEIK 107
DB 61 RFSGSGSGTDFTLTITSSLOPEDFATYYQGRNRAPTFGQGTKEIK 107

RESULT 12

US-09-801-185A-9
Sequence 9, Application US/09801185A
Publication No. US20030092059A1
GENERAL INFORMATION:
APPLICANT: BASF Aktiengesellschaft
TITLE OF INVENTION: Human Antibodies that Bind Human TNFalpha
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 28 State Street
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/801,185A
FILING DATE: 07-Mar-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/599,226
FILING DATE: 09-FEB-1996
APPLICATION NUMBER: US 60/031,476
FILING DATE: 25-NOV-1996
APPLICATION NUMBER: US 09/125,098
FILING DATE: 07-AUG-1998

Tue Jun 3 08:30:30 2003

us-09-644-668a-13.rapb

Search completed: June 3, 2003, 08:52:52
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OM protein - protein search, using sw model

Run on: June 3, 2003, 08:10:19 ; Search time 16.2509 Seconds

(without alignments)
193.728 Million cell updates/sec

Title: US-09-644-668A-13

Perfect score: 556
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Searched: 262574 seqs, 29422922 residues

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Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	509	91.5	109	4	US-09-025-769B-28
2	509	91.5	109	4	US-09-025-769B-43
3	505	90.8	109	2	US-07-934-373C-3
4	505	90.8	109	3	US-08-437-642B-3
5	505	90.8	109	4	US-08-146-206C-3
6	505	90.8	109	5	PCT-US93-07832-3
7	503	90.5	107	2	US-07-934-373C-18
8	503	90.5	107	3	US-08-437-642B-18
9	503	90.5	107	4	US-08-146-206C-18
10	503	90.5	107	5	PCT-US93-07832-18
11	503	90.5	108	3	US-08-974-893-3
12	493	88.7	117	4	US-09-042-353-48
13	493	88.7	117	4	US-08-758-417A-113
14	490	88.1	109	4	US-09-157-370-3
15	489	87.9	108	3	US-08-974-893-2
16	488	87.8	107	3	US-08-599-226-1
17	488	87.8	107	4	US-09-125-098-1
18	487	87.6	107	3	US-08-599-226-9
19	487	87.6	107	4	US-09-125-098-9
20	487	87.6	108	2	US-08-652-816A-5
21	486	87.4	116	1	US-08-053-131-185
22	486	87.4	116	2	US-08-096-762-185
23	485	87.2	108	3	US-08-812-586-45
24	485	87.2	108	4	US-09-025-769B-14
25	485	87.2	129	1	US-08-217-918-2
26	484	87.1	111	2	US-08-687-352B-7
27	484	87.1	111	4	US-09-109-207C-7

28	484	87.1	111	4	US-09-296-005-7	Sequence 7, Appl
29	484	87.1	263	4	US-09-069-821-3	Sequence 3, Appl
30	484	87.1	183	4	US-09-420-592A-6	Sequence 6, Appl
31	482.5	86.8	114	1	US-08-202-047-25	Sequence 25, Appl
32	482.5	86.8	114	3	US-08-964-690-25	Sequence 25, Appl
33	482	86.7	108	2	US-08-652-816A-2	Sequence 2, Appl
34	482	86.7	108	2	US-08-378-933-32	Sequence 32, Appl
35	482	86.7	108	2	US-08-378-933-34	Sequence 34, Appl
36	479	86.2	107	1	US-08-276-852-84	Sequence 84, Appl
37	479	86.2	107	1	US-08-899-575-84	Sequence 84, Appl
38	479	86.2	107	1	US-08-899-575-84	Sequence 84, Appl
39	479	86.2	107	5	PCT-US95-08743-84	Sequence 84, Appl
40	479	86.2	108	2	US-08-652-816A-4	Sequence 4, Appl
41	479	86.2	108	2	US-08-652-816A-53	Sequence 53, Appl
42	479	86.2	108	2	US-08-379-057-29	Sequence 29, Appl
43	478	86.0	108	4	US-08-983-607-29	Sequence 29, Appl
44	477	85.8	107	4	US-09-240-274-40	Sequence 40, Appl
45	476.5	85.7	114	2	US-08-561-521-43	Sequence 43, Appl

ALIGNMENTS

RESULT 1
US-09-025-769B-28
Sequence 28, Application US/09025769B
Patent No. 6300064
GENERAL INFORMATION:
APPLICANT: Knappik, Achim
APPLICANT: Pack, Peter
APPLICANT: Ilaag, Vic
APPLICANT: Ge, Liming
APPLICANT: Moroney, Simon
APPLICANT: Plueckthum, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
NUMBER OF SEQUENCES: 373
CORRESPONDENCE ADDRESS:
ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
STREET: 1251 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10021
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/025,769B
FILING DATE: 18-FEB-1998
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: James F. Haley, Jr., Esq.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: MORPHO/5
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)596-9000
TELEFAX: (212)596-9090
INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
LENGTH: 109 amino acids
TYPE: amino acid
STRANDNESS: linear
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-025-769B-28
Query Match 91.5%, Score 509, DB 4, Length 109;
Best Local Similarity 93.5%, Pred. No. 4e-41;
Matches 100; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGDRTVITTCRASQGISWLMAYQOKPEKAPKSLIYAASLSQGVPS 60
DB 1 DIQMTQSPSSLSASVGDRTVITTCRASQGISWLMAYQOKPEKAPKSLIYAASLSQGVPS 60
QY 61 RFGSGSGTDFLTITLISLOPEDPATYTCOQYNSYPTFGQTKVEIK 107
DB 61 RFGSGSGTDFLTITLISLOPEDPATYTCOQYNSYPTFGQTKVEIK 107

RESULT 2

US-09-025-769B-43

Sequence 43, Application US/09025769B
Patent No. 6300064
GENERAL INFORMATION:
APPLICANT: Knappik, Achim
APPLICANT: Pack, Peter
APPLICANT: Ilag, Vic
APPLICANT: Ge, Liming
APPLICANT: Moroney, Simon
APPLICANT: Plueckhuhn, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
NUMBER OF SEQUENCES: 373
CORRESPONDENCE ADDRESS:
ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
STREET: 1251 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10021
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/025,769B
FILING DATE: 18-FEB-1998
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: James F. Haley, Jr., Esq.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: MORPHO/5
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)596-9000
TELEFAX: (212)596-9090
INFORMATION FOR SEQ ID NO: 43:
SEQUENCE CHARACTERISTICS:
LENGTH: 109 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-025-769B-43

Query Match 91.5%; Score 509; DB 4; Length 109;
Best Local Similarity 93.5%; Pred. No. 4e-41; Mismatches 4; Indels 0; Gaps 0;
Matches 100; Conservative 3;

QY 1 DIQMTQSPSSLSASVGDRTVITTCRASQGISWLMAYQOKPEKAPKSLIYAASLSQGVPS 60
DB 1 DIQMTQSPSSLSASVGDRTVITTCRASQGISWLMAYQOKPEKAPKSLIYAASLSQGVPS 60
QY 61 RFGSGSGTDFLTITLISLOPEDPATYTCOQYNSYPTFGQTKVEIK 107
DB 61 RFGSGSGTDFLTITLISLOPEDPATYTCOQYNSYPTFGQTKVEIK 107

RESULT 3
US-07-934-373C-3
Sequence 3, Application US/07934373C
Patent No. 5821337

GENERAL INFORMATION:
APPLICANT: Paul J. Carter
APPLICANT: Leonard G. Presta
TITLE OF INVENTION: Immunoglobulin Variants
NUMBER OF SEQUENCES: 48
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/934,373C
FILING DATE: 21-Aug-1992
CLASSIFICATION: 530
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/05126
FILING DATE: 15-JUN-1992
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 07/715272
FILING DATE: 14-JUN-1991
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER: 40,378
REFERENCE/DOCKET NUMBER: P0709P2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1994
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 109 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-07-934-373C-3

Query Match 90.8%; Score 505; DB 2; Length 109;
Best Local Similarity 92.5%; Pred. No. 9.5e-41; Mismatches 5; Indels 0; Gaps 0;
Matches 99; Conservative 3;

QY 1 DIQMTQSPSSLSASVGDRTVITTCRASQGISWLMAYQOKPEKAPKSLIYAASLSQGVPS 60
DB 1 DIQMTQSPSSLSASVGDRTVITTCRASQGVSSYLMAYQOKPEKAPKSLIYAASLSQGVPS 60
QY 61 RFGSGSGTDFLTITLISLOPEDPATYTCOQYNSYPTFGQTKVEIK 107
DB 61 RFGSGSGTDFLTITLISLOPEDPATYTCOQYNSYPTFGQTKVEIK 107

RESULT 4
US-08-437-642B-3
Sequence 3, Application US/08437642B
Patent No. 6054297
GENERAL INFORMATION:
APPLICANT: Paul J. Carter
APPLICANT: Leonard G. Presta
TITLE OF INVENTION: Immunoglobulin Variants
NUMBER OF SEQUENCES: 47
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible

```
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/437,642B
FILING DATE: 09-MAY-1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/934373
FILING DATE: 21-AUG-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/146206
FILING DATE: 17-NOV-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/05126
FILING DATE: 15-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/715272
FILING DATE: 14-JUN-1991
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER: 40,378
REFERENCE/DOCKET NUMBER: P0709P2C1
TELEPHONE: 650/225-1994
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 109 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-08-437-642B-3

Query Match          90.8%; Score 505; DB 3; Length 109;
Best Local Similarity 92.5%; Pred. No. 9.5e-41;
Matches 99; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 1 DIQMTSPSSLSASVGDRTVITCRASQGISWLAHYQKPKAPKSLIYAASLSQGVPS 60
Db 1 DIQMTSPSSLSASVGDRTVITCRASQGVPSYLAHYQKPKAPKSLIYAASLSQGVPS 60
QY 61 RFGSGSGTDFTLTITSSLOPEPFAITYCOQVNSYPTTGGQTKVEIK 107
Db 61 RFGSGSGTDFTLTITSSLOPEPFAITYCOQVNSLPTTGGQTKVEIK 107

RESULT 5
US-08-146-206C-3
Sequence 3, Application US/08146206C
GENERAL INFORMATION:
APPLICANT: Carter, Paul J.
APPLICANT: Presta, Leonard G.
TITLE OF INVENTION: Method for Making Humanized Antibodies
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESS: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/146,206C
FILING DATE: 17-NO. 6407213-1993
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/715272
FILING DATE: 14-JUN-1991
```

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ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER: 40,378
REFERENCE/DOCKET NUMBER: P0709P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1994
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 109 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-08-146-206C-3

Query Match          90.8%; Score 505; DB 4; Length 109;
Best Local Similarity 92.5%; Pred. No. 9.5e-41;
Matches 99; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 1 DIQMTSPSSLSASVGDRTVITCRASQGISWLAHYQKPKAPKSLIYAASLSQGVPS 60
Db 1 DIQMTSPSSLSASVGDRTVITCRASQGVPSYLAHYQKPKAPKSLIYAASLSQGVPS 60
QY 61 RFGSGSGTDFTLTITSSLOPEPFAITYCOQVNSYPTTGGQTKVEIK 107
Db 61 RFGSGSGTDFTLTITSSLOPEPFAITYCOQVNSLPTTGGQTKVEIK 107

RESULT 6
PCT-US93-07832-3
Sequence 3, Application PC/TUS9307832
GENERAL INFORMATION:
APPLICANT: Genentech, Inc.
TITLE OF INVENTION: Immunoglobulin Variants
NUMBER OF SEQUENCES: 40
CORRESPONDENCE ADDRESS:
ADDRESS: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/07832
FILING DATE: 19930820
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/715272
FILING DATE: 14-JUN-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/05126
FILING DATE: 15-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/934373
FILING DATE: 21-AUG-1992
ATTORNEY/AGENT INFORMATION:
NAME:
REGISTRATION NUMBER:
REFERENCE/DOCKET NUMBER: 709P2PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE:
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 109 amino acids
TYPE: amino acid
TOPOLOGY: linear
PCT-US93-07832-3
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Query Match 90.8%; Score 505; DB 5; Length 109;
Best Local Similarity 92.5%; Pred. No. 9.5e-41;
Matches 99; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 1 DIOMTOSPSLSASVGRVITTCRASGSSMLAWYQKPKAPKSLIYAASSLSGSPS 60
DB 1 DIOMTOSPSLSASVGRVITTCRASGSSMLAWYQKPKAPKSLIYAASSLSGSPS 60

QY 61 RFSGSGSGTDFTLTISLSLOPEDPATYCCOQYNSYPPFPGGTKEIK 107
DB 61 RFSGSGSGTDFTLTISLSLOPEDPATYCCOQYNSYPPFPGGTKEIK 107

RESULT 7
US-07-934-373C-18
; Sequence 18, Application US/07934373C
; Patent No. 5821337
; GENERAL INFORMATION:
; APPLICANT: Paul J. Carter
; APPLICANT: Leonard G. Presta
; TITLE OF INVENTION: Immunoglobulin Variants
; NUMBER OF SEQUENCES: 48
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Winpatin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/934,373C
; FILING DATE: 21-Aug-1992
; CLASSIFICATION: 530
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/05126
; FILING DATE: 15-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/715272
; FILING DATE: 14-JUN-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee, Wendy M.
; REGISTRATION NUMBER: 40,378
; REFERENCE/DOCKET NUMBER: P0709P2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1994
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
US-07-934-373C-18

Query Match 90.5%; Score 503; DB 2; Length 107;
Best Local Similarity 92.5%; Pred. No. 1.4e-40;
Matches 99; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 1 DIOMTOSPSLSASVGRVITTCRASGSSMLAWYQKPKAPKSLIYAASSLSGSPS 60
DB 1 DIOMTOSPSLSASVGRVITTCRASGSSMLAWYQKPKAPKSLIYAASSLSGSPS 60

QY 61 RFSGSGSGTDFTLTISLSLOPEDPATYCCOQYNSYPPFPGGTKEIK 107
DB 61 RFSGSGSGTDFTLTISLSLOPEDPATYCCOQYNSYPPFPGGTKEIK 107

RESULT 8

US-08-437-642B-18
; Sequence 18, Application US/08437642B
; Patent No. 6054297
; GENERAL INFORMATION:
; APPLICANT: Paul J. Carter
; APPLICANT: Leonard G. Presta
; TITLE OF INVENTION: Immunoglobulin Variants
; NUMBER OF SEQUENCES: 47
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Winpatin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/437,642B
; FILING DATE: 09-May-1995
; CLASSIFICATION: 530
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: 07/934373
; FILING DATE: 21-AUG-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/146206
; FILING DATE: 17-NOV-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/05126
; FILING DATE: 15-JUN-1992
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: 07/715272
; FILING DATE: 14-JUN-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee, Wendy M.
; REGISTRATION NUMBER: 40,378
; REFERENCE/DOCKET NUMBER: P0709P2C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1994
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
US-08-437-642B-18

Query Match 90.5%; Score 503; DB 3; Length 107;
Best Local Similarity 92.5%; Pred. No. 1.4e-40;
Matches 99; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 1 DIOMTOSPSLSASVGRVITTCRASGSSMLAWYQKPKAPKSLIYAASSLSGSPS 60
DB 1 DIOMTOSPSLSASVGRVITTCRASGSSMLAWYQKPKAPKSLIYAASSLSGSPS 60

QY 61 RFSGSGSGTDFTLTISLSLOPEDPATYCCOQYNSYPPFPGGTKEIK 107
DB 61 RFSGSGSGTDFTLTISLSLOPEDPATYCCOQYNSYPPFPGGTKEIK 107

RESULT 9
US-08-146-206C-18
; Sequence 18, Application US/08146206C
; Patent No. 6407213
; GENERAL INFORMATION:
; APPLICANT: Carter, Paul J.
; APPLICANT: Presta, Leonard G.
; TITLE OF INVENTION: Method for Making Humanized Antibodies
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:

ADDRESSER: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/146,206C
FILING DATE: 17-NO. 6407213-1993
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/715272
FILING DATE: 14-JUN-1991
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER: 40,378
REFERENCE/DOCKET NUMBER: P0709P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/952-9881
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 107 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-08-146-206C-18

Query Match 90.5%; Score 503; DB 4; Length 107;
Best Local Similarity 92.5%; Pred. No. 1.4e-40;
Matches 99; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

OY 1 DIQMTQSPSSLSASVGRVTITCRASQGISWLAHYQOKPEKAPSLIYAASSLSGVPS 60
DB 1 DIQMTQSPSSLSASVGRVTITCRASQGISWLAHYQOKPEKAPSLIYAASSLSGVPS 60
61 RPSGSGSGTDFLTITSSLOPEDFATYYCOQVNSYPPTGQGTKEIK 107
61 RPSGSGSGTDFLTITSSLOPEDFATYYCOQVNSLPWTFGQGTKEIK 107

RESULT 10

PCT-US93-07832-18
Sequence 18, Application PC/TUS9307832
GENERAL INFORMATION:
APPLICANT: Genentech, Inc.
TITLE OF INVENTION: Immunoglobulin Variants
NUMBER OF SEQUENCES: 40
CORRESPONDENCE ADDRESS:
ADDRESSER: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/07832
FILING DATE: 19930820
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/715272
FILING DATE: 14-JUN-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/05126

FILING DATE: 15-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/934373
FILING DATE: 21-AUG-1992
ATTORNEY/AGENT INFORMATION:
NAME:
REGISTRATION NUMBER:
REFERENCE/DOCKET NUMBER: 709P2PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE:
TELEFAX: 415/952-9881
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 107 amino acids
TYPE: amino acid
TOPOLOGY: linear
PCT-US93-07832-18

Query Match 90.5%; Score 503; DB 5; Length 107;
Best Local Similarity 92.5%; Pred. No. 1.4e-40;
Matches 99; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

OY 1 DIQMTQSPSSLSASVGRVTITCRASQGISWLAHYQOKPEKAPSLIYAASSLSGVPS 60
DB 1 DIQMTQSPSSLSASVGRVTITCRASQGISWLAHYQOKPEKAPSLIYAASSLSGVPS 60
61 RPSGSGSGTDFLTITSSLOPEDFATYYCOQVNSYPPTGQGTKEIK 107
61 RPSGSGSGTDFLTITSSLOPEDFATYYCOQVNSLPWTFGQGTKEIK 107

RESULT 11

US-08-974-899-3
Sequence 3, Application US/08974899
Patent No. 6037454
GENERAL INFORMATION:
APPLICANT: Presta, Leonard G.
TITLE OF INVENTION: Humanized Anti-CD11a Antibodies
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSER: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/974, 899
FILING DATE:
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/031971
FILING DATE: 11/27/96
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER: 40,378
REFERENCE/DOCKET NUMBER: P1014R1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/952-9881
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 108 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-08-974-899-3

APPLICATION NUMBER: US 08/209,741
 FILING DATE: 09-MAR-1994
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/352,322
 FILING DATE: 07-DEC-1994

? APPLICATION NUMBER: US/08/758,417A
 ? FILING DATE: 02-Dec-1996
 ? CLASSIFICATION: <unknown>
 ?
 ? PRIOR APPLICATION DATA:
 ? APPLICATION NUMBER: US 08/728,463
 ? FILING DATE: 10-OCT-1996
 ? APPLICATION NUMBER: US 08/544,404

FILING DATE: 10-OCT-1995
APPLICATION NUMBER: US 08/352,322
FILING DATE: 07-DEC-1994
APPLICATION NUMBER: US 08/209,741
FILING DATE: 09-MAR-1994
APPLICATION NUMBER: US 08/165,699
FILING DATE: 10-DEC-1993
APPLICATION NUMBER: US 08/161,739
FILING DATE: 03-DEC-1993
APPLICATION NUMBER: US 08/155,301
FILING DATE: 18-NOV-1993
APPLICATION NUMBER: US 08/096,762
FILING DATE: 22-JUL-1993
APPLICATION NUMBER: US 08/053,131
FILING DATE: 26-APR-1993
APPLICATION NUMBER: US 07/990,860
FILING DATE: 16-DEC-1992
ATTORNEY/AGENT INFORMATION:
NAME: Serafini, Andrew T.
REGISTRATION NUMBER: 41,103
REFERENCE/DOCKET NUMBER: 014643-009030US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 313:
SEQUENCE CHARACTERISTICS:
LENGTH: 117 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 313:
US-08-758-417A-313

Query Match 88.7%; Score 493; DB 4; Length 117;
Best Local Similarity 100.0%; Pred. No. 1.4e-39;
Matches 95; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DIQMTQSSSSLSASVGDVVTITTCRASQGISLWAWYQKPEKAPSLIYAASLSQGVPS 60
DB 23 DIQMTQSSSSLSASVGDVVTITTCRASQGISLWAWYQKPEKAPSLIYAASLSQGVPS 82
QY 61 RFSGSGSGTDFTLTITSSLOPEDFATYYCOQYNSYP 95
DB 83 RFSGSGSGTDFTLTITSSLOPEDFATYYCOQYNSYP 117

RESULT 14
US-09-157-370-3
Sequence 3, Application US/09157370A
Patent No. 6262238
GENERAL INFORMATION:
APPLICANT: STRIPE, Boris
APPLICANT: STEINBACHER, Stefan
TITLE OF INVENTION: PROCESS FOR MODIFYING THE STABILITY OF ANTIBODIES
FILE REFERENCE: P6341-8072
CURRENT APPLICATION NUMBER: US/09/157,370A
CURRENT FILING DATE: 1998-09-21
EARLIER APPLICATION NUMBER: 08/765,179
EARLIER FILING DATE: 1997-01-14
EARLIER APPLICATION NUMBER: PCT/EP95/02626
EARLIER FILING DATE: 1995-07-06
EARLIER APPLICATION NUMBER: DE/P44 25 115.7
EARLIER FILING DATE: 1994-07-15
NUMBER OF SEQ ID NOS: 10
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 3
LENGTH: 109
TYPE: PRT
ORGANISM: Homo sapiens
US-09-157-370-3

Query Match 88.1%; Score 480; DB 4; Length 109;
Best Local Similarity 90.7%; Pred. No. 2.4e-39;

Matches 97; Conservative 3; Mismatches 7; Indels 0; Gaps 0;
QY 1 DIQMTQSSSSLSASVGDVVTITTCRASQGISLWAWYQKPEKAPSLIYAASLSQGVPS 60
DB 1 DIQMTQSSSSLSASVGDVVTITTCRASQGISLWAWYQKPEKAPSLIYAASLSQGVPS 60
QY 61 RFSGSGSGTDFTLTITSSLOPEDFATYYCOQYNSYPPTFGQGTVEIK 107
DB 61 RFSGSGSGTDFTLTITSSLOPEDFATYYCOQYNSYPPTFGQGTVEIK 107

RESULT 15
US-08-974-899-2
Sequence 2, Application US/08974899
Patent No. 6037454
GENERAL INFORMATION:
APPLICANT: Presta, Leonard G.
APPLICANT: Jardieu, Paula M.
TITLE OF INVENTION: Humanized Anti-CD11a Antibodies
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 MB floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/974,899
FILING DATE:
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/031971
FILING DATE: 11/27/96
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER: 40,378
REFERENCE/DOCKET NUMBER: P1014R1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1994
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 108 amino acids
TYPE: Amino Acid
TOPOLOGY: linear
US-08-974-899-2

Query Match 87.9%; Score 489; DB 3; Length 108;
Best Local Similarity 88.8%; Pred. No. 3e-39;
Matches 95; Conservative 5; Mismatches 7; Indels 0; Gaps 0;
QY 1 DIQMTQSSSSLSASVGDVVTITTCRASQGISLWAWYQKPEKAPSLIYAASLSQGVPS 60
DB 1 DIQMTQSSSSLSASVGDVVTITTCRASQGISLWAWYQKPEKAPSLIYAASLSQGVPS 60
QY 61 RFSGSGSGTDFTLTITSSLOPEDFATYYCOQYNSYPPTFGQGTVEIK 107
DB 61 RFSGSGSGTDFTLTITSSLOPEDFATYYCOQYNSYPPTFGQGTVEIK 107

Search completed: June 3, 2003, 08:24:16
Job time: 17.2509 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 3, 2003, 08:09:29 ; Search time 17.727 Seconds
(without alignments)
531.460 Million cell updates/sec

Title: US-09-644-668a-15

Perfect score: 512

Sequence: 1 QVQLVESGGGVQPGSRSLRL.....LYLQMSLRAEDTAVYYCAR 98

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	512	100.0	98	2	529546
2	512	100.0	119	2	F36005
3	512	100.0	121	2	G36005
4	512	100.0	122	2	E36005
5	512	100.0	134	2	E31679
6	509	99.4	114	2	S46390
7	507	99.0	120	2	S31112
8	505	98.6	98	2	PL0116
9	505	98.6	122	2	S31119
10	503	98.2	118	2	S31116
11	502	98.0	121	2	S19666
12	501	97.9	119	2	S31111
13	501	97.9	122	2	S31117
14	501	97.9	128	2	S48797
15	501	97.9	132	2	S31603
16	500	97.7	114	2	S46392
17	500	97.7	123	2	S38493
18	499	97.5	137	2	S31701
19	496	96.5	113	2	S38490
20	496	96.9	139	2	S31674
21	495	96.7	130	2	PL0098
22	494	96.5	133	2	A49028
23	492	96.1	130	2	S31601
24	490	95.7	133	2	S31510
25	489	95.5	97	2	S44115
26	488	95.3	98	2	S29543
27	488	95.3	134	2	S31688
28	488	95.3	135	2	S31598
29	488	95.3	140	2	S70442

ALIGNMENTS

30	487	95.1	94	2	PL0120	Ig heavy chain V-I
31	480	93.8	114	2	S46391	Ig heavy chain V r
32	480	93.8	122	1	M3HUM	Ig heavy chain V-I
33	478	93.4	117	2	S36270	Ig heavy chain V r
34	476	93.0	133	2	S31590	Ig heavy chain V r
35	475	92.8	109	2	PH1644	Ig heavy chain V r
36	475	92.8	109	2	PH1646	Ig heavy chain V r
37	475	92.8	111	2	PH1645	Ig heavy chain V r
38	474	92.6	117	2	S36259	Ig heavy chain V r
39	469	91.6	115	2	S36284	Ig heavy chain V r
40	468	91.4	111	2	PH1643	Ig heavy chain V r
41	466	91.0	151	2	A60943	Ig heavy chain pre
42	465	90.8	118	2	S31677	Ig heavy chain V r
43	464	90.6	108	2	PH1642	Ig heavy chain V r
44	456	89.1	118	2	PH1662	Ig heavy chain V r
45	456	89.1	122	2	S69910	Ig V-D-J region (K

RESULT 1

S29546

Ig heavy chain V region (COS-8 / DP-46) - human (fragment)

C:Species: Homo sapiens (man)

C>Date: 07-Jan-1994 #sequence_revision 17-Nov-1995 #text_change 23-Jul-1999

C/Accession: S29546; S26888

R/Tomlinson, M.; Walter, G.; Cook, G.P.; Winter, G.

submitted to the EMBL Data Library, October 1992

A:Reference number: S29543

A:Accession: S29546

A:Molecule type: DNA

A:Residues: 1-98 <TOM>

A/Cross-references: EMBL: Z17394; NID: G32843; PIDN: CAA78997.1; PID: G32844

A/Note: designated COS-8

R/Tomlinson, I.M.; Walter, G.; Marks, J.D.; Llewellyn, M.B.; Winter, G.

J. Mol. Biol. 227, 776-798, 1992

A/Title: The repertoire of human germline V(H) sequences reveals about fifty groups of

A/Reference number: S26885; MUID: 93021117; PMID: 1404388

A/Accession: S26888

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-98 <TOM>

A/Cross-references: EMBL: Z12346; NID: G32912; PIDN: CAA78216.1; PID: G32913

A/Note: designated DP-46

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: heterotrimer; immunoglobulin

F:15-98/Domain: immunoglobulin homology <IM>

Query Match 100.0%; Score 512; DB 2; Length 98;

Best local similarity 100.0%; Pred. No. 5.8e-42;

Matches 98; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QVQLVESGGGVQPGSRSLRLCAASGFTFSYAMHWROAEGKLEWAVSYGSKNY 60

DB 1 QVQLVESGGGVQPGSRSLRLCAASGFTFSYAMHWROAEGKLEWAVSYGSKNY 60

QY 61 ADSVKGRTTISRDNKNTLYLQMSLRAEDTAVYYCAR 98

DB 61 ADSVKGRTTISRDNKNTLYLQMSLRAEDTAVYYCAR 98

RESULT 2

F36005

Ig heavy chain V region (M49) - human

C:Species: Homo sapiens (man)

C>Date: 21-Dec-1990 #sequence_revision 21-Dec-1990 #text_change 16-Dec-1998

C/Accession: F36005

R/Schroeder Jr., H.W.; Wang, J.Y.

Proc. Natl. Acad. Sci. U.S.A. 87, 6146-6150, 1990

A/Title: Preferential utilization of conserved immunoglobulin heavy chain variable gene

A/Reference number: A36005; MUID: 90349571; PMID: 2117275

A/Accession: F36005

A>Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-119 <SCH>
 A:Cross-references: GB:M34026
 C:Genetics:
 A:Gene: GDB:IGH@; IGHDI1
 A:Cross-references: GDB:118731; OMIM:146910
 A:Map position: 14q32.33-14q32.33
 C:Superfamily: immunoglobulin V region; immunoglobulin heavy chain variable gene
 C:Keywords: heterotetramer; immunoglobulin
 P:15-98/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 512; DB 2; Length 119;
 Best Local Similarity 100.0%; Pred. No. 7.1e-42;
 Matches 98; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QVQLVSGGAVVQPGKSLRLSCAASGFTFSYAMHWVRQAPGKGLEWVAIVSYDGSNKYY 60
 DB 1 QVQLVSGGAVVQPGKSLRLSCAASGFTFSYAMHWVRQAPGKGLEWVAIVSYDGSNKYY 60
 QY 61 ADSVKGRTISRDNKNTLYLQMSLRADTAIVYCAR 98
 DB 61 ADSVKGRTISRDNKNTLYLQMSLRADTAIVYCAR 98

RESULT 3

G36005
 Ig heavy chain V region (M74) - human
 C:Species: Homo sapiens (man)
 C>Date: 21-Dec-1990 #sequence_revision 21-Dec-1990 #text_change 16-Dec-1998
 C:Accession: G36005
 R:Schroeder Jr., H.W.; Wang, J.Y.
 Proc. Natl. Acad. Sci. U.S.A. 87, 6146-6150, 1990
 A>Title: Preferential utilization of conserved immunoglobulin heavy chain variable gene
 A:Reference number: A36005; MUID:90349571; PMID:2117273
 A:Accession: G36005
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-121 <SCH>
 A:Cross-references: GB:M34031
 C:Genetics:
 A:Gene: GDB:IGH@; IGHDI1
 A:Cross-references: GDB:118731; OMIM:146910
 A:Map position: 14q32.33-14q32.33
 C:Superfamily: immunoglobulin V region; immunoglobulin heavy chain variable gene
 C:Keywords: heterotetramer; immunoglobulin
 P:15-98/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 512; DB 2; Length 121;
 Best Local Similarity 100.0%; Pred. No. 7.2e-42;
 Matches 98; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QVQLVSGGAVVQPGKSLRLSCAASGFTFSYAMHWVRQAPGKGLEWVAIVSYDGSNKYY 60
 DB 1 QVQLVSGGAVVQPGKSLRLSCAASGFTFSYAMHWVRQAPGKGLEWVAIVSYDGSNKYY 60
 QY 61 ADSVKGRTISRDNKNTLYLQMSLRADTAIVYCAR 98
 DB 61 ADSVKGRTISRDNKNTLYLQMSLRADTAIVYCAR 98

RESULT 4

E36005
 Ig heavy chain V region (M72) - human
 C:Species: Homo sapiens (man)
 C>Date: 21-Dec-1990 #sequence_revision 21-Dec-1990 #text_change 16-Dec-1998
 C:Accession: E36005
 R:Schroeder Jr., H.W.; Wang, J.Y.
 Proc. Natl. Acad. Sci. U.S.A. 87, 6146-6150, 1990
 A>Title: Preferential utilization of conserved immunoglobulin heavy chain variable gene
 A:Reference number: A36005; MUID:90349571; PMID:2117273
 A:Accession: E36005
 A:Status: preliminary

A:Molecule type: mRNA
 A:Residues: 1-122 <SCH>
 A:Cross-references: GB:M34030
 C:Genetics:
 A:Gene: GDB:IGH@; IGHDI1
 A:Cross-references: GDB:118731; OMIM:146910
 A:Map position: 14q32.33-14q32.33
 C:Superfamily: immunoglobulin V region; immunoglobulin heavy chain variable gene
 C:Keywords: heterotetramer; immunoglobulin
 P:15-98/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 512; DB 2; Length 122;
 Best Local Similarity 100.0%; Pred. No. 7.3e-42;
 Matches 98; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QVQLVSGGAVVQPGKSLRLSCAASGFTFSYAMHWVRQAPGKGLEWVAIVSYDGSNKYY 60
 DB 1 QVQLVSGGAVVQPGKSLRLSCAASGFTFSYAMHWVRQAPGKGLEWVAIVSYDGSNKYY 60
 QY 61 ADSVKGRTISRDNKNTLYLQMSLRADTAIVYCAR 98
 DB 61 ADSVKGRTISRDNKNTLYLQMSLRADTAIVYCAR 98

RESULT 5

S31679
 Ig heavy chain V region - human (fragment)
 C:Species: Homo sapiens (man)
 C>Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
 C:Accession: S31679
 R:Cutlinder, A.M.; Gauchier, L.; Boubli, L.; Fougereau, M.; Tonnelie, C.
 Submitted to the EMBL Data Library, June 1992.
 A:Description: Mechanisms that generate human immunoglobulin diversity operate from
 A:Reference number: S31585
 A:Accession: S31679
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-134 <CU>
 A:Cross-references: EMBL:Z14203; NID:930965; PIDN:CAA78572.1; PID:930966
 C:Superfamily: immunoglobulin V region; immunoglobulin heavy chain variable gene
 C:Keywords: heterotetramer; immunoglobulin
 P:34-117/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 512; DB 2; Length 134;
 Best Local Similarity 100.0%; Pred. No. 8e-42;
 Matches 98; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QVQLVSGGAVVQPGKSLRLSCAASGFTFSYAMHWVRQAPGKGLEWVAIVSYDGSNKYY 60
 DB 20 QVQLVSGGAVVQPGKSLRLSCAASGFTFSYAMHWVRQAPGKGLEWVAIVSYDGSNKYY 79
 QY 61 ADSVKGRTISRDNKNTLYLQMSLRADTAIVYCAR 98
 DB 80 ADSVKGRTISRDNKNTLYLQMSLRADTAIVYCAR 117

RESULT 6

S46390
 Ig heavy chain V region - human
 C:Species: Homo sapiens (man)
 C>Date: 27-Jan-1995 #sequence_revision 27-Jan-1995 #text_change 20-Jun-2000
 C:Accession: S46390
 R:Figini, M.; Marks, J.D.; Winter, G.; Griffiths, A.D.
 J. Mol. Biol. 239, 68-78, 1994
 A>Title: In vitro assembly of repertoires of antibody chains on the surface of phage
 A:Reference number: S46390; MUID:94254092; PMID:8156048
 A:Accession: S46390
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-114 <FIG>
 A:Cross-references: EMBL:Z31686; NID:9509782; PIDN:CAA83491.1; PID:91335143
 C:Superfamily: immunoglobulin V region; immunoglobulin heavy chain variable gene
 C:Keywords: heterotetramer; immunoglobulin

F;15-98/Domain: immunoglobulin homology <IMM>

Query Match	99.4%	Score 509;	DB 2;	Length 114;
Best Local Similarity	99.0%	Pred. No. 1.3e-41;		
Matches 97;	Conservative 1;	Mismatches 0;	Indels 0;	Gaps 0;

1 0VQVLVEGGGCVVQVQGRSLRLSCAASGFTTSSYAMHWVRQAPGKGLEWVAIVSYDGSNKYY 60
:
1 EVQVLVEGGGCVVQVQGRSLRLSCAASGFTTSSYAMHWVRQAPGKGLEWVAIVSYDGSNKYY 60

[illegible]

RESULT 7
S31112

Ig heavy chain - human
C:Species: Homo sapiens (man)
C:Date: 02-Dec-1993 #sequence

R:Raaphorst, F.M., Timmers, E., Kenter, M.J.H., van Tol, M.J.D., Vosse, J.M., Schuurman, E., J. Remunoi. 22, 247-251, 1992
A:Title: Restored utilization of germ-line V(H)3 genes and short diverse third complement A:Reference number: S31104; MUID:92111633; PMID:1730252

A/Status: preliminary; nucleic acid sequence not shown; translation not shown
A/Molecule type: mRNA
A/Residues: 1-120 <RAA>

A:Cross-references: EMBL:X62961
 A:Note: the nucleotide sequence was submitted to the EMBL Data Library, October 1991
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotrimer; immunoglobulin
 C:15-98/Domain: immunoglobulin homology <Imm>

Query Match	99.0%;	Score 507;	DB 2;	Length 120;
Best Local Similarity	100.0%;	Pred. No. 2.1e-41;		
Matches	97;	Conservative	0;	Mismatches 0;
				Indels 0;
				Gaps 0;

1 QVQLVESGGGVQPGRLSLRLSCAASGFTSSYAMHWRAQPKGLEWVAISYDGSNKYY 60
1 QVQLVESGGGVQPGRLSLRLSCAASGFTSSYAMHWRAQPKGLEWVAISYDGSNKYY 60	

```

61 ADSVKGFTISRDNKNTLYLOMNSLRADTAVYYCA 97
|||
61 ADSVKGFTISRDNKNTLYLOMNSLRADTAVYYCA 97

```

RESULT 8
PL0116

Ig heavy chain V-III region (AW-Vx) - human (Fragment)
C:Species: Homo sapiens (man)
C:Date: 07-Jun-1990 #sequence_revision 07-Jun-1990 #text_change 23-Jul-1999

C/Accession: P10116; S26892
R/Bird, J.; Galli, N.; Link, M.; Stiles, D.; Sklar, J.
J. Exp. Med. 168, 229-245, 1988
A/Title: Contributing rearrangement but absence of somatic hypermutation in immunoglobulin
R/Reference number: P10116; MUID:68286083; PMID:2840480

A;Accession: PL0116
A;Molecule type: mRNA
A;Reidses: 1-98 <Bis>
A;Experimental source: B cells from patient AM with acute lymphoblastic leukemia, ALL
A;Note: the sequence shows the V region (AM-Vx) from a nonproductive DNA rearrangement

R:Tomlinson, I.M.; Walter, G.; Marks, J.D.; Llewellyn, M.B.; Winter, G.
J. Mol. Biol. 227, 776-798, 1992
A:Title: The repertoire of human germline (VH) sequences reveals about fifty groups of V
A:Reference number: 526885; MUID:93021117; PMID:1404388
A:Accession: S26892

A,Status: preliminary
A,Molecule type: DNA
A,Residues: 1-98 <TOM>
A,Cross-references: EMBL:g12349; NID:g32918; PID:CAAG78219; h1; PID:g32919
A,Superfamily: immunoglobulin V region; immunoglobulin h1

C;Keywords: acute lymphoblastic leukemia; heterorecramer; immunoglobulin F;15-98/Domain: immunoglobulin homology <IM> F;31-35/Region: complementarily-determining 1 F;49-65/Region: complementarily-determining 2

Query Match	98.6%	Score 505;	DB 2;	Length 98;
Best Local Similarity	98.0%;	Pred. No. 2.7e-41;		
Matches 96;	Conservative	1;	Mismatches	0;
			Gaps	0;

Oy 1 QVQLVESGGGVQPGKSLRLTSCAASGFTSSSYAMHWVRQAPEGLEWVAIVISYDGSNKYY 60
Db 1 QVQLVESGGGVQPGKSLRLTSCAASGFTSSSYGMHWVRQAPGKGLEWVAIVISYDGSNKYY 60	

```
QY      61 ADSVKGFTISRDNSKNTLYIQMNSLRADPTAVVYCAR 98
        |||||
        61 ADSVKGFTISRDNSKNTLYIQMNSLRADPTAVVYCAR 98
```

RESULT 9
S31119

Ig heavy chain - human
C/Species: Homo sapiens (man)
C/Date: 02-Dec-1993 #sequence

R; Raaphorst, P.M., Timmers, E.; Kenter, M.J.H.; van Tol, M.J.D.; Vossen, J.M.; Schuurman
Eur. J. Immunol. 22, 247-251, 1992

A; Title: Restricted utilization of germ-line V(H)3 genes and short diverse third comple
S31104; MUID:9211633; PMID:1730252

A; Reference number: S31104; MUID:9211633; PMID:1730252

A/Accession: S3119
A/Status: preliminary; nucleic acid sequence not shown; translation not shown
A/Molecule type: mRNA
A/Residues: 1-122 <RAA>
A/Cross-references: EMBL:X62970

A>Note: the nucleotide sequence was submitted to the EMBL Data Library, October 1991
C:Superfamily: Immunoglobulin V region; Immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMM>

Query match	56.6%	Score 505	DB 4	Length 122
Best Local Similarity	98.0%	Pred. No. 3.4e-41		
Matches 96	Conservative 1	Mismatches 1	Indels 0	Gaps 0

1 QVGVVDSGGGVVQFENSRIRKUSLCMAASGIFSSIAMHWKQAPGKLEWVAHISIDSNKI 60
D5 1 QVGVVDSGGGVVQFENSRIRKUSLCMAASGIFSSIAMHWKQAPGKLEWVAHISIDSNKI 60
1 QVGVVDSGGGVVQFENSRIRKUSLCMAASGIFSSIAMHWKQAPGKLEWVAHISIDSNKY 60

D6
07
D8

61 ADSVKRFTISRDNSSNLTLLQNNSLRAEDTAVVYCAK 98
:
61 ADSVKRFTISRDNSSNLTLLQNNSLRAEDTAVVYCAK 98

RESULT 10
S31116
Id heavy

C:\Species: Homo sapiens (man)
C:\Date: 02-Dec-1993 #sequence_revision 26-May-1995 #text_change 17-Mar-1999
C:\Accession: S31116

R. Raaphorst, F.M.; Timmers, E.; Kenter, M.J.H.; van Tol, M.J.D.; Vossen, J.M.; Schuurman Eur. J. Immunol. 22, 247-251, 1992
A>Title: Restricted utilization of germ-line V(H)3 genes and short diverse third comple
A/Reference number: S31104; MUID:92111633; PMID:1730252
A/Accession: S3116

A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: mRNA
A:Residues: 1-118 <RNA>
A:Cross-references: EMBL:K62966
A:Note: the nucleotide sequence was submitted to the EMBL Data Library. Oct99b

Query Match 98.2%; Score 503; DB 2; Length 118;
 Best Local Similarity 98.0%; E 1e-41;
 A, Role: the nucleotide sequence was submitted to the EMBL Data Library, October 1998
 C, Superfamily: Immunoglobulin V region; immunoglobulin homology
 C, Keywords: heterotrimer; immunoglobulin
 F, 15-98/Domain: immunoglobulin homology <IMM>

Matches 96; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QVQLVESGGGVQPGSRSLRSCAASGFTFSYAMHWYRQAPGKLEWAVAVISYDGSNKYY 60
Db 1 QVQLVESGGGVQPGSRSLRSCAASGFTFSYAMHWYRQAPGKLEWAVAVISYDGSNKYY 60
QY 61 ADSVKGRTISRDNKNTLYLQMSLRADTAIVYCAR 97
Db 61 ADSVKGRTISRDNKNTLYLQMSLRADTAIVYCAR 97

RESULT 11

ig heavy chain V region (VH3DJH4) - human

C/Species: Homo sapiens (man)

C/Date: 22-Jan-1993 #sequence_revision 22-Jan-1993 #text_change 20-Jun-2000

C/Accession: S19666

R/Author: J.D.; Hoogenboom, H.R.; Bonnett, T.P.; McCafferty, J.; Griffiths, A.D.; Winter, J. Mol. Biol. 227, 581-597, 1991

A/Title: By-passing immunization. Human antibodies from V-gene libraries displayed on phage

A/Reference number: S19663; MUID:92085276; PMID:1748994

A/Accession: S19666

A/Molecule type: mRNA

A/Residues: 1-121 <VAR>

A/Cross-references: EMBL:X61646; NID:937688; PIDN:CAA43827.1; PID:91335369

C/Suprafamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: heterotrimer; immunoglobulin

P:15-98/Domain: immunoglobulin homology <IMM>

Query Match 98.0%; Score 502; DB 2; Length 121;

Best Local Similarity 96.9%; Pred. No. 6.5e-41;

Matches 95; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 QVQLVESGGGVQPGSRSLRSCAASGFTFSYAMHWYRQAPGKLEWAVAVISYDGSNKYY 60
Db 1 QVQLVESGGGVQPGSRSLRSCAASGFTFSYAMHWYRQAPGKLEWAVAVISYDGSNKYY 60
QY 61 ADSVKGRTISRDNKNTLYLQMSLRADTAIVYCAR 98
Db 61 ADSVKGRTISRDNKNTLYLQMSLRADTAIVYCAR 98

RESULT 12

S3111

ig heavy chain - human

C/Species: Homo sapiens (man)

C/Date: 02-Dec-1993 #sequence_revision 26-May-1995 #text_change 17-Mar-1999

C/Accession: S31111

R/Author: R.M.; Timmers, E.; Kenter, M.J.H.; van Tol, M.J.D.; Vossen, J.M.; Schuurman

Ent. J. Immunol. 22, 247-251, 1992

A/Title: Restricted utilization of germ-line V(H)3 genes and short diverse third complement

A/Reference number: S31104; MUID:92111633; PMID:1730252

A/Accession: S31111

A/Status: preliminary; nucleic acid sequence not shown; translation not shown

A/Molecule type: mRNA

A/Residues: 1-119 <RAA>

A/Cross-references: EMBL:X62959

C/Suprafamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: heterotrimer; immunoglobulin

P:15-98/Domain: immunoglobulin homology <IMM>

Query Match 97.9%; Score 501; DB 2; Length 119;

Best Local Similarity 96.0%; Pred. No. 7.9e-41;

Matches 96; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 QVQLVESGGGVQPGSRSLRSCAASGFTFSYAMHWYRQAPGKLEWAVAVISYDGSNKYY 60
Db 1 QVQLVESGGGVQPGSRSLRSCAASGFTFSYAMHWYRQAPGKLEWAVAVISYDGSNKYY 60
QY 61 ADSVKGRTISRDNKNTLYLQMSLRADTAIVYCAR 98
Db 61 ADSVKGRTISRDNKNTLYLQMSLRADTAIVYCAR 98

RESULT 13

S31117

ig heavy chain - human

C/Species: Homo sapiens (man)

C/Date: 02-Dec-1993 #sequence_revision 26-May-1995 #text_change 17-Mar-1999

C/Accession: S31117

R/Author: R.M.; Timmers, E.; Kenter, M.J.H.; van Tol, M.J.D.; Vossen, J.M.; Schuurman

Ent. J. Immunol. 22, 247-251, 1992

A/Title: Restricted utilization of germ-line V(H)3 genes and short diverse third complement

A/Reference number: S31104; MUID:92111633; PMID:1730252

A/Accession: S31117

A/Status: preliminary; nucleic acid sequence not shown; translation not shown

A/Molecule type: mRNA

A/Residues: 1-122 <RAA>

A/Cross-references: EMBL:X62967

C/Suprafamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: heterotrimer; immunoglobulin

P:15-98/Domain: immunoglobulin homology <IMM>

Query Match 97.9%; Score 501; DB 2; Length 122;

Best Local Similarity 96.0%; Pred. No. 8.1e-41;

Matches 96; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 QVQLVESGGGVQPGSRSLRSCAASGFTFSYAMHWYRQAPGKLEWAVAVISYDGSNKYY 60
Db 1 QVQLVESGGGVQPGSRSLRSCAASGFTFSYAMHWYRQAPGKLEWAVAVISYDGSNKYY 60
QY 61 ADSVKGRTISRDNKNTLYLQMSLRADTAIVYCAR 98
Db 61 ADSVKGRTISRDNKNTLYLQMSLRADTAIVYCAR 98

RESULT 14

S48797

ig heavy chain V region (anti-Sm, VH3/Dxp4/JH6) - human (fragment)

C/Species: Homo sapiens (man)

C/Date: 13-Jan-1995 #sequence_revision 13-Sep-1998 #text_change 23-Jul-1999

C/Accession: S48797; S26893

R/Author: R.M.; Timmers, E.; Kenter, M.J.H.; van Tol, M.J.D.; Vossen, J.M.; Schuurman

Ent. J. Immunol. 22, 247-251, 1992

A/Title: The repertoire of human germline V(H) sequences reveals about fifty groups

A/Reference number: S26885; MUID:92021117; PMID:1404388

A/Accession: S26893

A/Molecule type: DNA

A/Residues: 1-98 <TOM>

A/Cross-references: EMBL:Z12350; NID:932922; PIDN:CAA78220.1; PID:932923

C/Suprafamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: heterotrimer; immunoglobulin

P:15-98/Domain: immunoglobulin homology <IMM>

Query Match 97.9%; Score 501; DB 2; Length 128;

Best Local Similarity 96.0%; Pred. No. 8.5e-41;

Matches 96; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 QVQLVESGGGVQPGSRSLRSCAASGFTFSYAMHWYRQAPGKLEWAVAVISYDGSNKYY 60
Db 1 QVQLVESGGGVQPGSRSLRSCAASGFTFSYAMHWYRQAPGKLEWAVAVISYDGSNKYY 60
QY 61 ADSVKGRTISRDNKNTLYLQMSLRADTAIVYCAR 98
Db 61 ADSVKGRTISRDNKNTLYLQMSLRADTAIVYCAR 98

RESULT 15

S31603

Ig heavy chain V region - human

C/Species: Homo sapiens (man)

C/Date: 03-Mar-1994 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999

C/Accession: S31603

R/Cuisinier, A.M.; Gauthier, L.; Boubil, L.; Fougereau, M.; Tonnelie, C.

submitted to the EMBL Data Library, June 1992

A/Description: Mechanisms that generate human immunoglobulin diversity operate from the

A/Reference number: S31585

A/Accession: S31603

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-132 <cut>

A/Cross-references: EMBL:Z14168; NID:G30999; PID:CAA78537.1; PID:G31000

C/Superfamily: Immunoglobulin V region; Immunoglobulin homology

C/Keywords: heterotetramer; immunoglobulin

F/30-113/Domain: Immunoglobulin homology <IMM>

Query Match 97.9%; Score 501; DB 2; Length 132;

Best Local Similarity 96.9%; Pred. No. 8.8e-41; Mismatches 2; Indels 0; Gaps 0;

Matches 95; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 QVOLVESGGVYQPGSRSLRLSCAASGFTFSSYAMHWROAPGKLEWVAVISYDGSNKYY 60
|||
Db 16 QVOLVESGGVYQPGSRSLRLSCAASGFTFSSYGMHWROAPGKLEWVAVISYDGSNKYY 75
|||

OY 61 ADSVKGFTISRDNKNTLLYQMNSLRADDTAVYYCAR 98
|||
Db 76 ADSVKGFTISRDNKNTLLYQMNSLRADDTAVYYCAR 113
|||

Search completed: June 3, 2003, 08:22:39
Job time : 18.727 secs

GenCore version 5.1.6
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OM protein - protein search, using SW model

Run on: June 3, 2003, 08:09:29 ; Search time 21.5256 Seconds
(without alignments)
531.460 Million cell updates/sec

Title: US-09-644-668a-23

Sequence: 1 QVALVESGGGVQPGSRSLRL.....PNVIGAFDVWGQCTMTVSS 119

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :
1: p1r1:
2: p1r2:
3: p1r3:
4: p1r4:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	574.5	90.8	122	2	S31117 Ig heavy chain - h
2	566	89.4	119	2	F36005 Ig heavy chain V r
3	565.5	89.3	128	2	S48797 Ig heavy chain V r
4	562.5	88.9	137	2	S31701 Ig heavy chain V r
5	561	88.6	130	2	S31601 Ig heavy chain V r
6	559	88.3	133	2	A49028 Ig heavy chain V-I
7	558.5	88.2	118	2	S31116 Ig heavy chain - h
8	551	87.0	121	2	S19666 Ig heavy chain V r
9	550	86.9	132	2	S31603 Ig heavy chain V r
10	549	86.7	135	2	S31598 Ig heavy chain V r
11	548.5	86.7	139	2	S31674 Ig heavy chain V r
12	548	86.6	121	2	G36005 Ig heavy chain V r
13	547.5	86.5	122	2	E36005 Ig heavy chain V r
14	545.5	86.2	140	2	S70442 Ig heavy chain pre
15	541	85.5	134	2	S31679 Ig heavy chain V r
16	540.5	85.4	120	2	S31112 Ig heavy chain - h
17	539.5	85.2	108	2	PH1642 Ig heavy chain V r
18	536.5	84.8	114	2	S46390 Ig heavy chain V r
19	536	84.7	123	2	S38493 Ig heavy chain - h
20	533	84.2	130	2	PL0098 Ig heavy chain pre
21	528.5	83.5	114	2	S46391 Ig heavy chain V r
22	527	83.3	109	2	PH1646 Ig heavy chain V r
23	524	82.8	121	1	PH1643 Ig heavy chain V-I
24	523	82.6	111	2	PH1643 Ig heavy chain V r
25	521.5	82.4	114	2	S46392 Ig heavy chain V r
26	521.5	82.4	122	2	S68910 Ig V-D-J region (K
27	519.5	82.1	133	2	S31510 Ig heavy chain pre
28	518.5	81.9	151	2	A60943 Ig heavy chain V-I
29	517.5	81.8	122	1	M3HUM

30	517	81.7	119	2	S31111 Ig heavy chain - h
31	513	81.0	111	2	PH1645 Ig heavy chain V r
32	511	80.7	109	2	PH1644 Ig heavy chain V r
33	508	80.3	113	2	S38490 Ig heavy chain - h
34	507.5	80.2	118	2	S31672 Ig heavy chain V r
35	506.5	80.0	118	2	PH1662 Ig heavy chain V r
36	504	79.6	125	2	S37455 Ig mu chain - huma
37	503.5	79.5	136	2	S31587 Ig heavy chain V r
38	502.5	79.4	122	2	S31119 Ig heavy chain - h
39	500	79.0	98	2	PL0116 Ig heavy chain V-I
40	499	78.8	121	2	I55673 Ig heavy chain - h
41	498.5	78.8	147	2	I37780 Ig variable region
42	498	78.7	119	2	S31108 Ig heavy chain - h
43	498	78.7	139	2	I37781 Ig variable region
44	497	78.5	98	2	S29546 Ig heavy chain V r
45	497	78.5	119	2	S31107 Ig heavy chain - h

ALIGNMENTS

RESULT 1
S31117
Ig heavy chain - human
C/Species: Homo sapiens (man)
C/Date: 02-Dec-1993 #sequence_revision 26-May-1995 #text_change 17-Mar-1999
C/Accession: S31117
R/Rapport: F.M.; Timmers, E.; Kenner, M.J.H.; van Tol, M.J.D.; Vossen, J.M.; Schuurm
Eur. J. Immunol. 22, 247-251, 1992
A/Title: Restricted utilization of germ-line V(H)3 genes and short diverse third compl
A/Reference number: S31104; MUID:92111633; PMID:1730252
A/Accession: S31117
A/Status: preliminary; nucleic acid sequence not shown; translation not shown
A/Molecule type: mRNA
A/Residues: 1-122 <RA>
A/Cross-References: EMBL:X62967
A/Note: the nucleotide sequence was submitted to the EMBL Data Library, October 1991
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin
F15-98/Domain: immunoglobulin homology <IM>

Query Match 90.8%; Score 574.5; DB 2; Length 122;
Best Local Similarity 91.0%; Pred. No. 2.6e-46;
Matches 111; Conservative 2; Mismatches 6; Indels 3; Gaps 1;

QY 1 QVALVESGGGVQPGSRSLRLSCAAGFTPPSSGGMWVROAPKGLKEMVAIVYDGSNKTY 60
DB 1 QVALVESGGGVQPGSRSLRLSCAAGFTPPSSGGMWVROAPKGLKEMVAIVYDGSNKTY 60
QY 61 ADSVKGRTISRDNKNTLYLQMSLRADPAVFYCAR---APNVIGAFDVWGQCTMTV 117
DB 61 ADSVKGRTISRDNKNTLYLQMSLRADPAVFYCAR---APNVIGAFDVWGQCTMTV 120

QY 118 SS 119
DB 121 SS 122

RESULT 2
F36005
Ig heavy chain V region (M49) - human
C/Species: Homo sapiens (man)
C/Date: 21-Dec-1990 #sequence_revision 21-Dec-1990 #text_change 16-Dec-1998
C/Accession: F36005
R/Schneider Jr., H.W.; Wang, J.Y.
Proc. Natl. Acad. Sci. U.S.A. 87, 6146-6150, 1990
A/Title: Preferential utilization of conserved immunoglobulin heavy chain variable gene
A/Reference number: A36005; MUID:90349571; PMID:2117273
A/Accession: F36005
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-119 <SCH>
A/Cross-References: GB:M34026

C/Genetics:
A:Gene: GDB:IGH@; IGHDI1
A:Cross-references: GDB:118731; OMIM:146910
A:Map position: 14q32.33-14q32.33
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
P:15-98/Domain: immunoglobulin homology <IMM>

Query Match 89.4%; Score 566; DB 2; Length 119;
Best Local Similarity 91.6%; Pred. No. 1.6e-45;
Matches 109; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

QY 1 QVQLVSGGAVQPGKSLRLSCAASGFTSSYGMHWVRQAPGKLEWVAIVYDGSNKYY 60
DB 1 QVQLVSGGAVQPGKSLRLSCAASGFTSSYGMHWVRQAPGKLEWVAIVYDGSNKYY 60
QY 61 ADSVKGRTISRDNSKNTLYLQNMSLRAEDTAVFYCARAPNYTGAFDVWGQGTMTVSS 119
DB 61 ADSVKGRTISRDNSKNTLYLQNMSLRAEDTAVFYCARAPNYTGAFDVWGQGTMTVSS 119

RESULT 3

548797
Ig heavy chain V region (anti-Sm, VH3/DXP4/JH6) - human (fragment)

C/Species: Homo sapiens (man)
C/Date: 13-Jan-1995 #sequence_revision 13-Sep-1998 #text_change 23-Jul-1999
C/Accession: S48797; S26893
R:Mahmoudi, M.; Edwards, J.; Cairns, B.; Bell, D.
submitted to the EMBL Data Library, October 1994
A/Description: Molecular characterization of natural human anti-Sm autoantibodies.
A/Reference number: S48797
A/Accession: S48797
A:Molecule type: mRNA
A:Residues: 1-128 <MAH>
A:Cross-references: EMBL:Z46379; NID:G587147; PIDN:CAA86512.1; PID:G1340168
R:Tomlinson, I.M.; Walter, G.; Marks, J.D.; Llewellyn, M.B.; Winter, G.
J. Mol. Biol. 227, 776-798, 1992
A/Title: The repertoire of human germline V(H) sequences reveals about fifty groups of
A/Reference number: S26885; MIMD:93021117; PMID:1404388
A/Accession: S26893
A:Molecule type: DNA
A:Residues: 1-98 <TOM>
A:Cross-references: EMBL:Z12350; NID:G32922; PIDN:CAA78220.1; PID:G32923
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
P:15-98/Domain: immunoglobulin homology <IMM>

Query Match 89.3%; Score 565.5; DB 2; Length 128;
Best Local Similarity 85.9%; Pred. No. 1.9e-45;
Matches 110; Conservative 2; Mismatches 7; Indels 9; Gaps 1;

QY 1 QVQLVSGGAVQPGKSLRLSCAASGFTSSYGMHWVRQAPGKLEWVAIVYDGSNKYY 60
DB 1 QVQLVSGGAVQPGKSLRLSCAASGFTSSYGMHWVRQAPGKLEWVAIVYDGSNKYY 60
QY 61 ADSVKGRTISRDNSKNTLYLQNMSLRAEDTAVFYCARAPNYTGAFDVWGQGTMTVSS 111
DB 61 ADSVKGRTISRDNSKNTLYLQNMSLRAEDTAVFYCARAPNYTGAFDVWGQGTMTVSS 120
QY 112 GTMTVSS 119
DB 121 GTMTVSS 128

RESULT 4

531701

Ig heavy chain V region - human (fragment)

C/Species: Homo sapiens (man)
C/Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C/Accession: S31701
R:Chislier, A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnelle, C.
submitted to the EMBL Data Library, June 1992
A/Description: Mechanisms that generate human immunoglobulin diversity operate from the

A/Reference number: S31585
A/Accession: S31701
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-137 <CU>
A:Cross-references: EMBL:Z14177; NID:G31020; PIDN:CAA78546.1; PID:G31021
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
P:34-117/Domain: immunoglobulin homology <IMM>

Query Match 88.9%; Score 562.5; DB 2; Length 137;
Best Local Similarity 90.8%; Pred. No. 3.8e-45;
Matches 108; Conservative 4; Mismatches 6; Indels 1; Gaps 1;

QY 1 QVQLVSGGAVQPGKSLRLSCAASGFTSSYGMHWVRQAPGKLEWVAIVYDGSNKYY 60
DB 20 QVQLVSGGAVQPGKSLRLSCAASGFTSSYGMHWVRQAPGKLEWVAIVYDGSNKYY 79
QY 61 ADSVKGRTISRDNSKNTLYLQNMSLRAEDTAVFYCARAPNYTGAFDVWGQGTMTVSS 119
DB 60 PDSVKGRTISRDNSKNTLYLQNMSLRAEDTAVFYCARAPNYTGAFDVWGQGTMTVSS 137

RESULT 5

531601

Ig heavy chain V region - human

C/Species: Homo sapiens (man)
C/Date: 03-Mar-1994 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C/Accession: S31601
R:Chislier, A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnelle, C.
submitted to the EMBL Data Library, June 1992
A/Description: Mechanisms that generate human immunoglobulin diversity operate from
A/Reference number: S31585
A/Accession: S31601
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-110 <CU>
A:Cross-references: EMBL:Z14192; NID:G31018; PIDN:CAA78561.1; PID:G31019
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
P:30-113/Domain: immunoglobulin homology <IMM>

Query Match 88.6%; Score 561; DB 2; Length 130;
Best Local Similarity 91.6%; Pred. No. 5e-45;
Matches 109; Conservative 3; Mismatches 3; Indels 4; Gaps 2;

QY 1 QVQLVSGGAVQPGKSLRLSCAASGFTSSYGMHWVRQAPGKLEWVAIVYDGSNKYY 60
DB 16 QVQLVSGGAVQPGKSLRLSCAASGFTSSYGMHWVRQAPGKLEWVAIVYDGSNKYY 75
QY 61 ADSVKGRTISRDNSKNTLYLQNMSLRAEDTAVFYCARAPNYTGAFDVWGQGTMTVSS 119
DB 76 ADSVKGRTISRDNSKNTLYLQNMSLRAEDTAVFYCARAPNYTGAFDVWGQGTMTVSS 130

RESULT 6

A49028

Ig heavy chain V-III region - human (fragment)

C/Species: Homo sapiens (man)
C/Date: 21-Jan-1994 #sequence_revision 18-Nov-1994 #text_change 23-Jul-1999
C/Accession: A49028
R:Timmers, B.; Kenter, M.; Thompson, A.; Kraakman, M.E.; Berman, J.E.; Alt, F.W.; SC
Eur. J. Immunol. 21, 2355-2363, 1991
A/Title: Diversity of immunoglobulin heavy chain gene segment rearrangement in B lymphoblastoid cell lines
A/Reference number: A49028; MIMD:92008140; PMID:1515549
A/Accession: A49028
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-133 <TIM>
A:Cross-references: GB:564471; NID:G236904; PIDN:AA82001.1; PID:G236905
A:Experimental source: X-linked agammaglobulinemia patients; B lymphoblastoid cell lines
C:Superfamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: heterotetramer; immunoglobulin F₁₅-98/Domain: immunoglobulin homology <IMM>

Query Match	Score	DB 2;	Length
88.34;	559;		133;
87.04;	559;		133;

y
 1 QVQLVSGGGVNPGRSLRLSCAASGTFSSYGMHWTRQAPKGLIEWAVIYWDGSNKYY 60
 |||||
 b
 1 QVQLVESGGGVNPGRSLRLSCAASGTFSSYGMHWLDAFGKLEWAVIYWDGSNKYY 60
 |||||

γ	117	VSS	119
δ	121	VSS	123

A, Note: the nucleotide sequence was submitted to the EMBL Data Library, October 1991
C, Superfamily: Immunoglobulin V region; Immunoglobulin homology
K, Keywords: heterotrimer; immunoglobulin
E, 15-98/Domain: immunoglobulin homology <Imm>

1 QVQLVESGGGVVQGRSLRLSCAASGFTSSYGMMHVRQAPGKGLMVAIVTIDGSKYY 600

1 QVQLVESGGGVVQGRSLRLSCAASGFTSSYGMMHVRQAPGKGLMVAIVTIDGSKYY 600

RESULT 8

```

IG heavy chain V region (VH3DJH4) - human
C/Species: Homo sapiens (man)
C/Date: 22-Jan-1993 #sequence_revision 22-Jan-1993 #text_change 20-Jun-2000
C/Accession: S19663
R/Marks: J.D.; Hoogenboom, H.R.; Bonnett, T.P.; McCafferty, J.; Griffiths, A.D.; Winter
J. Mol. Biol. 222, 581-597, 1991
A/Title: By-passing immunization. Human antibodies from V-gene libraries displayed on phage
A/Reference number: S19663; MUID:92085276; PMID:1748994
A/Accession: S19666
A/Molecule type: mRNA
A/Residues: 1-121 <MAR>

```

Query Match	87.0%;	Score 551;	DB 2;	length 121;
Best Local Similarity	88.4%;	Pred. No. 3.9e-44;		

Matches 107; Conservative 5; Mismatches 7; Indels 2; Gaps 1;

Qy 1 QVQLVESGGGVQPGRSLRLSCAASGTFSSYGMHWYQAPGKLEWVAIWYDGSNKYY 600
|||:|||||
Db 1 QVQLVQSGGVSVPGRSLRLSCAASGTFSSYGMHWYQAPGKLEWVAISYDGSNKYY 600

QY	119 S 119
	—
Db	121 S 121

A_Cross-references: EMBL:Z14168; NID:g30999; PID:CAA75537.1; PID:g310000
C_Superfamily: immunoglobulin V region, immunoglobulin homology
C_Keywords: heterotrimer; immunoglobulin
P_30-113/Domain: immunoglobulin homology <Im>

Query Match	86.9%;	Score 550;	DB 2;	Length 132;
Best Local Similarity	89.9%;	Pred. No. 5.3e-44;		
Matches 107; Conservative	3;	Mismatches 7;	Indels 2;	Gaps 1

Dy 61 ADSVKGRFTISRDNKNTLYIQMNSLRADTAIFYCARAPNYTGAFDWMGQMTVYSS 113

Dd 76 ADSVKGRFTISRDNKNTLYIQMGRLRADTAVYYCAQLFFY--FDYMGGTLVTYSS 132

A; Cross-references: EMBL:Z14170, NID:g31001, PIDD:CAA78539.1, PID:g31002
C; Superfamily: Immunoglobulin V region, Immunoglobulin homology
C; Keywords: heterotrimer; immunoglobulin
F; 31-114/Domain: Immunoglobulin homology <Im>

QY 1 QVQLVESGGGVDPGRSLRLSCAASGFTSSYGMHWYRQAPGKGLEWAVIWDGSNKKY 60
DQ 1 QVQLVESGGGVDPGRSLRLSCAASGFTSSYGMHWYRQAPGKGLEWAVIWDGSNKKY 60
Db 17 QVQLVESGGGVDPGRSLRLSCAASGFTSSYGMHWYRQAPGKGLEWAVIWDGSNKKY 76

QY 61 ADSVKGRTISRDNKNTLYLQNMNSLRADTAIFYCARAPNYIGA-PDVGQGTMTVSS 119
 DB 77 ADSVKGRTISRDNKNTLYLQNMNSLRADTAIFYCARAPNYIGA-PDVGQGTMTVSS 135

RESULT 11

S31674
 Ig heavy chain V region - human (fragment)
 C/Species: Homo sapiens (man)
 C/Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
 C/Accession: S31674
 R/CuSinter, A.M.; Gauthier, L.; Boublil, L.; Fougereau, M.; Tonnelie, C.
 submitted to the EMBL Data Library, June 1992
 A/Description: Mechanisms that generate human immunoglobulin diversity operate from the
 A/Reference number: S31585
 A/Accession: S31674
 A/Status: preliminary
 A/Molecule type: mRNA
 A/Residues: 1-139 <CUI>
 A/Cross-references: EMBL:Z14204; NID:G30967; PIDN:CAA78573.1; PID:G30968
 C/Superfamily: immunoglobulin V region; immunoglobulin homology
 C/Keywords: heterotetramer; immunoglobulin
 F/34-117/Domain: immunoglobulin homology <IMM>

Query Match 86.7%; Score 548.5; DB 2; Length 139;
 Best Local Similarity 89.2%; Pred. No. 7.6e-44;
 Matches 107; Conservative 4; Mismatches 8; Indels 1; Gaps 1;

QY 1 QVQLVESGGGVQPGKSLRLSCAASGFTFSYGMHWRAQPGKLEWAVIWDGSKNKKY 60
 DB 20 QVQLVESGGGVQPGKSLRLSCAASGFTFSYGMHWRAQPGKLEWAVIWDGSKNKKY 79
 QY 61 ADSVKGRTISRDNKNTLYLQNMNSLRADTAIFYCARAP-NYIGA-PDVGQGTMTVSS 119
 DB 80 ADSVKGRTISRDNKNTLYLQNMNSLRADTAIFYCARAP-NYIGA-PDVGQGTMTVSS 139

RESULT 12

G36005
 Ig heavy chain V region (M74) - human
 C/Species: Homo sapiens (man)
 C/Date: 21-Dec-1990 #sequence_revision 21-Dec-1990 #text_change 16-Dec-1998
 C/Accession: G36005
 R/Schroeder Jr., H.W.; Wang, J.Y.
 Proc. Natl. Acad. Sci. U.S.A. 87, 6146-6150, 1990
 A/Title: Preferential utilization of conserved immunoglobulin heavy chain variable gene
 A/Reference number: A36005; MUID:90349571; PMID:2117273
 A/Accession: G36005
 A/Status: preliminary
 A/Molecule type: mRNA
 A/Residues: 1-121 <SCH>
 A/Cross-references: GB:M34031
 A/Genetics: GDB:IGH@; IGHDIY1
 A/Cross-references: GDB:118731; OMIM:146910
 A/Map position: 14q32.33-14q32.33
 C/Superfamily: immunoglobulin V region; immunoglobulin homology
 C/Keywords: heterotetramer; immunoglobulin
 F/15-98/Domain: immunoglobulin homology <IMM>

Query Match 86.6%; Score 548; DB 2; Length 121;
 Best Local Similarity 89.3%; Pred. No. 7.4e-44;
 Matches 108; Conservative 2; Mismatches 9; Indels 2; Gaps 1;

QY 1 QVQLVESGGGVQPGKSLRLSCAASGFTFSYGMHWRAQPGKLEWAVIWDGSKNKKY 60
 DB 1 QVQLVESGGGVQPGKSLRLSCAASGFTFSYGMHWRAQPGKLEWAVIWDGSKNKKY 60
 QY 61 ADSVKGRTISRDNKNTLYLQNMNSLRADTAIFYCARAPNYIGA-PDVGQGTMTVSS 118
 DB 61 ADSVKGRTISRDNKNTLYLQNMNSLRADTAIFYCARAPNYIGA-PDVGQGTMTVSS 120

QY 119 S 119
 DB 121 S 121

RESULT 13

E36005
 Ig heavy chain V region (M72) - human
 C/Species: Homo sapiens (man)
 C/Date: 21-Dec-1990 #sequence_revision 21-Dec-1990 #text_change 16-Dec-1998
 C/Accession: E36005
 R/Schroeder Jr., H.W.; Wang, J.Y.
 Proc. Natl. Acad. Sci. U.S.A. 87, 6146-6150, 1990
 A/Title: Preferential utilization of conserved immunoglobulin heavy chain variable
 A/Reference number: A36005; MUID:90349571; PMID:2117273
 A/Accession: E36005
 A/Status: preliminary
 A/Molecule type: mRNA
 A/Residues: 1-122 <SCH>
 A/Cross-references: GB:M34030
 A/Genetics: GDB:IGH@; IGHDIY1
 A/Cross-references: GDB:118731; OMIM:146910
 A/Map position: 14q32.33-14q32.33
 C/Superfamily: immunoglobulin V region; immunoglobulin homology
 C/Keywords: heterotetramer; immunoglobulin
 F/15-98/Domain: immunoglobulin homology <IMM>

Query Match 86.5%; Score 547.5; DB 2; Length 122;
 Best Local Similarity 87.7%; Pred. No. 8.3e-44;
 Matches 107; Conservative 4; Mismatches 8; Indels 3; Gaps 1;

QY 1 QVQLVESGGGVQPGKSLRLSCAASGFTFSYGMHWRAQPGKLEWAVIWDGSKNKKY 60
 DB 1 QVQLVESGGGVQPGKSLRLSCAASGFTFSYGMHWRAQPGKLEWAVIWDGSKNKKY 60
 QY 61 ADSVKGRTISRDNKNTLYLQNMNSLRADTAIFYCARAP-NYIGA-PDVGQGTMTV 117
 DB 61 ADSVKGRTISRDNKNTLYLQNMNSLRADTAIFYCARAP-NYIGA-PDVGQGTMTV 120
 QY 118 SS 119
 DB 121 SS 122

RESULT 14

S70442
 Ig heavy chain precursor V region (mu) - human (fragment)
 C/Species: Homo sapiens (man)
 C/Date: 24-Jul-1998 #sequence_revision 24-Jul-1998 #text_change 21-Jan-2000
 C/Accession: S70442
 R/CuSinter, A.M.; Fumoux, F.; Fougereau, M.; Tonnelie, C.
 Mol. Immunol. 29, 1363-1373, 1992
 A/Title: IGM kappa/lambda B2V human B cell clone: an early step of differentiation c
 A/Reference number: S70442; MUID:93024508; PMID:1383695
 A/Accession: S70442
 A/Status: not compared with conceptual translation
 A/Molecule type: mRNA
 A/Residues: 1-140 <CUI>
 C/Superfamily: immunoglobulin V region; immunoglobulin homology
 F/34-117/Domain: immunoglobulin homology <IMM>

Query Match 86.2%; Score 545.5; DB 2; Length 140;
 Best Local Similarity 88.4%; Pred. No. 1.5e-43;
 Matches 107; Conservative 5; Mismatches 6; Indels 3; Gaps 2;

QY 1 QVQLVESGGGVQPGKSLRLSCAASGFTFSYGMHWRAQPGKLEWAVIWDGSKNKKY 60
 DB 20 QVQLVESGGGVQPGKSLRLSCAASGFTFSYGMHWRAQPGKLEWAVIWDGSKNKKY 79
 QY 61 ADSVKGRTISRDNKNTLYLQNMNSLRADTAIFYCARAPNYIGA-PDVGQGTMTVSS 118
 DB 80 ADSVKGRTISRDNKNTLYLQNMNSLRADTAIFYCARAPNYIGA-PDVGQGTMTVSS 138

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OM protein - protein search, using sw model

Run on: June 3, 2003, 08:02:44 ; Search time 10.9659 Seconds

(without alignments)
450.095 Million cell updates/sec

Title: US-09-644-668a-23

Perfect score: 633
Sequence: 1 QVQLVSGGGVQVQPSRLRL.....PNYIGAFVWGQGTMTVYVS 119

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database : SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	524	82.8	121	1	HV3J_HUMAN
2	517.5	81.8	122	1	HV3J_HUMAN
3	488	77.1	119	1	HV3I_HUMAN
4	483.5	76.4	122	1	HV3H_HUMAN
5	483.5	76.4	126	1	HV3K_HUMAN
6	453.5	71.6	136	1	HV1E_MOUSE
7	453	71.6	119	1	HV3L_HUMAN
8	448.5	70.9	116	1	HV3T_HUMAN
9	440.5	69.6	114	1	HV3B_HUMAN
10	430	67.9	120	1	HV3E_HUMAN
11	428.5	67.7	120	1	HV3U_HUMAN
12	427	67.5	117	1	HV3C_HUMAN
13	423.5	66.9	117	1	HV3O_HUMAN
14	421	66.5	115	1	HV3F_HUMAN
15	418.5	66.1	116	1	HV05_CARAU
16	418.5	66.1	119	1	HV3M_HUMAN
17	416.5	65.8	119	1	HV3N_HUMAN
18	416	65.7	115	1	HV3D_HUMAN
19	411.5	65.0	119	1	HV38_MOUSE
20	408.5	64.5	122	1	HV3A_MOUSE
21	407.5	64.4	122	1	HV20_MOUSE
22	397.5	62.8	119	1	HV37_MOUSE
23	397.5	62.8	119	1	HV3P_MOUSE
24	396	62.6	117	1	HV02_CANFA
25	395.5	62.5	114	1	HV01_CANFA
26	394.5	62.3	122	1	HV21_MOUSE
27	394	62.2	115	1	HV32_MOUSE
28	394	62.2	116	1	HV3R_MOUSE
29	394	62.2	123	1	HV18_MOUSE
30	394	62.2	142	1	HV01_RAT
31	392	61.9	113	1	HV30_MOUSE
32	392	61.9	123	1	HV23_MOUSE
33	391.5	61.8	119	1	HV40_MOUSE

34	391	61.8	123	1	HV19_MOUSE
35	388.5	61.4	111	1	HV35_MOUSE
36	388	61.3	113	1	HV34_MOUSE
37	388	61.3	123	1	HV24_MOUSE
38	388	61.3	144	1	HV26_MOUSE
39	387	61.1	113	1	HV27_MOUSE
40	387	61.1	123	1	HV22_MOUSE
41	387	61.1	123	1	HV25_MOUSE
42	384	60.7	113	1	HV31_MOUSE
43	383	60.5	115	1	HV33_MOUSE
44	382	60.3	98	1	HV57_MOUSE
45	381	60.2	113	1	HV28_MOUSE
					P01788 mus musculus
					P01804 mus musculus
					P01803 mus musculus
					P01796 mus musculus
					P01795 mus musculus
					P01791 mus musculus
					P01794 mus musculus
					P01800 mus musculus
					P01802 mus musculus
					P18528 mus musculus
					P01797 mus musculus

ALIGNMENTS

RESULT 1		HV3J_HUMAN		STANDARD;		PRT; 121 AA.	
ID	HV3J_HUMAN						
AC	P01771;						
DT	21-JUL-1986 (Rel. 01, Created)						
DR	21-JUL-1986 (Rel. 01, Last sequence update)						
DE	15-JUL-1999 (Rel. 38, Last annotation update)						
DS	Ig heavy chain V-II region HIL.						
OS	Homo sapiens (Human)						
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;						
CC	Mammalia; Eutheria; Primates; Carnivora; Hominidae; Homo.						
LN	NCBI_Taxid=9606;						
OX	[1]						
RP	SEQUENCE.						
RX	MEDLINE:79124695; PubMed:420800;						
RA	Chiu Y.-Y.H., Lopez de Castro J.A., Poljak R.J.;						
RT	"Amino acid sequence of the VH region of human myeloma						
RL	cryoimmunoglobulin IgG H1."						
CC	Biochemistry 18:553-560(1979).						
CC	-I- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGG1 MYELOMA						
CC	PROTEIN.						
DR	PIR; A02054; GIHQHL.						
DR	HSSP; P01772; 2F84.						
DR	InterPro; IPR003006; Ig_MHC.						
DR	InterPro; IPR003596; Ig_V.						
DR	Pfam; PF00047; Ig_1.						
DR	SMART; SM00406; IGV_1.						
KW	Immunoglobulin V region.						
FT	MOD RES 1						
FT	NON TER 121						
FT	PIR						
FT	SEQUENCE 121 AA; 13566 MW; 480FC53610E5DAB CRC64;						
Query Match							
Best Local Similarity 82.8%; Score 524; DB 1; Length 121;							
Matches 97; Conservative 11; Mismatches 11; Indels 2; Gaps 1;							
QY	1	QVQLVSGGGVQVQPSRLRLSCAAGFTPSYGMWVQAPKGLGAWAVIMYDSNRY	60				
DB	1	QVQLVQAGGGVQVQPSRLSLCIAAGFTPSNYGMWVQAPKGLGAWAVIMYDSNRY	60				
QY	61	ADSVGRFTISRDNSKNTLYIQMNSLRADITAVFYCAPNYIGA--PDWVGQGTMTVVS	118				
DB	61	GSVVGRTISRDNKRTLYVMZNSLRTEIDTAVFYCAADPDLITAFSPDYMGGLVTVS	120				
QY	119	S 119					
DB	121	S 121					
RESULT 2							
ID	HV3G_HUMAN						
AC	P01768;						
DT	21-JUL-1986 (Rel. 01, Created)						
DR	21-JUL-1986 (Rel. 01, Last sequence update)						
DT	15-JUL-1999 (Rel. 38, Last annotation update)						

DE Ig heavy chain V-III region CAM.
 OS Homo sapiens (Human).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 NCBI_TaxID=9606;
 [1]
 RP SEQUENCE.
 RX MEDLINE=81013859; PubMed=6774332;
 RA Lehman D.W., Putnam F.W.;
 RT "Amino acid sequence of the variable region of a human mu chain:
 location of a possible JH segment.";
 RL Proc. Natl. Acad. Sci. U.S.A. 77:3239-3243(1980).
 CC -1- MISCELLANEOUS: THIS MU CHAIN WAS ISOLATED FROM THE PLASMA OF A
 PATIENT WITH MACROGLOBULINEMIA.
 CC PIR; A02051; M3H0AM.
 DR HSSP; P01772; 2FB4.
 DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR003596; Ig_V.
 DR Pfam; PF00047; Ig_V.
 DR SMART; SM00406; IGV; 1.
 KW Immunoglobulin V region.
 FT MOD_RES 1
 FT NON_TER 122
 SQ SEQUENCE 122 AA; 13668 MW; AA2D0F17D52F1C2 CRC64;
 PYRROLIDONE CARBOXYLIC ACID.
 Query Match 81.8%; Score 517.5; DB 1; Length 122;
 Best Local Similarity 79.5%; Pred. No. 1.5e-47;
 Matches 97; Conservative 12; Mismatches 10; Indels 3; Gaps 1;
 QY 1 QVQLVSGGAVVQPGKSLRLSCAASGFTPSYSGMHWRQAPGKLEWAVIYDGSNKYY 60
 DB 1 QVQLVSGGAVVQPGKSLRLSCAASGFTPSYNAHWKQPGKLEWAVIYGBBKY 60
 QY 61 ADSVKGRTISRDNSKNTLYIQNNSLRAPDTAVFYCARAPNYIS---AFDWGGTMTV 117
 DB 61 ADSVKGRTISRDNSKNTLYIQNNSLRAPDTAVFYCARAPNYIS---AFDWGGTMTV 117
 QY 118 SS 119
 DB 121 SS 122
 RESULT 3
 HV31_HUMAN STANDARD; PRT; 119 AA.
 ID HV31_HUMAN
 AC P01770;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Ig heavy chain V-III region NIE.
 OS Homo sapiens (Human).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 NCBI_TaxID=9606;
 [1]
 RP SEQUENCE.
 RX MEDLINE=77070269; PubMed=826475;
 RA Ponsing H., Hilschmann N.;
 RT "The rule of antibody structure. The primary structure of a
 monoclonal IgG1 immunoglobulin (myeloma protein NIE). III. The
 chymotryptic peptides of the H-chain, alignment of the tryptic
 peptides and discussion of the complete structure.";
 RL Hoppe-Seyler's Z. Physiol. Chem. 357:1571-1604(1976).
 [2]
 RP DISULFIDE BOND.
 RX MEDLINE=77070267; PubMed=1002129;
 RA Dreker L., Schwarz J., Reichel W., Hilschmann N.;
 RT "Rule of antibody structure. The primary structure of a monoclonal
 IgG1 immunoglobulin (myeloma protein NIE). I: Purification and
 characterization of the protein, the L- and H-chains, the
 cyanogen bromide cleavage products, and the disulfide bridges.";
 RL Hoppe-Seyler's Z. Physiol. Chem. 357:1515-1540(1976).
 CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGG1 MYELOMA

CC PROTEIN.
 DR PIR; A02053; GHUNI.
 DR HSSP; P01772; 2FB4.
 DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR003596; Ig_V.
 DR Pfam; PF00047; Ig_V.
 DR SMART; SM00406; IGV; 1.
 KW Immunoglobulin V region.
 FT MOD_RES 1
 FT DISULFID 22
 FT NON_TER 96
 SQ SEQUENCE 119 AA; 13242 MW; C96935A6E55E165B CRC64;
 PYRROLIDONE CARBOXYLIC ACID.
 Query Match 77.1%; Score 488; DB 1; Length 119;
 Best Local Similarity 78.2%; Pred. No. 1.8e-44;
 Matches 93; Conservative 11; Mismatches 15; Indels 0; Gaps 0;
 QY 1 QVQLVSGGAVVQPGKSLRLSCAASGFTPSYSGMHWRQAPGKLEWAVIYDGSNKYY 60
 DB 1 QVQLVSGGAVVQPGKSLRLSCAASGFTPSYTIHWKQPGKLEWAVIYGBBKY 60
 QY 61 ADSVKGRTISRDNSKNTLYIQNNSLRAPDTAVFYCARAPNYIGADWGGTMTV 119
 DB 61 ADSVKGRTISRDNSKNTLYIQNNSLRAPDTAVFYCARAPNYIGADWGGTMTV 119
 RESULT 4
 HV31_HUMAN STANDARD; PRT; 122 AA.
 ID HV31_HUMAN
 AC P01769;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Ig heavy chain V-III region GA.
 OS Homo sapiens (Human).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 NCBI_TaxID=9606;
 [1]
 RP SEQUENCE.
 RX MEDLINE=74175307; PubMed=420843;
 RA Florent G., Lehman D., Putnam F.W.;
 RT "The switch point in mu heavy chains of human IgM immunoglobulins.";
 RL Biochemistry 13:2482-2498(1974).
 CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A WALDENSTROM'S
 MACROGLOBULIN.
 CC PIR; A02052; M3H0GA.
 DR HSSP; P01772; 2FB4.
 DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR003596; Ig_V.
 DR Pfam; PF00047; Ig_V.
 DR SMART; SM00406; IGV; 1.
 KW Immunoglobulin V region.
 FT MOD_RES 1
 FT NON_TER 122
 SQ SEQUENCE 122 AA; 13166 MW; 74E5B6959E84100A CRC64;
 PYRROLIDONE CARBOXYLIC ACID.
 Query Match 76.4%; Score 483.5; DB 1; Length 122;
 Best Local Similarity 69.7%; Pred. No. 5.5e-44;
 Matches 85; Conservative 24; Mismatches 10; Indels 3; Gaps 1;
 QY 1 QVQLVSGGAVVQPGKSLRLSCAASGFTPSYSGMHWRQAPGKLEWAVIYDGSNKYY 60
 DB 1 QVQLVSGGAVVQPGKSLRLSCAASGFTSTYNAHWKQPGKLEWAVIYGBBKY 60
 QY 61 ADSVKGRTISRDNSKNTLYIQNNSLRAPDTAVFYCARAPNYIGAF---DVGGGTMTV 117
 DB 61 AASVKGRTISRBBSKNTLYIQNNSLRAPDTAVFYCARAPNYIGAF---DVGGGTMTV 117
 QY 118 SS 119
 DB 121 SS 122

RESULT 5

ID HV3K_HUMAN STANDARD; PRT; 126 AA.
 AC P01772;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Ig heavy chain V-III region KOL.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxId=9606;
 RN [1]
 SEQUENCE, AND DISULFIDE BONDS.
 RX MEDLINE=83289131; PubMed=6884994;
 RA Schmidt W.E., Jung H.-D., Palm W., Hilschmann N.;
 RT "Three-dimensional structure determination of antibodies. Primary
 structure of crystallized monoclonal immunoglobulin IgG1 KOL, I.",
 RL Hoppe-seyler's Z. Physiol. Chem. 364:713-747(1983).
 RN [2]
 RP X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS).
 RX MEDLINE=81072295; PubMed=7441755;
 RA Marguaret M., Deisenhofer J., Huber R., Palm W.;
 RT "Crystallographic refinement and atomic models of the intact
 immunoglobulin molecule KOL and its antigen-binding fragment at 3.0 A
 and 1.0-A resolution.";
 RL J. Mol. Biol. 141:369-391(1980).
 DR PIR; A02055; GIHUKL.
 DR PDB; 2PB4; 12-JUL-89.
 DR InterPro; IPR003006; IG_MHC.
 DR InterPro; IPR003596; IG_V.
 DR Pfam; PF00047; Ig; 1.
 DR SMART; SM00406; IGV; 1.
 KM Immunoglobulin V region; 3D-structure.
 KW MOD RES
 FT DIULFID 1 96
 FT DISULFID 105 110
 FT STRAND 3 7
 FT TURN 11 12
 FT TURN 14 15
 FT STRAND 18 25
 FT TURN 29 31
 FT STRAND 34 39
 FT TURN 41 42
 FT STRAND 46 51
 FT TURN 53 54
 FT STRAND 58 60
 FT TURN 62 67
 FT STRAND 68 73
 FT TURN 74 77
 FT STRAND 78 83
 FT HELIX 88 90
 FT STRAND 92 99
 FT TURN 106 108
 FT STRAND 107 109
 FT STRAND 113 113
 FT STRAND 120 124
 FT NON_TER 126
 SQ SEQUENCE 126 AA; 13718 MW; EAD71B52B16F876 CRC64;

Query Match 76.4%; Score 483.5; DB 1; Length 126;
 Best Local Similarity 71.2%; Pred. No. 5.7e-44;
 Matches 94; Conservative 12; Mismatches 7; Indels 19; Gaps 2;

QY 1 QVAVESGGVVGPGSRISLISCAASGFTSSYGMMVWQAQPKGLEWVAIVYDGSNKXY 60
 DB 1 QVAVESGGVVGPGSRISLISCAASGFTSSYGMMVWQAQPKGLEWVAIVYDGSNKXY 60
 QY 61 ADVKGRFTIRDSNKTLYIQMNSLRPDTAVFYCAR-----APNYTGAFD 107

DB 61 ADVKGRFTIRDSNKTLYIQMNSLRPDTAVFYCARDGHGFCSSASCPGPDY----- 115
 QY 108 VWGQGTWTVSS 119
 DB 116 -WGQGTWTVSS 126

RESULT 6

ID HV16_MOUSE STANDARD; PRT; 136 AA.
 AC P01783;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 15-JUL-1999 (Rel. 38, Last sequence update)
 DE Ig heavy chain V region MOPC 21 precursor (Fragment).
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxId=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=81234548; PubMed=6788376;
 RA Botwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.,
 RA Baltimore D.;
 RT "Heavy chain variable region contribution to the NpB family of
 antibodies: somatic mutation evident in a gamma 2a variable region.";
 RL Cell 24:625-637(1981).
 RN [2]
 RP SEQUENCE OF 17-136.
 RX MEDLINE=77100368; PubMed=401950;
 RA Adelungo K., Milstein C., Secher D.S.;
 RT "Molecular analysis of spontaneous somatic mutants.";
 RL Nature 265:299-304(1977).
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 or send an email to license@ebi.ac.uk).

CC EMBL; J00522; AAD15290.1; -.
 DR PIR; A02066; GIMS21.
 DR HSSP; P01772; 2PB4.
 DR InterPro; IPR003006; IG_MHC.
 DR InterPro; IPR003596; IG_V.
 DR Pfam; PF00047; Ig; 1.
 DR SMART; SM00406; IGV; 1.
 KM Immunoglobulin V region; signal.
 KW NON_TER
 FT SIGNAL 1 1
 FT CHAIN 17 16
 FT DOMAIN 115 119
 FT DOMAIN 120 136
 FT DISULFID 38 112
 FT CONFLICT 75 78
 FT CONFLICT 89 90
 FT CONFLICT 115 115
 FT CONFLICT 120 120
 FT NON_TER 136
 SQ SEQUENCE 136 AA; 15071 MW; 2276A98BDBE7016 CRC64;

Query Match 71.6%; Score 453.5; DB 1; Length 136;
 Best Local Similarity 75.6%; Pred. No. 8.8e-41;
 Matches 90; Conservative 9; Mismatches 19; Indels 1; Gaps 1;

QY 2 VQAVESGGVVGPGSRISLISCAASGFTSSYGMMVWQAQPKGLEWVAIVYDGSNKXY 61
 DB 18 VQAVESGGVVGPGSRISLISCAASGFTSSYGMMVWQAQPKGLEWVAIVYDGSNKXY 77
 QY 62 DSVKGRFTIRDSNKTLYIQMNSLRPDTAVFYCARPNY-IGAFDVGQGTWTVSS 119

DB 78 DTVKGRFTISRDNPKOTLFLQMTSLSESDTAMYYCARWGNYPYANDYWGQGTLYTVSS 136

RESULT 7

HY3L_HUMAN

ID HY3L_HUMAN STANDARD; PRT; 119 AA.

AC P01773;

DT 21-JUL-1986 (Rel. 01, Created)

DT 21-JUL-1986 (Rel. 01, Last sequence update)

DT 15-JUL-1999 (Rel. 38, Last annotation update)

DB Ig heavy chain V-II region BUR.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

OX NCBI_TaxId=9606;

RN [1]

RP SEQUENCE (MELOMA PROTEIN BUR).

MEDLINE=79151016; PubMed=107164;

RA Putnam F.W., Liu Y.-S.V., Low T.L.K.;

RT "Primary structure of a human IgA1 immunoglobulin. IV. Streptococcal

RT IgA1 protease, digestion, Fab and Fc fragments, and the complete

RT amino acid sequence of the alpha 1 heavy chain."

RL J. Biol. Chem. 254:2865-2874(1979).

DR PIR; A02056; ALHUBR.

DR HSSP; P01772; 2PB4.

DR InterPro; IPR003006; IG_MHC.

DR InterPro; IPR003596; IG_V.

DR Pfam; PF00047; IgV_1.

DR SMART; SM00406; IgV_1.

KW Immunoglobulin V region; Glycoprotein.

FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.

FT DISULFID 22 96

FT CARBOHYD 28 28

FT NON_TER 119 119

SQ SEQUENCE 119 AA; 12981 MW; 12A709A75344D024 CRC64;

Query Match

Best Local Similarity 71.6%; Score 453; DB 1; Length 119;

Matches 84; Conservative 12; Mismatches 22; Indels 0; Gaps 0;

QY 1 QVQLVESGGGVQVQPGSRSLRLSCAASGFTSSYGMHWVRQAPGKGLKLVAVIWDGSKNTYY 60

DB 1 QVQLVESGGGVQVQPGSRSLRLSCAASGFTSSYGMHWVRQAPGKGLKLVAVIWDGSKNTYY 60

QY 61 ADSVKGRTISRDNKNTLYLQMSLRBEDTAVFYCARAPNTYIGAFDVGSGGTMYTVSS 118

DB 61 ADSVKGRTISRDNKNTLYLQMSLRBEDTAVFYCARAPNTYIGAFDVGSGGTMYTVSS 118

RESULT 8

HY3T_HUMAN

ID HY3T_HUMAN STANDARD; PRT; 116 AA.

AC P01781;

DT 21-JUL-1986 (Rel. 01, Created)

DT 21-JUL-1986 (Rel. 01, Last sequence update)

DT 15-JUN-2002 (Rel. 41, Last annotation update)

DB Ig heavy chain V-III region GAL.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

OX NCBI_TaxId=9606;

RN [1]

RP SEQUENCE.

MEDLINE=75059123; PubMed=4803843;

RA Watanabe S., Barnikol H.O., Horn J., Bertram J., Hilschmann N.;

RT "The primary structure of a monoclonal IgM-immunoglobulin

RT (macroglobulin Gal.), II: the amino acid sequence of the H-chain (mu-

RT type), subgroup H III. Architecture of the complete IgM-molecule."

RL Hoppe-Seyler's Z. Physiol. Chem. 354:1505-1509(1973).

RN [2]

RP REVISION TO 28-33.

RA Hilschmann N.;

RL Submitted (JUN-1975) to the PIR data bank.

CC -1- MISCELLANEOUS; THIS MU CHAIN WAS ISOLATED FROM A WALDENSTROM'S

MACROGLOBULIN.

DR PIR; A02064; M3HUGL.

DR HSSP; P01772; 2PB4.

DR InterPro; IPR003006; IG_MHC.

DR InterPro; IPR003596; IG_V.

DR Pfam; PF00047; IgV_1.

DR SMART; SM00406; IgV_1.

KW Immunoglobulin V region.

FT NON_TER 116 116

SQ SEQUENCE 116 AA; 12730 MW; 2C67CA9AAAAA1282 CRC64;

Query Match

Best Local Similarity 70.9%; Score 448.5; DB 1; Length 116;

Matches 88; Conservative 10; Mismatches 18; Indels 3; Gaps 1;

QY 1 QVQLVESGGGVQVQPGSRSLRLSCAASGFTSSYGMHWVRQAPGKGLKLVAVIWDGSKNTYY 60

DB 1 QVQLVESGGGVQVQPGSRSLRLSCAASGFTSSYGMHWVRQAPGKGLKLVAVIWDGSKNTYY 60

QY 61 ADSVKGRTISRDNKNTLYLQMSLRBEDTAVFYCARAPNTYIGAFDVGSGGTMYTVSS 119

DB 61 ADSVKGRTISRDNKNTLYLQMSLRBEDTAVFYCARAPNTYIGAFDVGSGGTMYTVSS 119

RESULT 9

HY3B_HUMAN

ID HY3B_HUMAN STANDARD; PRT; 114 AA.

AC P01763;

DT 21-JUL-1986 (Rel. 01, Created)

DT 21-JUL-1986 (Rel. 01, Last sequence update)

DT 15-JUL-1999 (Rel. 38, Last annotation update)

DB Ig heavy chain V-III region WEA.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

OX NCBI_TaxId=9606;

RN [1]

RP SEQUENCE.

MEDLINE=83273707; PubMed=6410398;

RA Goni F., Frangione B.;

RT "Amino acid sequence of the Fv region of a human monoclonal IgM

RT (protein WEA) with antibody activity against 3,4-pyruvylated

RT galactose in Klebsiella polysaccharides K30 and K33."

RL Proc. Natl. Acad. Sci. U.S.A. 80:4837-4841(1983).

CC -1- MISCELLANEOUS: THIS CHAIN WAS OBTAINED FROM A MONOCLONAL ANTIBODY

CC AGAINST 3,4-PYRUVYLATED GALACTOSE AND ISOLATED FROM A PATIENT WITH

CC WALDENSTROM'S MACROGLOBULINEMIA.

DR PIR; A02046; M3HUME.

DR HSSP; P01772; 2PB4.

DR InterPro; IPR003006; IG_MHC.

DR InterPro; IPR003596; IG_V.

DR Pfam; PF00047; IgV_1.

DR SMART; SM00406; IgV_1.

KW Immunoglobulin V region.

FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.

FT NON_TER 114 114

SQ SEQUENCE 114 AA; 12256 MW; D88294FB418A07B7 CRC64;

Query Match

Best Local Similarity 73.1%; Score 440.5; DB 1; Length 114;

Matches 87; Conservative 14; Mismatches 13; Indels 5; Gaps 1;

QY 1 QVQLVESGGGVQVQPGSRSLRLSCAASGFTSSYGMHWVRQAPGKGLKLVAVIWDGSKNTYY 60

DB 1 QVQLVESGGGVQVQPGSRSLRLSCAASGFTSSYGMHWVRQAPGKGLKLVAVIWDGSKNTYY 60

QY 61 ADSVKGRTISRDNKNTLYLQMSLRBEDTAVFYCARAPNTYIGAFDVGSGGTMYTVSS 119

DB 61 ADSVKGRTISRDNKNTLYLQMSLRBEDTAVFYCARAPNTYIGAFDVGSGGTMYTVSS 119

RESULT 10

HV3E_HUMAN
ID HV3E_HUMAN STANDARD; PRT; 120 AA.
AC P01766;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V-II region BRO.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=7117674; PubMed=65324;
RA Capra J.D., Hopper J.E.;
RT "Comparative studies on monocytic IgM lambda and IgG kappa from an individual patient. III. The complete amino acid sequence of the VH region of the IgM paraprotein.";
RL Immunohistochemistry 13:995-999(1976).
CC -1- MISCELLANEOUS: THIS CHAIN WAS OBTAINED FROM IGM ISOLATED FROM THE SERUM OF A PATIENT WITH MALIGNANT LYMPHOMA OF THE WALDENSTROM TYPE.
CC PIR: A02049; M3HUBM.
DR HSP; P01772; 2PB4.
DR InterPro: IPR003006; IG_MHC.
DR InterPro: IPR003596; IG_V.
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00406; IGv; 1.
DR Immunoglobulin V region.
KW NON TER
FT 120
SQ SEQUENCE 120 AA; 13327 MW; D3F0428F7C2B6410 CRC64;
Query Match 67.9%; Score 430; DB 1; Length 120;
Best Local Similarity 70.7%; Pred. No. 2.2e-38;
Matches 87; Conservative 12; Mismatches 12; Indels 12; Gaps 3;
QY 1 QVQLVSGGAVGQGRSLRLSCAASGFTFSYGMHWVRQAPGKGLEWVAIVMYGSSNRY 60
DB 1 EVQLVSGGGLVQPGSRIRLSCAASGFTFSYMMWVRQVTKGLEWVAISGTAG-DOYY 59
QY 61 ADVYKGRFTISRDNKNTLYLQNNSLRAEDTAVFYCARPYIGA-PDVGCGMTWYSS 119
DB 60 ADVYKGRFTISRDNKNTLYLQNNSLRAEDTAVFYCARPYIGASPVLDGMYLYYYS- -VWGQ 117
QY 112 GTM 114
DB 118 GTL 120
RESULT 11
HV3U_HUMAN STANDARD; PRT; 120 AA.
AC P01783;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V-II region DOB.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=80020921; PubMed=114209;
RA Steiner L.A., Garcia Pardo A., Margolies M.N.;
RT "Amino acid sequence of the heavy-chain variable region of the RT crystallizable human myeloma protein Dob.";
RL Biochemistry 18:4068-4080(1979).
RN [2]
RP CRYSTALLIZATION.
RX MEDLINE=80020920; PubMed=114208;
RA Steiner L.A., Lopes A.D.;
RT "The crystallizable human myeloma protein Dob has a hinge-region

RT deletion.";
RL Biochemistry 18:4054-4067(1979).
CC -1- MISCELLANEOUS: THIS GAMMA-1 MYELOMA PROTEIN HAS A DELETION IN THE HINGE REGION. THERE ARE NO LIGHT-HEAVY OR INTER-HEAVY CHAIN DISULFIDE BONDS.
CC PIR: A02065; G1HUBD.
DR HSP; P01772; 2PB4.
DR InterPro: IPR003006; IG_MHC.
DR InterPro: IPR003596; IG_V.
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00406; IGv; 1.
DR Immunoglobulin V region.
KW NON TER
FT 120
SQ SEQUENCE 120 AA; 13440 MW; 880DDB307C4B2627 CRC64;
Query Match 67.7%; Score 428.5; DB 1; Length 120;
Best Local Similarity 68.3%; Pred. No. 3.2e-38;
Matches 82; Conservative 14; Mismatches 23; Indels 1; Gaps 1;
QY 1 QVQLVSGGAVGQGRSLRLSCAASGFTFSYGMHWVRQAPGKGLEWVAIVMYGSSNRY 60
DB 1 EVQLVSGGGLVQPGSRIRLSCAASGFTFSYMMWVRQVTKGLEWVAISGTAG-DOYY 59
QY 61 ADVYKGRFTISRDNKNTLYLQNNSLRAEDTAVFYCARPYIGA-PDVGCGMTWYSS 119
DB 61 ADVYKGRFTISRDNKNTLYLQNNSLRAEDTAVFYCARPYIGASPVLDGMYLYYYS- -VWGQ 120
RESULT 12
HV3C_HUMAN STANDARD; PRT; 117 AA.
AC P01764;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V-II region VH26 precursor.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=81101090; PubMed=6450418;
RA Matlyssens G., Rabbitts T.H.;
RT "Structure and multiplicity of genes for the human immunoglobulin RT heavy chain variable region.";
RL Proc. Natl. Acad. Sci. U.S.A. 77:6561-6565(1980).
CC -----
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CC -----
DR EMBL: J00236; AAA53516.1; -;
DR EMBL: M35415; AAA58735.1; -;
DR PIR: A02047; H3HUB2.
DR HSP; P01772; 2PB4.
DR Genew; HGNC:5545; IGHW@.
DR InterPro: IPR003006; IG_MHC.
DR InterPro: IPR003596; IG_V.
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00406; IGv; 1.
DR Immunoglobulin V region; Signal.
KW SIGNAL
FT CHAIN 1
FT NON TER 117
FT 117
SQ SEQUENCE 117 AA; 12582 MW; E826733FLAOCB0P1 CRC64;
Query Match 67.5%; Score 427; DB 1; Length 117;
Best Local Similarity 82.7%; Pred. No. 4.5e-38;

Matches 81; Conservative 7; Mismatches 10; Indels 0; Gaps 0;

QY 1 QVQLVESGGGVVQPGSRSLRLSCAASGFTSSYGMHWVRQAPGKLEWVAIVYDGSKYY 60
 DB 20 EVQLLESGGGLVQPGGSLRLSCAASGFTSSYANSWVRQAPGKLEWVAISLGGSTYY 79

QY 61 ADSVKGRFTISRDNKNTLYLQNMNLSRAEDTAVFYCAR 98
 DB 80 GDSVKGRFTISRDNKNTLYLQNMNLSRAEDTAVFYCAR 117

RESULT 13
 HV30 HUMAN STANDARD; PRT; 117 AA.

AC P01776;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE 15 heavy chain V-III region WAS.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 NCBI_TaxID=9606;
 RX MEDLINE=74142702; PubMed=4522793;
 RA Capra J.D., Kehoe J.M.;
 RT "Variable region sequences of five human immunoglobulin heavy chains
 of the Vh3 subgroup: definitive identification of four heavy chain
 hypervariable regions.";
 RL Proc. Natl. Acad. Sci. U.S.A. 71:845-848(1974).
 CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IG1 MYELOMA
 CC PROTEIN.
 DR HSSP; P01772; 2PB4.
 DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR003596; Ig_V.
 DR Pfam; PF00047; Ig; 1.
 DR SMART; SM00406; IgV; 1.
 KM Immunoglobulin V region.
 FT NON TER 117
 SQ SEQUENCE 117 AA; 13091 MW; 201DEF0B1E53D9BF CRC64;

Query Match 66.9%; Score 423.5; DB 1; Length 117;
 Best Local Similarity 68.4%; Pred. No. 1.1e-37;
 Matches 80; Conservative 20; Mismatches 16; Indels 1; Gaps 1;

QY 1 QVQLVESGGGVVQPGSRSLRLSCAASGFTSSYGMHWVRQAPGKLEWVAIVYDGSKYY 60
 DB 1 EVQLLESGGGLVQPGGSLRLSCAASGFTSSYANSWVRQAPGKLEWVAISLGGSTYY 79

QY 61 ADSVKGRFTISRDNKNTLYLQNMNLSRAEDTAVFYCAR-APNTIGAFDVWGQGTWY 116
 DB 61 ADVNKRFTISRDNKNTLYLQNMNLSRAEDTAVFYCAR-APNTIGAFDVWGQGTWY 117

RESULT 14
 HV30 HUMAN STANDARD; PRT; 115 AA.

AC P01767;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE 15 heavy chain V-III region BUT.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 NCBI_TaxID=9606;
 RX MEDLINE=78137069; PubMed=416441;
 RA Torano A., Putnam F.W.;
 RT "Complete amino acid sequence of the alpha 2 heavy chain of a human

RT 1GA2 immunoglobulin of the Azm (2) allotype.";
 RL Proc. Natl. Acad. Sci. U.S.A. 75:966-969(1978).
 CC -1- MISCELLANEOUS: THE SEQUENCE OF THE ALPHA-2, AZM(2) ALLOTYPE, C
 CC REGION OF THIS MYELOMA PROTEIN IS ALSO GIVEN.
 DR PIR; A02050; AZHUBU.
 DR HSSP; P01789; 1MCP.
 DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR003596; Ig_V.
 DR Pfam; PF00047; Ig; 1.
 DR SMART; SM00406; IgV; 1.
 KM Immunoglobulin V region.
 FT NON TER 115
 SQ SEQUENCE 115 AA; 12379 MW; 208876A7DF52DC64 CRC64;

Query Match 66.5%; Score 421; DB 1; Length 115;
 Best Local Similarity 68.9%; Pred. No. 1.9e-37;
 Matches 82; Conservative 17; Mismatches 16; Indels 4; Gaps 2;

QY 1 QVQLVESGGGVVQPGSRSLRLSCAASGFTSSYGMHWVRQAPGKLEWVAIVYDGSKYY 60
 DB 1 EVQLVGGGLVQPGGSLRLSCAASGFTVSBHSMWVRQAPGKLEWVAI-YRGSTYY 59

QY 61 ADSVKGRFTISRDNKNTLYLQNMNLSRAEDTAVFYCARAPNTIGAFDVWGQGTWY 119
 DB 60 ADSVKGRFTISRDNKNTLYLQNMNLSRAEDTAVFYCAR---LAARLFGKPTTVYSS 115

RESULT 15
 HV05 CARAU STANDARD; PRT; 116 AA.

AC P19181;
 DT 01-NOV-1990 (Rel. 16, Created)
 DT 01-NOV-1990 (Rel. 16, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE 15 heavy chain V region 5A precursor.
 OS Carassius auratus (Goldfish).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
 OC Cyprinidae; Carassius.
 NCBI_TaxID=7957;
 RX MEDLINE=88144476; PubMed=312551;
 RA Wilson M.R., Middleton D., Watt G.W.;
 RT "Immunoglobulin heavy chain variable region gene evolution: structure
 and family relationships of two genes and a pseudogene in a teleost
 fish.";
 RL Proc. Natl. Acad. Sci. U.S.A. 85:1566-1570(1988).
 DR HSSP; P01772; 2PB4.
 DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR003596; Ig_V.
 DR Pfam; PF00047; Ig; 1.
 DR SMART; SM00406; IgV; 1.
 KM Immunoglobulin V region; Signal.
 FT CHAIN 1
 FT SIGNAL 19
 FT CHAIN 20
 FT DOMAIN 20 116 IG HEAVY CHAIN V REGION 5A.
 FT DOMAIN 50 49 FRAMEWORK-1.
 FT DOMAIN 55 54 COMPLEMENTARITY-DETERMINING-1.
 FT DOMAIN 69 68 FRAMEWORK-2.
 FT DOMAIN 85 84 COMPLEMENTARITY-DETERMINING-2.
 FT DISULFID 85 116 FRAMEWORK-3.
 FT NON TER 116 BY SIMILARITY.
 SQ SEQUENCE 116 AA; 12808 MW; 9C2279E2DF199B12 CRC64;

Query Match 66.1%; Score 418.5; DB 1; Length 116;
 Best Local Similarity 83.7%; Pred. No. 3.5e-37;
 Matches 82; Conservative 6; Mismatches 9; Indels 1; Gaps 1;

QY 1 QVQLVESGGGVVQPGSRSLRLSCAASGFTSSYGMHWVRQAPGKLEWVAIVYDGSKYY 60
 DB 20 EVQLVESGGGLVQPGGSLRLSCAASGFTVSSYHSMWVRQAPGKLEWVAI-YSGSTYY 78

Oy 61 ADVKGRFTISRDNKNTLYLOMSIRADTAVFYCAR 98
|||
Db 79 ADVKGRFTISRDNKNTLYLOMSIRADTAVFYCAR 116
|||

Search completed: June 3, 2003, 08:15:45
Job time : 10.9659 secs

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OM protein - protein search, using sw model

Run on: June 3, 2003, 08:07:54 ; Search time 59.2969 Seconds

(without alignments)
413,506 Million cell updates/sec

Title: US-09-644-668A-23

Sequence: 1 QVQLVSGGGVQPGSRSLRL.....PNYIGAFDVGQGTMTVSS 119

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

- 1: SP:archaea:*
- 2: SP:bacteria:*
- 3: SP:fungi:*
- 4: SP:human:*
- 5: SP:invertebrate:*
- 6: SP:mammal:*
- 7: SP:mhc:*
- 8: SP:organelle:*
- 9: SP:phage:*
- 10: SP:plant:*
- 11: SP:rodent:*
- 12: SP:virus:*
- 13: SP:vertebrate:*
- 14: SP:unclassified:*
- 15: SP:viirus:*
- 16: SP:bacteriopl:*
- 17: SP:archaeopl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	558.5	88.2	613	4	Q8WUK1
2	536	84.7	113	4	Q9UL90
3	522	82.5	116	4	Q9UL93
4	498.5	78.8	147	4	Q9Y509
5	495.5	78.3	122	4	Q9UL84
6	490	77.4	121	4	Q9UL71
7	475.5	75.1	118	4	Q9UL91
8	475.5	75.1	573	4	Q8WU38
9	472	74.6	557	4	Q96BB9
10	465.5	73.5	471	4	Q8TC77
11	453.5	71.6	118	4	Q9UL72
12	449.5	71.0	112	4	Q9HCC1
13	446	70.5	119	11	Q920E7
14	441.5	69.7	473	11	Q91205
15	431.5	68.2	494	4	Q96K68
16	429	67.8	479	11	Q91WP5

17	424	67.0	95.	4	Q9ULB6	Q9ULB6 homo sapien
18	423.5	66.9	487	11	Q99XA4	Q99XA4 mus musculu
19	401	63.3	131	4	Q9UL88	Q9UL88 homo sapien
20	397	62.7	486	11	Q91Z07	Q91Z07 mus musculu
21	391.5	61.8	484	11	Q8VEA0	Q8VEA0 mus musculu
22	390.5	61.7	469	11	Q8RV99	Q8RV99 mus musculu
23	387.5	61.2	298	11	Q9QYF0	Q9QYF0 mus musculu
24	386	61.0	480	11	Q91X81	Q91X81 mus musculu
25	380	60.0	104	4	Q9UL87	Q9UL87 mus musculu
26	379.5	60.0	124	4	Q9UL92	Q9UL92 homo sapien
27	366.5	57.9	457	11	Q9UL94	Q9UL94 mus musculu
28	365.5	57.7	124	6	Q9N0M4	Q9N0M4 oryctolagus
29	362.5	57.3	124	6	Q9N0M6	Q9N0M6 oryctolagus
30	359.5	56.8	482	11	Q91X92	Q91X92 mus musculu
31	358	56.6	112	4	Q9UL93	Q9UL93 homo sapien
32	355.5	56.2	121	4	Q9NNG4	Q9NNG4 mus musculu
33	353	55.8	125	4	Q9UL95	Q9UL95 mus musculu
34	343.5	54.3	159	4	Q96QSO	Q96QSO mus musculu
35	340	53.7	484	11	Q9UL96	Q9UL96 mus musculu
36	339.5	53.6	143	11	Q924R7	Q924R7 mus musculu
37	339	53.6	614	4	Q96GA5	Q96GA5 mus musculu
38	334.5	52.8	143	11	Q91VA2	Q91VA2 mus musculu
39	334	52.8	119	4	Q9UL94	Q9UL94 homo sapien
40	330.5	52.2	463	11	Q9ULC4	Q9ULC4 mus musculu
41	326.5	51.6	143	11	Q91V67	Q91V67 mus musculu
42	326.5	51.6	241	11	Q921A6	Q921A6 mus musculu
43	325	51.3	119	4	Q9UL73	Q9UL73 homo sapien
44	322.5	50.9	145	11	Q924R4	Q924R4 mus musculu
45	321	50.7	146	11	Q924R8	Q924R8 mus musculu

ALIGNMENTS

RESULT 1

Q8WUK1 PRELIMINARY; PRT; 613 AA.

AC Q8WUK1
DT 01-MAR-2002 (TREMBLrel. 20, Created)
DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Hypothetical 67.3 kDa protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
RN NCBI_TaxID=9606;
RP SEQUENCE FROM N.A.
RC TISSUE=TONSIL;
RA Strauberg R.;
RL Submitted (DRC-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC020240; AA020240.1; -
DR InterPro; IPR003599; IG.
DR InterPro; IPR003597; IG CL.
DR InterPro; IPR003006; IG MHC.
DR InterPro; IPR003596; IG V.
DR Pfam; PF00047; IG 5.
DR SMART; SM00409; IG 2.
DR SMART; SM00407; IG 1; 4.
DR SMART; SM00406; IG 1.
DR PROSITE; PS00290; IG MHC; UNKNOWN_3.
DR Hypothetical protein
SQ SEQUENCE 613 AA; 67296 MW; 60CTF5950671E315 CRC64;

Query Match 88.2%; Score 558.5; DB 4; Length 613;
Best Local Similarity 90.0%; Pred. No. 3.6e-50;

Matches 108; Conservative 4; Mismatches 7; Indels 1; Gaps 1;

QY 1 QVQLVSGGGVQPGSRSLRLCAASGFTSSYGMHWVQAPKGLWVAIVYDGSNKYY 60
DB 20 QVQLVSGGGVQPGSRSLRLCAASGFTSSYGMHWVQAPKGLWVAIVYDGSNKYY 79
QY 61 ADVKGRFTISRDNSKNTLYIQMNSLRADETAVFYCAR-PNYIGAFDVGQGTMTVSS 119

OC Mammalia, Eutheria, Primates, Catarrhini, Hominoidea, Homo.
OX NCBI TaxID=9606;
RN [1]
RP
RC SEQUENCE FROM N.A.
RD TISSUE=MAMMARY GLAND;
RA Isogai T., Ota T., Hayaishi K., Sugiyama T., Otsuki T., Suzuki Y.,
RA Nishikawa T., Nagai K., Sugano S., Shiratori A., Sudo H.,
RA Wagatsuma M., Hosokiri T., Kaku Y., Kodaira H., Kondo H., Sugawara M.,
RA Takahashi M., Chiba Y., Ishida S., Murakawa K., Ono Y., Takiguchi S.,
RA Watanabe S., Kimura K., Murakami K., Ishii S., Kawai Y., Saito K.,
RA Yamamoto J., Wakamatsu A., Nakamura Y., Nagahara K., Maeno Y.,
RA Niinomiya K., Iwayanagi T.,
RT "NEO human cDNA sequencing project";
RL submitted (May-2001) to the EMBL/GenBank/DBJ databases.
RR EMBL; AK027379, BAB55072.1;
DR InterPro; IPR003006; IG_MHC.
DR Pfam; PF00047; IG; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN.1.
SO SEQUENCE 494 AA; 5108 MW;

Query Match

68-241-6000

Best Local Similarity	70.7%;	score 431.5;	DB 4;	Length 494;
Matches	87;	Conservative	70.7%;	Pred. No. 5.9e-37;

QY 1 QVQLVESGGGVNPGRSPRTTC... 18; Indels 5; Gaps 2;

Db
20 EVQLVESGGGLYKPCCKGKLEWVAWIYDGSNKYY 60

61 ADSVKGREFTISPDNSKAMT W 79

Db
80 RDSVKGRFTISPDNAKNSIYVQSSDIAVEFCARAPNYIGA-----FDVWGQGTMYT 116

QY 117 VSS 119
- - - - -
- - - - - CAR - DSCNGAI CYGFSFPGQGLVT 138

Db 139 VSS 141

Search completed: June 3, 2003, 08:20:48
Job time : 60.2969 secs

FE : 24-AUG-2000; 2000MO-0523356.
XY

The heavy chain of

PR 24-AUG-1999; 99US-0150452.
 XX
 PA (MEDA-) MEDAREX INC.
 XX
 PI Korman AJ, Halk EL, Lonberg N;
 XX
 DR WPI, 2001-202933/20.
 XX
 PT Novel human sequence antibody that binds to human cytotoxic T
 PT lymphocyte associated antigen-4, useful for inducing, augmenting or
 PT prolonging immune response to antigen or for suppressing immune
 PT response in patient
 XX
 PS Claim 27; Fig 8; 127pp; English.
 XX
 CC The present sequence represents the heavy chain variable region of
 CC human antibody 1B2. This antibody specifically binds to human
 CC cytotoxic T lymphocyte associated antigen-4 (CTLA-4). Such antibodies
 CC are used in methods for inducing, augmenting or prolonging an immune
 CC response to an antigen in a patient, where the antibodies block
 CC binding of human CTLA-4 to human B7 ligands. The antibodies are
 CC also useful for treating autoimmune disease in a subject caused or
 CC exacerbated by increased activity of T cells and for treating prostate
 CC cancer, melanoma or epithelial cancer. A polyvalent or polyclonal
 CC antibody preparation comprising two antibodies of the invention are
 CC useful for suppressing a immune response in a patient. They are used for
 CC treating cancer, infectious diseases and promoting beneficial autoimmune
 CC reactions for the treatment of diseases with inflammatory or allergic
 CC components. The polyvalent or polyclonal preparations are useful for
 CC treating autoimmune diseases such as rheumatoid arthritis, myasthenia
 CC gravis and lupus erythematosus, multiple sclerosis, insulin-dependent
 CC diabetes mellitus, transplant rejection, and inflammation, graft versus
 CC host disease.
 CC
 SQ Sequence 119 AA;
 Query Match 100.0%; Score 633; DB 22; Length 119;
 Best Local Similarity 100.0%; Pred. No. 1,3e-50;
 Matches 119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 QVQLVSGGAVQPGKSLRLSCAASGFTSSVGMHWRAQPGKLEWAVIWDGSKYY 60
 DB 1 QVQLVSGGAVQPGKSLRLSCAASGFTSSVGMHWRAQPGKLEWAVIWDGSKYY 60
 QY 61 ADSVKGRTISRNSKNTLYLQNSLRADTAVFYCARAPNYIGADPWGQGTMTVSS 119
 DB 61 ADSVKGRTISRNSKNTLYLQNSLRADTAVFYCARAPNYIGADPWGQGTMTVSS 119
 DB 61 ADSVKGRTISRNSKNTLYLQNSLRADTAVFYCARAPNYIGADPWGQGTMTVSS 119
 RESULT 2
 ID AAY93734
 AC AAY93734 standard; Protein; 451 AA.
 XX
 DT 03-OCT-2000 (first entry)
 XX
 DB The heavy chain of immunoglobulin clone 11.2.1.
 KW Cytotoxic T-lymphocyte antigen-4; CTLA-4; antibody; immune system;
 KW hyperimmunity disorder; autoimmune disease; diabetes; graft rejection;
 KW proliferative disorder; cancer; immunodeficient disorder.
 XX
 OS Homo sapiens.
 XX
 PN WO200037504-A2.
 PD 29-JUN-2000.
 XX
 PF 23-DEC-1999; 99WO-US30895.
 XX
 PR 23-DEC-1998; 98US-0113647.
 XX

PA (PRIZ) PRIZER INC.
 PA (ABGE-) ABGENIX INC.
 XX
 PI Hanson DC, Neveu MJ, Mueller EE, Hanke JH, Gilman SC, Davis CG;
 PI Corvalan JR;
 XX
 DR WPI, 2000-442647/38.
 XX
 DR N-PSDB; AAA46898.
 XX
 PT Novel antibodies capable of binding cytotoxic T-lymphocyte antigen
 PT (CTLA)-4 containing specified heavy and light chain sequences, useful
 PT for treating, e.g. immune disorders
 XX
 PS Claim 2; Fig 22q; 157pp; English.
 XX
 CC The present sequence represents a heavy chain of an antibody of the
 CC invention. The antibody is directed cytotoxic T-lymphocyte antigen
 CC (CTLA)-4. Antibodies of the invention are composed of a heavy chain
 CC variable region, comprising a modified contiguous sequence from a
 CC FRI-FR3 sequence encoded by a human VH3-33 family gene. The
 CC modifications are contained in CDR1, CDR2 and/or framework regions.
 CC The antibodies may be used to inhibit CTLA-4 and down-regulate the
 CC immune system to treat hyperimmunity disorders (e.g. autoimmune
 CC disease, diabetes and graft rejection) and proliferative disorders
 CC (e.g. cancer). CTLA-4 stimulatory agents may be used to up-regulate
 CC immune system to up-regulate immunodeficient disorders.
 CC
 SQ Sequence 451 AA;
 Query Match 90.8%; Score 575; DB 21; Length 451;
 Best Local Similarity 88.8%; Pred. No. 1.1e-44;
 Matches 111; Conservative 1; Mismatches 7; Indels 6; Gaps 1;
 QY 1 QVQLVSGGAVQPGKSLRLSCAASGFTSSVGMHWRAQPGKLEWAVIWDGSKYY 60
 DB 1 QVQLVSGGAVQPGKSLRLSCAASGFTSSVGMHWRAQPGKLEWAVIWDGSKYY 60
 QY 61 ADSVKGRTISRNSKNTLYLQNSLRADTAVFYCARAPN-----YIGADPWGQGTMT 114
 DB 61 ADSVKGRTISRNSKNTLYLQNSLRADTAVFYCARAPNATLYYYYYGMDPWGQGTMT 120
 QY 115 VTSS 119
 DB 121 VTSS 125
 RESULT 3
 ID ABP45098
 AC ABP45098 standard; Protein; 249 AA.
 XX
 DT 19-AUG-2002 (first entry)
 XX
 DB Human Bly's binding scFv SEQ ID 1109.
 KW Bly's; B lymphocyte stimulator; TNF superfamily; human; cytostatic;
 KW tumor necrosis factor; B cell proliferation; B cell differentiation;
 KW immunosuppressive; immunostimulant; immunomodulatory; antirheumatic;
 KW antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;
 KW systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;
 KW common variable immunodeficiency; acquired immunodeficiency syndrome.
 XX
 OS Homo sapiens.
 XX
 PN WO200202641-A1.
 PD 10-JAN-2002.
 XX
 PF 15-JUN-2001; 2001WO-US19110.
 XX
 PR 16-JUN-2000; 2000US-212210P.
 XX
 PR 17-OCT-2000; 2000US-240816P.
 XX

XX		(HOMA-) HUMAN GENOME SCI INC.
PA		(CAME-) CAMBRIDGE ANTIBODY TECHNOLOGY.
XX		
PI	Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;	
DR	WPI; 2002-114799/15.	
XX		
PT	Antibodies against B Lymphocyte Stimulating polypeptides, useful for	
XX	the diagnosis and treatment of cancers and immune disorders -	
PS	Claim 1, Page 1726-1727, 3148pp; English.	
XX		
CC	This invention describes novel antibodies that immunospecifically bind to	
CC	B Lymphocyte Stimulator (BLYS) polypeptides. BLYS is a member of the	
CC	tumour necrosis factor (TNF) super family and induces B cell	
CC	proliferation and differentiation. The antibodies of the invention have	
CC	cytostatic, immunosuppressive, immunostimulant, immunomodulatory,	
CC	antirheumatic and antiAIDS activity and can be used in vaccines to	
CC	inhibit the expression and activity of BLYS. The antibodies bind to BLYS	
CC	and so may be used to detect and quantitate the presence of BLYS in	
CC	biological samples and may be used in this way to diagnose disease	
CC	associated with aberrant expression of BLYS. They may also be	
CC	administered to treat diseases associated with aberrant BLYS expression	
CC	and actively such as cancer, immune, and autoimmune disorders and	
CC	diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,	
CC	immunodeficiency (e.g. common variable immunodeficiency (CVID) and	
CC	acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent	
CC	the antibodies and fragments of the antibodies described in the method	
XX	of the invention.	
SQ		
Sequence	249 AA;	
Query Match	90.8%; Score 574.5; DB 23; Length 249;	
Best Local Similarity	88.9%; Pred. No. 6.3e-45;	
Matches 112; Conservative	2; Mismatches 5; Indels 7; Gaps 1;	
OY	1 QVQLVESGGGVVQPGRSLRLCSAAGFPFSSTGGMHWQAPEKGLDWMVAIVMYDGSKRYY 60	
DB	1 QVQLVESGGGVVQPORSLRLSCASGFTFSSYGMMHWQAPEKGLEMAVVISYDSNRRYY 60	
OY	61 ADSVKGRETTISRDN SKNTLYIQMNSLRLEDTAVFYCARAP-----NYIGAFDVWGSGT 113	
DB	61 VDSVKGRTISRDN SKNTLYIQMNSLRLEDTAVFYCARASYDDITGYKKAFDIWGCGT 120	
OY	114 MVTWSS 119	
DB	121 MVTWSS 126	
RESULT 4		
ID	AAU81993 standard; Protein; 519 AA.	
XX	AAU81993	
AC	AAU81993;	
DT	09-APR-2002 (first entry)	
XX		
DE	Human secreted protein SECP19.	
XX		
KW	Human; SECP; antiinflammatory; cytosratic; cardiac;	
KW	immunosuppressive; antiviral; anti-HIV; antiaarthritis; antineumatic;	
KW	mucular active general; anticoagulant; noctropic; neuroprotective;	
KW	antiallergic; hypotensive; cardiovascular disorder; atherosclerosis;	
KW	hyperension; myocardial infarction; autoimmune disorder;	
KW	inflammatory disorder; AIDS; acquired immunodeficiency syndrome;	
KW	allergy; rheumatoid arthritis; cell proliferative disorder; cancer;	
KW	developmental disorder; Duchenne muscular dystrophy;	
KW	neurological disorder; epilepsy; Alzheimer's disease.	

```

OS Homo sapiens.
XX
XX WO200198353-A2.
XX
XX PD 27-DEC-2001.
XX
XX PF 20-JUN-2001, 2001WO-US19862.
XX
XX PR 20-JUN-2000, 2000US-212890P.
XX
XX PR 23-JUN-2000, 2000US-213466P.
XX
XX PR 27-JUN-2000, 2000US-214601P.
XX
XX PR 31-JUL-2000, 2000US-222372P.
XX
XX PR 08-SEP-2000, 2000US-231435P.
XX
XX PR 15-SEP-2000, 2000US-232889P.
XX
XX (INCY-) INCYTE GENOMICS, INC.
XX
XX PA Hillman JI, Tang YF, Yue H, Elliott VS, Tribouley CM, Lee EA,
XX
XX PI Ramm Kumar Y, Lal P, Xu Y, Warren BA, Hattalia AB, Baughn KR;
XX
XX PI Azimzal Y, Batra S, Burford N, Yao MG, Nguyen DB, Lu DM;
XX
XX PI Walla NK, Gandhi AR, Au-Young J, Patterson C;
XX
XX MP1, 2002-090431/12.
XX
XX N-PSDB; ABK28652.
XX
XX
XX PT Forty four human secreted proteins (referred to as SECP-1 to SECP-44),
XX
XX PT useful in the diagnosis, treatment and prevention of cardiovascular
XX
XX PT (e.g. atherosclerosis), autoimmune/inflammatory (e.g. allergies) and
XX
XX PT cell proliferative disorders -
XX
XX
XX PS Claim 1, Page 142-143, 195BP, English.
XX
XX
XX CC The invention relates to forty four human secreted proteins (referred to
XX
XX CC as SECP-1 to SECP-44) and the nucleic acids encoding them. Also
XX
XX CC included are a host cell transformed with the nucleic acid, a
XX
XX CC transgenic animal comprising the nucleic acid, an anti-SECP
XX
XX CC antibody, use of the SECP proteins in isolating agonists and antagonists
XX
XX CC of SECP activity and a method of isolating compounds which alter the
XX
XX CC expression of the SECP nucleic acid. The SECP polynucleotides and
XX
XX CC polypeptides are useful in the diagnosis, treatment and prevention of
XX
XX CC cardiovascular (e.g. atherosclerosis, hypertension, myocardial
XX
XX CC infarction), autoimmune/inflammatory (e.g. acquired immunodeficiency
XX
XX CC syndrome (AIDS), allergies, rheumatoid arthritis), cell proliferative
XX
XX CC (e.g. cancer), developmental (e.g. Duchenne and Becker muscular
XX
XX CC dystrophy), and neurological (e.g. epilepsy, Alzheimer's disease)
XX
XX CC disorders. Numerous other examples of each disorder are given in the
XX
XX CC specification. The present sequence represents a SECP protein.
XX
XX
XX SQ Sequence 519 AA;
XX
XX
XX Query Match 90.4%; Score 572; DB 23; Length 519;
XX
XX Best Local Similarity 90.2%; Pred. No. 2.3e-44;
XX
XX Matches 111; Conservative 4; Mismatches 4; Indels 4; Gaps 1;
XX
XX
XX QY 1 QVQLVESGGGVGVQPGSRSLRLSCAASGFTFSYGMHWYROAPGKGLIEWVAIVYDGSNKYY 60
XX
XX DB 20 QVQLVESGGGVGVQPGSRSLRLSCAASGFTFSYGMHWYROAPGKGLIEWVAIVYDGSNKYY 79
XX
XX
XX QY 61 ADSYKGFRTISRDNSKNTLYIQNNLSLAEDTAVFYCARA---ENYIGAPFVWGQGTMT 116
XX
XX DB 80 ADSYKGFRTISRDNSKNTLYIQNNLSLAEDTAVFYCARAGSGSDTLVAFPIWGQGTMT 139
XX
XX
XX QY 117 VSS 119
XX
XX DB 140 VSS 142
XX
XX
XX RESULT 5
XX
XX ID AA193707 standard; Protein: 463 AA.
XX
XX CC AA193707;
XX
XX

```

DT 03-OCT-2000 (first entry)
 XX The heavy chain of immunoglobulin clone 6.1.1.
 DE
 XX Cytotoxic T-lymphocyte antigen-4; CTLA-4; antibody; immune system;
 KW hyperimmunity disorder; autoimmune disease; diabetes; graft rejection;
 KM proliferative disorder; cancer; immunodeficient disorder.
 XX
 OS Homo sapiens.
 XX
 XX WO200037504-A2.
 XX
 XX 29-JUN-2000.
 XX
 XX 23-DEC-1999; 99WO-US30895.
 XX
 XX 23-DEC-1998; 98US-0113647.
 XX
 XX (PF12) PFIZER INC.
 XX (ABGE-) ABGENIX INC.
 XX
 XX Hanson DC, Neveu MJ, Mueller BE, Hanke JH, Gilman SC, Davis CG;
 PI Corvalan JR;
 XX
 XX WPI; 2000-442647/38.
 XX N-PSDB; AAA46870.
 XX
 XX Novel antibodies capable of binding cytotoxic T-lymphocyte antigen
 PT (CTLA)-4 containing specified heavy and light chain sequences, useful
 PT for treating, e.g. immune disorders -
 PS
 PS Claim 2; Fig 1D; 157pp; English.
 XX
 XX The present sequence represents a heavy chain of an antibody of the
 CC invention. The antibody is directed cytotoxic T-lymphocyte antigen
 CC (CTLA)-4. Antibodies of the invention are composed of a heavy chain
 CC variable region, comprising a modified contiguous sequence from a
 CC FRI-FR3 sequence encoded by a human VH3-33 family gene. The
 CC modifications are contained in CDR1, CDR2 and/or framework regions.
 CC The antibodies may be used to inhibit CTLA-4 and down-regulate the
 CC immune system to treat hyperimmunity disorders (e.g. autoimmune
 CC disease, diabetes and graft rejection) and proliferative disorders
 CC (e.g. cancer). CTLA-4 stimulatory agents may be used to up-regulate
 CC immune system to up-regulate immunodeficient disorders.
 XX
 XX Sequence 463 AA;
 SO
 Query Match 89.5%; Score 566.5; DB 21; Length 463;
 Best Local Similarity 89.9%; Pred. No. 6.5e-44;
 Matches 107; Conservative 5; Mismatches 6; Indels 1; Gaps 1;
 QY
 1 QVQLVESGGGVQPGSRSLRSCAAGFTSSSGYGMHWVROAPGKGLEWVAIVYDGSNKY 60
 DB 20 QVQLVESGGGVQPGSRSLRSCAAGFTSSSGYGMHWVROAPGKGLEWVAIVYDGSNKY 79
 QY 61 ADSVKGRTISRDNKNTLYLQWNSLRADTAVFECARAPNYIGADFWGOGMTVSS 119
 DB 80 ADSAKGRFTISRDNKNTLYLQWNSLRADTAVFECARAPNYIGADFWGOGMTVSS 137
 RESULT 6
 AA93732
 ID AAY93732 standard; Protein; 463 AA.
 XX
 XX AAY93732;
 XX
 XX 03-OCT-2000 (first entry)
 XX
 XX The heavy chain of immunoglobulin clone 6.1.1.
 DE
 XX Cytotoxic T-lymphocyte antigen-4; CTLA-4; antibody; immune system;
 KW hyperimmunity disorder; autoimmune disease; diabetes; graft rejection;
 KM proliferative disorder; cancer; immunodeficient disorder.

XX
 OS Homo sapiens.
 XX
 XX Key Location/Qualifiers
 XX Peptide 1..19
 XX /note= "signal peptide"
 XX
 XX WO200037504-A2.
 XX
 XX 29-JUN-2000.
 XX
 XX 23-DEC-1999; 99WO-US30895.
 XX
 XX 23-DEC-1998; 98US-0113647.
 XX
 XX (PF12) PFIZER INC.
 XX (ABGE-) ABGENIX INC.
 XX
 XX Hanson DC, Neveu MJ, Mueller BE, Hanke JH, Gilman SC, Davis CG;
 PI Corvalan JR;
 XX
 XX WPI; 2000-442647/38.
 XX N-PSDB; AAA46896.
 XX
 XX Novel antibodies capable of binding cytotoxic T-lymphocyte antigen
 PT (CTLA)-4 containing specified heavy and light chain sequences, useful
 PT for treating, e.g. immune disorders -
 PS
 PS Claim 2; Fig 22m; 157pp; English.
 XX
 XX The present sequence represents a heavy chain of an antibody of the
 CC invention. The antibody is directed cytotoxic T-lymphocyte antigen
 CC (CTLA)-4. Antibodies of the invention are composed of a heavy chain
 CC variable region, comprising a modified contiguous sequence from a
 CC FRI-FR3 sequence encoded by a human VH3-33 family gene. The
 CC modifications are contained in CDR1, CDR2 and/or framework regions.
 CC The antibodies may be used to inhibit CTLA-4 and down-regulate the
 CC immune system to treat hyperimmunity disorders (e.g. autoimmune
 CC disease, diabetes and graft rejection) and proliferative disorders
 CC (e.g. cancer). CTLA-4 stimulatory agents may be used to up-regulate
 CC immune system to up-regulate immunodeficient disorders.
 XX
 XX Sequence 463 AA;
 SO
 Query Match 89.5%; Score 566.5; DB 21; Length 463;
 Best Local Similarity 89.9%; Pred. No. 6.5e-44;
 Matches 107; Conservative 5; Mismatches 6; Indels 1; Gaps 1;
 QY
 1 QVQLVESGGGVQPGSRSLRSCAAGFTSSSGYGMHWVROAPGKGLEWVAIVYDGSNKY 60
 DB 20 QVQLVESGGGVQPGSRSLRSCAAGFTSSSGYGMHWVROAPGKGLEWVAIVYDGSNKY 79
 QY 61 ADSVKGRTISRDNKNTLYLQWNSLRADTAVFECARAPNYIGADFWGOGMTVSS 119
 DB 80 ADSAKGRFTISRDNKNTLYLQWNSLRADTAVFECARAPNYIGADFWGOGMTVSS 137
 RESULT 7
 AA93732
 ID AAY82629 standard; Protein; 143 AA.
 XX
 XX AAY82629;
 XX
 XX 02-AUG-2000 (first entry)
 XX
 XX Human FTHP monoclonal antibody clone 5B12-16-12 protein SEQ ID NO:42.
 DE
 XX Human; parathyroid hormone related protein; PTHrP; monoclonal antibody;
 KW hypercalcaemia; rheumatoid arthritis; bone cancer; metastasis; pain;
 KW fracture; cachexia; tooth disease; periodontal disease; gingivitis;
 KW sepsis; systemic inflammatory response syndrome; SIRS;
 KW hypophosphataemia; antitachycardic; cyostatic; antiinflammatory.

OS	Homo sapiens.
XX	
PN	JP2000080100-A.
XX	
PD	21-MAR-2000.
XX	
PF	12-OCT-1998; 98UP-0304793.
XX	
PR	17-JUN-1998; 98UP-0188196.
PR	26-JUN-1998; 98UP-0196729.
PA	(NIBS) JAPAN TOBACCO INC.
DR	
DR	WPI: 2000-286723/25.
N-FSD:	AAA13939.
PT	A human monoclonal antibody to parathyroid hormone related protein. -
PT	useful for treating hypercalcaemia, rheumatoid arthritis, cancer of bone
XX	including metastasis, and pain
XX	
XX	Claim 32; Page 76-77; 88pp; Japanese.
PS	
CC	The present invention describes a human monoclonal antibody to
CC	parathyroid hormone related protein (PTHrP). The monoclonal antibody or
CC	its fragments, following the stimulation of PTHrP has the following
CC	properties: (a) inhibits intracellular elevation of cAMP; (b) inhibits
CC	the release of calcium from bone; or (c) inhibits elevation of blood
CC	calcium content. The monoclonal antibody can be used in the treatment
CC	of hypercalcaemia, rheumatoid arthritis, cancer of bone including
CC	metastasis, pain, fracture, cachexia, diseases of teeth, periodontal
CC	diseases and gingivitis, sepsis, systemic inflammatory response syndrome
CC	(SIRS) and hypophosphataemia. It has antiarthritic, cyostatic and
CC	antiinflammatory activities. The present sequence represents a
CC	human PTHrP monoclonal antibody clone protein sequence from the
CC	present invention.
SQ	
XX	Sequence 143 AA;
Query Match	89.2%; Score 564.5; DB 21; Length 143;
Best Local Similarity	87.9%; Pred. No. 2,9e-44;
Matches 109; Conservative	2; Mismatches 8; Indels 5; Gaps 1
QY	1 QVQLVESGGGVQPGKSLRLCSAAGFTFSYGGMHWROAPGKGLBWAVIYYDSNKTY 60
DB	20 QVQLVESGGGVQPPRSRLRLCSAAGFTFSSSGMMHWROAPGKGLEWAVIYYDSNKTY 79
QY	61 ADSVGGRFTISRDNSKNTLYIQMNSLRADTVFYCAR-----ANNYIGAFDWGQTIV 115
DB	80 VDSVGRFTISRDNSKNTLYIQMNSLRADTVIYYCARRSSGWEDYYYGMVDWGQTTV 139
QY	116 TVSS 119 140 TVSS 143
Db	
RESULT 8	
ID AAY08598	standard; Protein; 223 AA.
XX AAY08598;	
AC AAY08598;	
XX	
DT 05-AUG-1999	(first entry)
XX	
DE Anti-human TNF-alpha monoclonal antibody H-chain protein.	
XX	
KW Monoclonal antibody; H chain; heavy chain; anti-human; TNF-alpha;	
KX tumour necrosis factor; light chain; L chain.	
XX	
OS Homo sapiens.	
XX	
PN JP1127855-A.	
XX	
PD 18-MAY-1999.	

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XX      27-OCT-1997;    97JP-0293994.
XX      27-OCT-1997;    97JP-0293994.
XX      (NIHA ) JAPAN ENERGY CORP.
XX      WPI; 1999-350318/30.
XX      DR N-PSDB; AAX77407.
XX
PT      Recombinant anti-human TNF-alpha human monoclonal antibody -
PT      produced stably with a high purity, and in large amounts
XX
PS      Claim 3; Page 12-13; 22pp; Japanese.
XX
CC      This invention describes novel recombinant anti-human TNF-alpha human
CC      monoclonal antibody consisting of a heavy (H) chain and a light (L)
CC      chain. The recombinant anti-human TNF-alpha human monoclonal antibody
CC      can be produced stably in a high purity and in a large amount.
XX
SQ      Sequence 223 AA;

Query Match          89.0%; Score 563.5; DB 20; Length 223;
Best Local Similarity 91.6%; Pred. No. 5.7e-44;
Matches 109; Conservative 4; Mismatches 5; Indels 1; Gaps 1;

QY      1 QVQLVESGGGVGVPGRSLRLSCAASGFTFSGYCMHWROAFGKGLIEWAVIWDGSNKRY 60
       ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      1 QVQLVESGGGVGPGRGSLRLSCAASGFTFSGYCMHWROAFGKGLIEWAVISYDGSNKYY 60

CY      61 ADSVKSGFTTSPDNKKTLYLQNMSLEADPTAVFYCARPVYICAPDVWGGMVTYS 119
       ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
       61 ADSVKSGFTTSPDNKKTLYLQNMSLEADPTAVFYCARPVYICAPDVWGGMVTYS 118

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XX	AA93701	standard; Protein; 463 AA.
XX	AA93701,	
XX	03-OCT-2000	(first entry)
XX		
XX		The heavy chain of immunoglobulin clone 4.1.1.
XX		
XX		Cytotoxic T-lymphocyte antigen-4; CTLA-4; antibody; immune system;
XX		hyperimmunity disorder; autoimmune disease; diabetes; graft rejection
XX		proliferative disorder; cancer; immunodeficient disorder.
XX		
XX	Homo sapiens.	
XX	WO200037504-A2.	
XX		
XX	29-JUN-2000.	
XX		
XX	23-DEC-1999;	99WO-US03895.
XX	23-DEC-1998;	98US-0113647.
XX		
XX	(PF12) PFIZER INC.	
XX	(ABGE-) ABGENIX INC.	
XX		
XX	Hanson DC, Neveu MJ, Mueller EE, Hanke JH, Gilman SC, Davis CG,	
XX	Corvaian UR;	
XX		
XX	WPI; 2000-442647/38.	
XX	DR	
XX	N-PSDB; AAA46864.	
XX		
XX		Novel antibodies capable of binding cytotoxic T-lymphocyte antigen
XX		(CTLA)-4 containing specified heavy and light chain sequences, useful
XX		for treating, e.g. immune disorders -
XX		
XX	Claim 2; Fig 1A; 157pp; English	

XX The present sequence represents a heavy chain of an antibody of the
CC invention. The antibody is directed cytotoxic T-lymphocyte antigen
CC (CTLA-4). Antibodies of the invention are composed of a heavy chain
CC variable region, comprising a modified contiguous sequence from a
CC FRI-FR3 sequence encoded by a human VH3-33 family gene. The
CC modifications are contained in CDR1, CDR2 and/or framework regions.
CC The antibodies may be used to inhibit CTLA-4 and down-regulate the
CC immune system to treat hyperimmunity disorders (e.g. autoimmune
CC disease, diabetes and graft rejection) and proliferative disorders
CC (e.g. cancer). CTLA-4 stimulatory agents may be used to up-regulate
CC immune system to up-regulate immunodeficient disorders.

XX Sequence 463 AA;

Query Match 88.9%; Score 562.5; DB 21; Length 463;
Best Local Similarity 89.1%; Pred. No. 1.5e-43;
Matches 106; Conservative 5; Mismatches 7; Indels 1; Gaps 1;

QY 1 QVQLVSGGAVVQPGSRLRSLSAASGFTSSYGMHWVRQAPGKLEWAVIYDGSKYY 60
DB 20 QVQLVSGGAVVQPGSRLRSLSAASGFTSSYGMHWVRQAPGKLEWAVIYDGSKYY 79

QY 61 ADSVKGRFTISRDNKNTLYLQNSLRADTAIVFYCARAPNYIGAPDWGQGMVYSS 119
DB 80 ADSVKGRFTISRDNKNTLYLQNSLRADTAIVFYCARG-GHFGPDPYWGQGLTVYSS 137

RESULT 10
ID AAY93727 standard; Protein; 463 AA.
XX AAY93727;

DT 03-OCT-2000 (first entry)

DE The heavy chain of immunoglobulin clone 4.1.1.

KW Cytotoxic T-lymphocyte antigen-4; CTLA-4; antibody; immune system;
KM hyperimmunity disorder; autoimmune disease; diabetes; graft rejection;
KW proliferative disorder; cancer; immunodeficient disorder.

OS Homo sapiens.

PN WO200037504-A2.

PD 29-JUN-2000.

PF 23-DEC-1999; 99WO-US30895.

PR 23-DEC-1998; 98US-0113647.

PA (PF12) PFIZER INC.
PA (ABGE-) ABGENIX INC.

PI Hanson DC, Neveu MJ, Mueller EE, Hanke JH, Gilman SC, Davis CG;
PI Corvalan JR;

DR WPI: 2000-442647/38.
DR N-PSDB; AAA46890.

PT Novel antibodies capable of binding cytotoxic T-lymphocyte antigen
PT for treating, e.g. immune disorders -

PS Claim 2; Fig 22c; 157pp; English.

XX The present sequence represents a heavy chain of an antibody of the
CC invention. The antibody is directed cytotoxic T-lymphocyte antigen
CC (CTLA-4). Antibodies of the invention are composed of a heavy chain
CC variable region, comprising a modified contiguous sequence from a
CC FRI-FR3 sequence encoded by a human VH3-33 family gene. The
CC modifications are contained in CDR1, CDR2 and/or framework regions.

CC The antibodies may be used to inhibit CTLA-4 and down-regulate the
CC immune system to treat hyperimmunity disorders (e.g. autoimmune
CC disease, diabetes and graft rejection) and proliferative disorders
CC (e.g. cancer). CTLA-4 stimulatory agents may be used to up-regulate
CC immune system to up-regulate immunodeficient disorders.

XX Sequence 463 AA;

Query Match 88.9%; Score 562.5; DB 21; Length 463;
Best Local Similarity 89.1%; Pred. No. 1.5e-43;
Matches 106; Conservative 5; Mismatches 7; Indels 1; Gaps 1;

QY 1 QVQLVSGGAVVQPGSRLRSLSAASGFTSSYGMHWVRQAPGKLEWAVIYDGSKYY 60
DB 20 QVQLVSGGAVVQPGSRLRSLSAASGFTSSYGMHWVRQAPGKLEWAVIYDGSKYY 79

QY 61 ADSVKGRFTISRDNKNTLYLQNSLRADTAIVFYCARAPNYIGAPDWGQGMVYSS 119
DB 80 ADSVKGRFTISRDNKNTLYLQNSLRADTAIVFYCARG-GHFGPDPYWGQGLTVYSS 137

RESULT 11
ID AAY93728 standard; Protein; 463 AA.
XX AAY93728;

DT 03-OCT-2000 (first entry)

DE The heavy chain of immunoglobulin clone 4.1.1.

KW Cytotoxic T-lymphocyte antigen-4; CTLA-4; antibody; immune system;
KM hyperimmunity disorder; autoimmune disease; diabetes; graft rejection;
KW proliferative disorder; cancer; immunodeficient disorder.

OS Homo sapiens.

Key Location/Qualifiers
FT Peptide 1..19
FT /note="signal peptide"

PN WO200037504-A2.

PD 29-JUN-2000.

PF 23-DEC-1999; 99WO-US30895.

PR 23-DEC-1998; 98US-0113647.

PA (PF12) PFIZER INC.
PA (ABGE-) ABGENIX INC.

PI Hanson DC, Neveu MJ, Mueller EE, Hanke JH, Gilman SC, Davis CG;
PI Corvalan JR;

DR WPI: 2000-442647/38.
DR N-PSDB; AAA46892.

PT Novel antibodies capable of binding cytotoxic T-lymphocyte antigen
PT for treating, e.g. immune disorders -

PS Claim 2; Fig 22e; 157pp; English.

XX The present sequence represents a heavy chain of an antibody of the
CC invention. The antibody is directed cytotoxic T-lymphocyte antigen
CC (CTLA-4). Antibodies of the invention are composed of a heavy chain
CC variable region, comprising a modified contiguous sequence from a
CC FRI-FR3 sequence encoded by a human VH3-33 family gene. The
CC modifications are contained in CDR1, CDR2 and/or framework regions.
CC The antibodies may be used to inhibit CTLA-4 and down-regulate the
CC immune system to treat hyperimmunity disorders (e.g. autoimmune
CC disease, diabetes and graft rejection) and proliferative disorders

CC (e.g. cancer). CTLA-4 stimulatory agents may be used to up-regulate
CC immune system to up-regulate immunodeficient disorders.

XX Sequence 463 AA;

Query Match 88.9%; Score 562.5; DB 21; Length 463;

Best Local Similarity 89.1%; Pred. No. 1.5e-43; Mismatches 7; Indels 1; Gaps 1;

Matches 106; Conservative 5;

QY 1 QVQLVSGGCVVQPGKSLRLSCAASGFTSSYGMHWVRQAPGKLEWVAIVTDSNKYY 60
DB 20 QVQLVSGGCVVQPGKSLRLSCAASGFTSSYGMHWVRQAPGKLEWVAIVTDSNKYY 79

QY 61 ADSVKGKFTISRDNKNTLYLQWNSLRADTAVFYCARAPNYIGAPDWGQGTNV 119
DB 80 ADSVKGKFTISRDNKNTLYLQWNSLRADTAVFYCARG-GHFGPPDYWGQGTNV 137

RESULT 12

ID ABP45508 standard; Protein; 252 AA.

XX ABP45508;

DT 19-AUG-2002 (first entry)

XX Human Blys binding scFv SEQ ID 1519.

XX Blys; B lymphocyte stimulator; TNF superfamily; human; cytosolic;
XX tumor necrosis factor; B cell proliferation; B cell differentiation;
XX immunosuppressive; immunostimulant; immunomodulatory; antirheumatic;
XX antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;
XX systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;
XX common variable immunodeficiency; acquired immunodeficiency syndrome.

XX Homo sapiens.

XX WO200202641-A1.

XX 10-JAN-2002.

XX 15-JUN-2001; 2001WO-US19110.

XX 16-JUN-2000; 2000US-212210P.

XX 17-OCT-2000; 2000US-240816P.

XX 16-MAR-2001; 2001US-276248P.

XX 21-MAR-2001; 2001US-277379P.

XX 25-MAY-2001; 2001US-293499P.

XX (HUMA-) HUMAN GENOME SGT INC.

XX (CAMP-) CAMBRIDGE ANTIBODY TECHNOLOGY.

XX Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;

XX WPI; 2002-114799/15.

XX Antisense against B lymphocyte stimulating polypeptides, useful for

XX the diagnosis and treatment of cancers and immune disorders -

XX Claim 1; Page 2215-2216; 3148pp; English.

CC This invention describes novel antibodies that immunospecifically bind to
CC B lymphocyte stimulator (Blys) polypeptides. Blys is a member of the
CC tumor necrosis factor (TNF) super family and induces B cell
CC proliferation and differentiation. The antibodies of the invention have
CC cytosolic, immunosuppressive, immunostimulant, immunomodulatory,
CC antirheumatic and antiAIDS activity and can be used in vaccines to
CC inhibit the expression and activity of Blys. The antibodies bind to Blys
CC and so may be used to detect and quantify the presence of Blys in
CC biological samples and may be used in this way to diagnose disease
CC associated with aberrant expression of Blys. They may also be
CC administered to treat diseases associated with aberrant Blys expression
CC and activity such as cancer, immune, and autoimmune disorders and

CC diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,
CC immunodeficiency (e.g. common variable immunodeficiency (CVID) and
CC acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent
CC the antibodies and fragments of the antibodies described in the method
CC of the invention.

XX Sequence 252 AA;

Query Match 88.7%; Score 561.5; DB 23; Length 252;

Best Local Similarity 87.9%; Pred. No. 9.9e-44; Mismatches 8; Indels 5; Gaps 1;

Matches 109; Conservative 2;

QY 1 QVQLVSGGCVVQPGKSLRLSCAASGFTSSYGMHWVRQAPGKLEWVAIVTDSNKYY 60
DB 1 QVQLVSGGCVVQPGKSLRLSCAASGFTSSYGMHWVRQAPGKLEWVAIVTDSNKYY 60

QY 61 ADSVKGKFTISRDNKNTLYLQWNSLRADTAVFYCAR-----APYICAPDWGQGTNV 115
DB 61 ADSVKGKFTISRDNKNTLYLQWNSLRADTAVFYCARQYDILGTYGSGFDYWGQGTNV 120

QY 116 TVSS 119

DB 121 TVSS 124

RESULT 13

ID AAU02501 standard; Protein; 120 AA.

XX AAU02501;

DT 29-AUG-2001 (first entry)

XX Anti-adipocyte monoclonal antibody heavy chain, FAT 1.

XX Antibody; adipocyte; heavy chain; light chain; obesity; fat;
XX heart disease; complementarity determining region; CDR.

XX Homo sapiens.

XX WO200127279-A1.

XX 19-APR-2001.

XX 11-OCT-2000; 2000WO-GB03900.

XX 12-OCT-1999; 99US-0158812.

XX (CAMP-) CAMBRIDGE ANTIBODY TECHNOLOGY.

XX Edwards BM, Main SH, Vaughan TV;

XX WPI; 2001-282031/29.

XX N-PSDB; AAS03401.

XX Panel of specific binding members of antibody molecules which bind to

XX whole adipocytes is used in the treatment of obesity and obesity

XX related diseases -

XX Claim 1; Page 95; 182pp; English.

CC AAU02501-AAU02635, and AAU02641-AAU02748 represent the amino acid
CC sequences of anti-adipocyte monoclonal antibody heavy chain, light
CC chain, and heavy chain complementarity determining regions (CDR) of the
CC invention. The antibodies can be used in the treatment of obesity and
CC obesity related diseases. The antibodies can be used to deliver drugs or
CC pro-drugs directly to the fat mass of an obese patient or the antibody
CC can be used as a therapeutic itself. Antibodies binding specifically to
CC adipocytes can be used to activate the immune system to destroy the cells
CC by complement mediated lysis. The antibodies may be labeled with a
CC detectable label such as radiolabel, fluorescent or chemical group and
CC used in methods of diagnosis in human subjects e.g. to determine the
CC presence of adipocyte antigen on the surface of an adipocyte to detect or

CC determine the presence or level of adipocytes in a cell or tissue sample.
CC The antibodies can be used as an alternative means of treatment for obese
CC patients other than undergoing surgery to remove excess fat. Antibodies
CC for different types of fat deposits can also be produced e.g. intra-
CC abdominal fat associated with heart disease.

CC Sequence 120 AA;

Query Match 88.5%; Score 560.5; DB 22; Length 120;
Best Local Similarity 90.8%; Pred. No. 5.6e-44;
Matches 109; Conservative 3; Mismatches 7; Indels 1; Gaps 1;

QY 1 QVQLVSGGAVVQPGKSLRLSCAASGFTSSYGMHWROAPGKLEWAVIYWGSKNKYY 60
Db 1 QVQLVSGGAVVQPGKSLRLSCAASGFTSSYGMHWROAPGKLEWAVIYWGSKNKYY 60
QY 61 ADSVKGRTTISRDNKNTLYLQWNSLRADTAIFYCARAPN-IGA FPDVWGQGT 119
Db 61 ADSVKGRTTISRDNKNTLYLQWNSLRADTAIFYCARAPNLAIFYADFWGQGTWTVSS 120

RESULT 14

ID ABP45616 standard; Protein; 252. AA.

AC ABP45616;

DT 19-AUG-2002 (first entry)

DE Human Blys binding scFv SEQ ID 1627.

XX Blys; B lymphocyte stimulator; TNF superfamily; human; cytostatic;
KW tumour necrosis factor; B cell proliferation; B cell differentiation;
KW immunosuppressive; immunostimulant; immunomodulatory; antirheumatic;
KW antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;
KW systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;
KW common variable immunodeficiency; acquired immunodeficiency syndrome.

OS Homo sapiens.

PN WO200202641-A1.

PD 10-JAN-2002.

PF 15-JUN-2001; 2001WO-US19110.

PR 16-JUN-2000; 2000US-212210P.

PR 17-OCT-2000; 2000US-240816P.

PR 16-MAR-2001; 2001US-276248P.

PR 21-MAR-2001; 2001US-277379P.

PR 25-MAY-2001; 2001US-293499P.

XX (HUMA-) HUMAN GENOME SCI INC.

PA (CAME-) CAMBRIDGE ANTIBODY TECHNOLOGY.

XX Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;

XX WPI, 2002-114799/15.

DR Claim 1; Page 2344-2345; 3148pp; English.

CC This invention describes novel antibodies that immunospecifically bind to
CC B lymphocyte stimulator (Blys) polypeptides. Blys is a member of the
CC tumour necrosis factor (TNF) super family and induces B cell
CC proliferation and differentiation. The antibodies of the invention have
CC cytostatic, immunosuppressive, immunostimulant, immunomodulatory,
CC antirheumatic and antiAIDS activity and can be used in vaccines to
CC inhibit the expression and activity of Blys. The antibodies bind to Blys
CC and so may be used to detect and quantitate the presence of Blys in
CC biological samples and may be used in this way to diagnose disease

CC associated with aberrant expression of Blys. They may also be
CC administered to treat diseases associated with aberrant Blys expression
CC and actively such as cancer, immune, and autoimmune disorders and
CC diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,
CC immunodeficiency (e.g. common variable immunodeficiency (CVID) and
CC acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent
CC the antibodies and fragments of the antibodies described in the method
CC of the invention.

CC Sequence 252 AA;

Query Match 88.5%; Score 560.5; DB 23; Length 252;
Best Local Similarity 86.5%; Pred. No. 1.2e-43;
Matches 109; Conservative 4; Mismatches 6; Indels 7; Gaps 1;

QY 1 QVQLVSGGAVVQPGKSLRLSCAASGFTSSYGMHWROAPGKLEWAVIYWGSKNKYY 60
Db 1 QVQLVSGGAVVQPGKSLRLSCAASGFTSSYGMHWROAPGKLEWAVIYWGSKNKYY 60
QY 61 ADSVKGRTTISRDNKNTLYLQWNSLRADTAIFYCARAPN-IGA FPDVWGQGT 113
Db 61 ADSVKGRTTISRDNKNTLYLQWNSLRADTAIFYCARAPNLAIFYADFWGQGT 120

QY 114 MWTYSS 119

Db 121 LTVYSS 126

RESULT 15

ID AAU79808 standard; Protein; 154 AA.

AC AAU79808;

DT 02-JUL-2002 (first entry)

DE Heavy chain variable region of s20 human antibody.

XX Heavy chain variable region; antibody; antibacterial; vaccine;
KW Pseudomonas aeruginosa infection inhibitor; lipopolysaccharide; LPS;
KW burn; prosthesis; cancer; cystic fibrosis; diabetes; heart disease;
KW otitis externa; swimmer's ear; osteomyelitis; corneal ulcer;
KW folliculitis; mastitis; pneumonia; meningitis; urinary tract infection;
KW endocarditis; peritonitis; geriatric; immunocompromised;
KW complementarity determining region; CDR.

OS Homo sapiens.

PN WO200220619-A2.

PD 14-MAR-2002.

PF 07-SEP-2001; 2001WO-US28019.

PR 07-SEP-2000; 2000US-230640P.

PR 03-JAN-2001; 2001US-259472P.

XX (SCHR/) SCHREIBER J R.

PA (KAMBOJ/) KAMBOJ K K.

PI Schreiber JR, Kamboj KK;

XX WPI, 2002-351767/38.

DR N-PSDB; ABK48972.

XX New human antibody that specifically binds to

CC lipopolysaccharide, useful for treating or preventing Pseudomonas
CC aeruginosa infection in patients with burns or prosthesis.
CC Claim 36; Fig 9; 84pp; English.
CC The invention describes an isolated human antibody or its antigen-binding
CC portion (I), that was expressed in a non-human animal and specifically

CC binds to lipopolysaccharide (LPS) of the opportunistic pathogen.
CC Pseudomonas aeruginosa (PA). (I) is useful for treating or preventing PA
CC infection in patients with burns, prosthesis, cancer, cystic fibrosis,
CC diabetes, heart disease, otitis externa (swimmer's ear), osteomyelitis,
CC corneal ulcers, folliculitis, mastitis, pneumonia, meningitis, urinary
CC tract infection, endocarditis, peritonitis and other diseases found in
CC geriatric or immunocompromised patients. (I) is also useful for detecting
CC the presence of PA in a biological sample. This is the amino acid
CC sequence of the B20 human monoclonal antibody heavy chain variable
CC region (containing complementarity determining regions (CDR) 1-3) that
CC binds PA lipopolysaccharide (LPS).
XX

SQ Sequence 154 AA;

Query Match 88.5%; Score 560; DB 23; Length 154;
Best Local Similarity 88.2%; Pred. No. 8.1e-44;
Matches 105; Conservative 5; Mismatches 9; Indels 0; Gaps 0;

OY	1	OVQLVESGGGVVQPGSRSLRLSCAASGFTSSYGMHWVRQAPGKGLEWAVIWDGSKYY	60
Db	1	OVQLVESGGGVVQPGSRSLRLSCAASGFTSSYGMHWVRQAPGKGLEWAVIWDGSKYY	60
OY	61	ADSVAGRFTISRDNKNTLYIQMNSLRADTAIFYCARAPNYIGAPDVWGQGTMTVSS	119
Db	61	ADSVAGRFTISRDNKNTLYIQMNSLRADTAIFYCARAPNYIGAPDVWGQGTMTVSS	119

Search completed: June 3, 2003, 08:14:48
Job time : 54.6109 secs

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OM protein - protein search, using sw model

Run on: June 3, 2003, 08:21:07 ; Search time 28.227 Seconds

(without alignments)
426.742 Million cell updates/sec

Title: US-09-644-668A-23
Perfect score: 1 QVQLVESGGGVQPGKSLRL.....FNITGAPFVWGQGTWVSS 119
Sequence: 633

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 383519 seqs, 101223694 residues

Total number of hits satisfying chosen parameters: 383519

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

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Published Applications NA:
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2: /cgn2_6/ptodata/1/pubppaa/PCT_NEM_PUB.pep.*
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14: /cgn2_6/ptodata/1/pubppaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	575	90.8	451	US-10-153-382-17	Sequence 17, Appl
2	574.5	90.8	249	US-09-880-748-1109	Sequence 1109, Ap
3	566.5	89.5	463	US-10-153-382-13	Sequence 13, Appl
4	562.5	88.9	463	US-10-153-382-3	Sequence 3, Appl1
5	562.5	88.9	252	US-10-153-382-5	Sequence 5, Appl1
6	561.5	88.5	252	US-09-880-748-1519	Sequence 1519, Ap
7	560.5	88.5	252	US-09-880-748-1627	Sequence 1627, Ap
8	556	87.8	251	US-09-880-748-955	Sequence 955, App
9	555	87.7	249	US-09-880-748-955	Sequence 955, App
10	554	87.5	244	US-10-153-382-9	Sequence 912, App
11	553.5	87.4	242	US-09-880-748-924	Sequence 924, App
12	553	87.4	252	US-09-880-748-988	Sequence 988, App
13	551.5	87.1	252	US-09-880-748-1201	Sequence 1201, Ap
14	551.5	87.1	254	US-09-880-748-1759	Sequence 1759, Ap
15	550.5	87.0	249	US-09-880-748-512	Sequence 512, App
16	549	86.7	125	US-09-848-798-8	Sequence 8, Appl1
17	549	86.7	125	US-09-848-798-20	Sequence 20, Appl
18	549	86.7	125	US-09-848-798-21	Sequence 21, Appl
19	549	86.7	125	US-09-848-798-22	Sequence 22, Appl

20	549	86.7	225	US-09-453-234-60	Sequence 60, Appl
21	549	86.7	225	US-09-453-234-92	Sequence 92, Appl
22	549	86.7	225	US-09-453-234-108	Sequence 108, App
23	548	86.6	225	US-09-453-234-68	Sequence 68, Appl
24	548	86.6	252	US-09-880-748-1731	Sequence 1731, Ap
25	546.5	86.3	254	US-09-880-748-983	Sequence 983, App
26	546	86.3	125	US-09-848-798-24	Sequence 24, Appl
27	545	86.1	119	US-10-073-644C-6	Sequence 6, Appl1
28	545	86.1	125	US-09-848-798-9	Sequence 9, Appl1
29	545	86.1	252	US-09-880-748-1394	Sequence 1394, Ap
30	544	85.9	225	US-09-453-234-102	Sequence 102, App
31	544	85.9	251	US-09-880-748-1332	Sequence 1332, Ap
32	543	85.8	123	US-10-243-265-2	Sequence 2, Appl1
33	543	85.8	225	US-09-453-234-106	Sequence 106, App
34	543	85.8	251	US-09-880-748-1309	Sequence 1309, Ap
35	543	85.8	225	US-09-880-748-1317	Sequence 1317, Ap
36	542	85.6	225	US-09-453-234-110	Sequence 110, App
37	541.5	85.5	247	US-09-880-748-1330	Sequence 1330, Ap
38	541.5	85.5	254	US-09-880-748-981	Sequence 981, App
39	541	85.5	125	US-09-848-798-23	Sequence 23, Appl
40	541	85.5	225	US-09-453-234-56	Sequence 56, Appl
41	540.5	85.4	254	US-09-880-748-881	Sequence 881, App
42	539.5	85.2	248	US-09-880-748-1890	Sequence 1890, App
43	539.5	85.2	249	US-09-880-748-197	Sequence 397, App
44	539.5	85.2	249	US-09-880-748-1102	Sequence 1102, Ap
45	539.5	85.2	249	US-09-880-748-1115	Sequence 1115, Ap

ALIGNMENTS

RESULT 1
US-10-153-382-17
; Sequence 17, Application US/10153382
; Publication No. US20030086930A1
; GENERAL INFORMATION:
; APPLICANT: PRIZER PRODUCTS INC.
; TITLE OF INVENTION: USES OF ANTI-CTLA-4 ANTIBODIES
; FILE REFERENCE: PC23019A
; CURRENT APPLICATION NUMBER: US/10/153,382
; CURRENT FILING DATE: 2002-05-22
; PRIOR APPLICATION NUMBER: 60/293042
; PRIOR FILING DATE: 2001-05-23
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 17
; LENGTH: 451
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-153-382-17

Query Match 90.8%; Score 575; DB 9; Length 451;
Best Local Similarity 88.8%; Pred. No. 6e-37; 7; Indels 6; Gaps 1;
Matches 111; Conservative 1; Mismatches 7; Indels 6; Gaps 1;

QY 1 QVQLVESGGGVQPGKSLRLSCAASGFTFSYGMHWYRQAPGKLEWYAVITWDGSKYY 60
Db 1 QVQLVESGGGVQPGKSLRLSCAASGFTFSYGMHWYRQAPGKLEWYAVITWDGSKYY 60

QY 61 ADSYKGFITSPNSKNTLYLQNNSLAEDTAIVYCYARP-----YTGAPFVWGQGT 114
Db 61 ADSYKGFITSPNSKNTLYLQNNSLAEDTAIVYCYARP-----YTGAPFVWGQGT 120

QY 115 VTVSS 119
Db 121 VTVSS 125

RESULT 2
US-09-880-748-1109
; Sequence 1109, Application US/09880748
; Publication No. US2003005937A1
; GENERAL INFORMATION:

Query Match	89.5%	Score 566.5	DB 9	Length 463
Best Local Similarity	89.9%	Pred. No. 2.8e-36		
Matches 107	Conservative 5	Mismatches 6	Indels 1	Gaps 1

QY	1	QNVLVESGGGVNPGRGRLRLSCAASGTFPSSGHHMYRQANGKGLERYAVIYVYDQSKNTY	60
		
Db	20	QNVLVESGGGVGGRSLRLSLCTASGTFPSSGHHMYRQANGKGLERYAVIYVYDQSKNTY	79
		
QY	61	ADSVKGRFTISRDNSKNTLYIWNMSLAEDTAVFYCARAPNYIGAFDVGQGTWTVSS	119
		
Db	80	ADSAKGFFTISRDNSKNTLYIWNMSLAEDTAVFYCARA-GILGFGFDVGQGTWTVSS	137

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Query Match      88.9%; Score 562.5; DB 9; Length 463;
Best Local Similarity 89.1%; Pred. No. 5,6e-36;
Matches 106; Conservative 5; Mismatches 7; Indels 1; Gaps 1;

QY      1 QVQLVSSGGGVVQPGSLRLSCAASFTTSSSYEMHWKRAQPGKLELVAVIYWDGSKITY 60
DB      20 QVQLVSSGGGVVQPGSLRLSCVASSFTTSSHHMHWRAPGKGLELVAVIYWDGRKKYY 79

QY      61 ADSVKRGFTISRNSRNTLLYLQWNSLRADPTAVFYCARAPNYIGAPDWMGQGTIVYSS 119
DB      80 ADSVKRGFTISRDSRNTLLFLQWNSLRADPTAVYICARG-GHFGPEPDWMGQGLIVYSS 137

RESULT 6
US-09-880-748-1519
; Sequence 1519, Application US/09880748
; Publication No. US20030059937A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind BlyS

```

FILE REFERENCE: PF523
CURRENT APPLICATION NUMBER: US/09/880,748
CURRENT FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: 60/212,210
PRIOR FILING DATE: 2000-06-15
PRIOR APPLICATION NUMBER: 60/240,816
PRIOR FILING DATE: 2000-10-17
PRIOR APPLICATION NUMBER: 60/276,248
PRIOR FILING DATE: 2001-03-16
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/293,499
PRIOR FILING DATE: 2001-05-25
NUMBER OF SEQ ID NOS: 3239
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1519
LENGTH: 252
TYPE: PRT
ORGANISM: Homo sapiens
US-09-880-748-1519

Query Match
Best Local Similarity 88.7%; Score 561.5; DB 9; Length 252;
Matches 109; Conservative 2; Mismatches 8; Indels 5; Gaps 1;

QY 1 QVQLVESGGGVVQGRSLRLSCAASGFTFSYGMHWVQAQPGKLEWYAVIWDGSKNTYY 60
1 QVQLVESGGGVVQGRSLRLSCAASGFTFSYGMHWVQAQPGKLEWYAVISYDGSNNTYY 60

QY 61 ADVSKGRFTISRDNKNTLYIQMNSLRADPAVYCARP-----NYIGAFPMWGQGT 115
61 ADVSKGRFTISRDNKNTLYIQMNSLRADPAVYCARQIDILTGYYGGDFYWGQGTWV 120

QY 116 TVSS 119
121 TVSS 124

RESULT 7
US-09-880-748-1627
Sequence 1627, Application US/09880748
Publication No. US2003005937A1
GENERAL INFORMATION:

APPLICANT: Ruben et al.
TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
FILE REFERENCE: PF523
CURRENT APPLICATION NUMBER: US/09/880,748
CURRENT FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: 60/212,210
PRIOR FILING DATE: 2000-06-15
PRIOR APPLICATION NUMBER: 60/240,816
PRIOR FILING DATE: 2000-10-17
PRIOR APPLICATION NUMBER: 60/276,248
PRIOR FILING DATE: 2001-03-16
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/293,499
PRIOR FILING DATE: 2001-05-25
NUMBER OF SEQ ID NOS: 3239
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1627
LENGTH: 252
TYPE: PRT
ORGANISM: Homo sapiens
US-09-880-748-1627

Query Match
Best Local Similarity 88.5%; Score 560.5; DB 9; Length 252;
Matches 109; Conservative 4; Mismatches 6; Indels 7; Gaps 1;
QY 1 QVQLVESGGGVVQGRSLRLSCAASGFTFSYGMHWVQAQPGKLEWYAVIWDGSKNTYY 60
1 QVQLVESGGGVVQGRSLRLSCAASGFTFSYGMHWVQAQPGKLEWYAVISYDGSNNTYY 60

QY 61 ADVSKGRFTISRDNKNTLYIQMNSLRADPAVYCARP-----YIGAFPMWGQGT 113
61 ADVSKGRFTISRDNKNTLYIQMNSLRADPAVYCARPDDILITGYKTFPMWGQGT 120

QY 114 MVTWSS 119
121 LVTWSS 126

RESULT 8
US-09-880-748-955
Sequence 955, Application US/09880748
Publication No. US2003005937A1
GENERAL INFORMATION:

APPLICANT: Ruben et al.
TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
FILE REFERENCE: PF523
CURRENT APPLICATION NUMBER: US/09/880,748
CURRENT FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: 60/212,210
PRIOR FILING DATE: 2000-06-15
PRIOR APPLICATION NUMBER: 60/240,816
PRIOR FILING DATE: 2000-10-17
PRIOR APPLICATION NUMBER: 60/276,248
PRIOR FILING DATE: 2001-03-16
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/293,499
PRIOR FILING DATE: 2001-05-25
NUMBER OF SEQ ID NOS: 3239
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 955
LENGTH: 251
TYPE: PRT
ORGANISM: Homo sapiens
US-09-880-748-955

Query Match
Best Local Similarity 87.8%; Score 556; DB 9; Length 251;
Matches 107; Conservative 7; Mismatches 4; Indels 8; Gaps 2;

QY 1 QVQLVESGGGVVQGRSLRLSCAASGFTFSYGMHWVQAQPGKLEWYAVIWDGSKNTYY 60
1 EVQLVESGGGVVQGRSLRLSCAASGFTFSYGMHWVQAQPGKLEWYAVIWDGSKNTYY 60

QY 61 ADVSKGRFTISRDNKNTLYIQMNSLRADPAVYCARP-----NYIGAFPMWGQGT 113
61 ADVSKGRFTISRDNKNTLYIQMNSLRADPAVYCARSHYDILITGLNY-WYFDLWGQGT 119

QY 114 MVTWSS 119
120 MVTWSS 125

RESULT 9
US-09-880-748-912
Sequence 912, Application US/09880748
Publication No. US2003005937A1
GENERAL INFORMATION:

APPLICANT: Ruben et al.
TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
FILE REFERENCE: PF523
CURRENT APPLICATION NUMBER: US/09/880,748
CURRENT FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: 60/212,210
PRIOR FILING DATE: 2000-06-15
PRIOR APPLICATION NUMBER: 60/240,816
PRIOR FILING DATE: 2000-10-17
PRIOR APPLICATION NUMBER: 60/276,248
PRIOR FILING DATE: 2001-03-16
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR FILING DATE: 2001-03-21

PRIOR APPLICATION NUMBER: 60/293,499
PRIOR FILING DATE: 2001-05-25
NUMBER OF SEQ ID NOS: 3239
SOFTWARE: Patent In Ver. 2.0
SEQ ID NO 912
LENGTH: 249
TYPE: PRF
ORGANISM: Homo sapiens
US-09-880-748-912

Query Match 87.4%; Score 555; DB 9; Length 249;
Best Local Similarity 84.9%; Pred. No. 1.2e-35;
Matches 107; Conservative 7; Mismatches 4; Indels 8; Gaps 2;

QY 1 QVQLVESGGGVQPGKSLRLSCAASGFTSSYGMHWVRQAPGKGLEWVAIVYDGSNKYY 60
DB 1 KQQLVESGGGVQPGKSLRLSCAASGFTSSYGMHWVRQAPGKGLEWVAIVYDGSNKYY 60
QY 61 ADSVKGRTISRDNKNTLYLQWNSLRADTAIFYCARAP-----NYIGAPDWGQGT 113
DB 61 ADSVKGRTISRDNKNTLYLQWNSLRADTAIFYCARSHYDILTGILNY-WYFDLWGRGT 119
QY 114 MVTWSS 119
DB 120 MVTWSS 125

RESULT 10
US-10-153-382-9
Sequence 9, Application US/10153382
Publication No. US20030086930A1
GENERAL INFORMATION:
APPLICANT: PRIZER PRODUCTS INC.
TITLE OF INVENTION: USES OF ANTI-CTLA-4 ANTIBODIES
FILE REFERENCE: PC23019A
CURRENT APPLICATION NUMBER: US/10/153,382
CURRENT FILING DATE: 2002-05-22
PRIOR APPLICATION NUMBER: 60/293042
PRIOR FILING DATE: 2001-05-23
NUMBER OF SEQ ID NOS: 39
SOFTWARE: Patent In Ver. 2.1
SEQ ID NO 9
LENGTH: 464
TYPE: PRF
ORGANISM: Homo sapiens
US-10-153-382-9

Query Match 87.5%; Score 554; DB 9; Length 464;
Best Local Similarity 87.4%; Pred. No. 2.5e-35;
Matches 104; Conservative 4; Mismatches 11; Indels 0; Gaps 0;

QY 1 QVQLVESGGGVQPGKSLRLSCAASGFTSSYGMHWVRQAPGKGLEWVAIVYDGSNKYY 60
DB 20 QVQLVESGGGVQPGKSLRLSCAASGFTSSYGMHWVRQAPGKGLEWVAIVYDGSNKYY 79
QY 61 ADSVKGRTISRDNKNTLYLQWNSLRADTAIFYCARAPNTYIGAPDWGQGTWTVSS 119
DB 80 GDSVKGRTISRDNKNTLYLQWNSLRADTAIFYCARSHYDILTGILNY-WYFDLWGRGT 138

RESULT 11
US-09-880-748-924
Sequence 924, Application US/09880748
Publication No. US20030059937A1
GENERAL INFORMATION:
APPLICANT: Ruben et al.
TITLE OF INVENTION: Antibodies that Immunospecifically Bind BlyS
FILE REFERENCE: PF523
CURRENT APPLICATION NUMBER: US/09/880,748
CURRENT FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: 60/212,210
PRIOR FILING DATE: 2000-06-15
PRIOR APPLICATION NUMBER: 60/240,816

PRIOR FILING DATE: 2000-10-17
PRIOR APPLICATION NUMBER: 60/276,248
PRIOR FILING DATE: 2001-03-16
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/293,499
NUMBER OF SEQ ID NOS: 3239
SOFTWARE: Patent In Ver. 2.0
SEQ ID NO 924
LENGTH: 247
TYPE: PRF
ORGANISM: Homo sapiens
US-09-880-748-924

Query Match 87.4%; Score 553.5; DB 9; Length 247;
Best Local Similarity 87.1%; Pred. No. 1.6e-35;
Matches 108; Conservative 3; Mismatches 8; Indels 5; Gaps 1;

QY 1 QVQLVESGGGVQPGKSLRLSCAASGFTSSYGMHWVRQAPGKGLEWVAIVYDGSNKYY 60
DB 1 QVQLVESGGGVQPGKSLRLSCAASGFTSSYGMHWVRQAPGKGLEWVAIVYDGSNKYY 60
QY 61 ADSVKGRTISRDNKNTLYLQWNSLRADTAIFYCAR-----APNYIGAPDWGQGTW 115
DB 61 ADSVKGRTISRDNKNTLYLQWNSLRADTAIFYCARPSYDILTGILNY-WYFDLWGRGT 120
QY 116 TVSS 119
DB 121 TVSS 124

RESULT 12
US-09-880-748-988
Sequence 988, Application US/09880748
Publication No. US20030059937A1
GENERAL INFORMATION:
APPLICANT: Ruben et al.
TITLE OF INVENTION: Antibodies that Immunospecifically Bind BlyS
FILE REFERENCE: PF523
CURRENT APPLICATION NUMBER: US/09/880,748
CURRENT FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: 60/212,210
PRIOR FILING DATE: 2000-06-15
PRIOR APPLICATION NUMBER: 60/240,816
PRIOR FILING DATE: 2000-10-17
PRIOR APPLICATION NUMBER: 60/276,248
PRIOR FILING DATE: 2001-03-16
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/293,499
NUMBER OF SEQ ID NOS: 3239
SOFTWARE: Patent In Ver. 2.0
SEQ ID NO 988
LENGTH: 252
TYPE: PRF
ORGANISM: Homo sapiens
US-09-880-748-988

Query Match 87.4%; Score 553; DB 9; Length 252;
Best Local Similarity 84.1%; Pred. No. 1.7e-35;
Matches 106; Conservative 8; Mismatches 4; Indels 8; Gaps 2;

QY 1 QVQLVESGGGVQPGKSLRLSCAASGFTSSYGMHWVRQAPGKGLEWVAIVYDGSNKYY 60
DB 1 EVQLVESGGGVQPGKSLRLSCAASGFTSSYGMHWVRQAPGKGLEWVAIVYDGSNKYY 60
QY 61 ADSVKGRTISRDNKNTLYLQWNSLRADTAIFYCARAP-----NYIGAPDWGQGT 113
DB 61 ADSVKGRTISRDNKNTLYLQWNSLRADTAIFYCARSHYDILTGILNY-WYFDLWGRGT 119
QY 114 MVTWSS 119

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OM protein - protein search, using sw model

Run on: June 3, 2003, 08:10:19 ; Search time 18.0734 Seconds

(without alignments)
193.728 Million cell updates/sec

Title: US-09-644-668A-23

Perfect score: 633
Sequence: 1 QVQLVESGGGVGVQPGRSLRL.....PNYICAFDVWGQGNVTVSS 119

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 26574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents AA:*
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6: /cgn2_6/ptodata/1/1aa/6D_COMB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	549	86.7	119	1	US-08-331-398A-46
2	549	86.7	119	2	US-08-331-397B-46
3	549	86.7	119	2	US-08-753-804A-46
4	549	86.7	119	4	US-09-227-693-46
5	549	86.7	125	4	US-09-240-274-8
6	549	86.7	125	4	US-09-240-274-20
7	549	86.7	125	4	US-09-240-274-21
8	549	86.7	125	4	US-09-240-274-22
9	546	86.3	125	4	US-09-240-274-24
10	545	86.1	125	4	US-09-240-274-9
11	544	85.9	120	1	US-07-942-245-35
12	541	85.5	125	4	US-09-240-274-23
13	538.5	85.1	126	4	US-09-240-274-149
14	537.5	84.9	126	4	US-09-240-274-26
15	535.5	84.6	126	4	US-09-240-274-10
16	535.5	84.6	126	4	US-09-240-274-14
17	535.5	84.6	126	4	US-09-240-274-150
18	535.5	84.6	126	4	US-09-079-029-11
19	533	84.2	125	4	US-09-240-274-140
20	531.5	84.0	126	4	US-09-240-274-153
21	529.5	83.6	126	4	US-09-240-274-25
22	527	83.3	127	4	US-09-240-274-18
23	526	83.1	121	4	US-09-202-181-4
24	525.5	83.0	126	4	US-08-983-607-38
25	525.5	83.0	126	4	US-09-240-274-152
26	524.5	82.9	128	4	US-09-240-274-1
27	522.5	82.5	126	4	US-09-240-274-13

28	521	82.3	117	4	US-09-025-769B-24	Sequence 24, Appl
29	520	82.1	120	2	US-08-652-558-39	Sequence 39, Appl
30	518.5	81.9	128	4	US-09-240-274-142	Sequence 142, Appl
31	517.5	81.8	126	4	US-09-240-274-16	Sequence 16, Appl
32	517.5	81.8	126	4	US-09-240-274-17	Sequence 17, Appl
33	516.5	81.6	126	4	US-09-240-274-14	Sequence 14, Appl
34	516.5	81.6	126	4	US-09-240-274-15	Sequence 15, Appl
35	516.5	81.6	126	4	US-09-240-274-147	Sequence 147, App
36	516.5	81.6	126	4	US-09-240-274-148	Sequence 148, App
37	516	81.5	116	1	US-08-211-202-141	Sequence 141, App
38	516	81.5	127	4	US-09-240-274-19	Sequence 19, Appl
39	515.5	81.4	123	1	US-08-478-039-94	Sequence 94, Appl
40	515.5	81.4	123	1	US-08-476-349A-94	Sequence 94, Appl
41	515	81.4	125	4	US-09-240-274-151	Sequence 151, App
42	515	81.4	127	4	US-09-240-274-11	Sequence 11, Appl
43	515	81.4	127	4	US-09-240-274-139	Sequence 139, App
44	513.5	81.1	124	4	US-09-240-274-4	Sequence 4, Appl
45	510.5	80.6	124	4	US-09-240-274-5	Sequence 5, Appl

ALIGNMENTS

RESULT 1
US-08-331-398A-46
Sequence 46, Application US/0833398A
Patent No. 5608039
GENERAL INFORMATION:
APPLICANT: Pastan, Ira
APPLICANT: Willingham, Mark
APPLICANT: Fitzgerald, David
APPLICANT: Brinkmann, Ulrich
APPLICANT: Pal, Lee
TITLE OF INVENTION: Single Chain B3 Antibody Fusion Proteins
TITLE OF INVENTION: and Their Uses (as amended)
NUMBER OF SEQUENCES: 68
CORRESPONDENCE ADDRESS:
ADDRESSER: Townsend and Townsend and Crew
STREET: One Market Plaza, Stewart Street Plaza
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94105-1492
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/331,398A
FILING DATE: 28-OCT-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/767,331
FILING DATE: 30-SEP-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/596,289
FILING DATE: 12-OCT-1990
ATTORNEY/AGENT INFORMATION:
NAME: Hunter, Tom
REGISTRATION NUMBER: 38,498
REFERENCE/DOCKET NUMBER: 015280-126110US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 543-9600
TELEFAX: (415) 543-5043
INFORMATION FOR SEQ ID NO: 46:
SEQUENCE CHARACTERISTICS:
LENGTH: 119 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURE:

NAME/KEY: Protein
LOCATION: 1..119
OTHER INFORMATION: /note="Human fetal immunoglobulin
OTHER INFORMATION: 56p1/CL Variable Heavy chain (V-H)"
US-08-331-397B-46

Query Match 86.7%; Score 549; DB 1; Length 119;
Best Local Similarity 89.1%; Pred. No. 4e-49;
Matches 106; Conservative 3; Mismatches 10; Indels 0; Gaps 0;

QY 1 QVQLVSGGCVGVQGRSLRLSCAASGFTFSYGMHWROAPGKLEWVAIVYDGSKYY 60
DB 1 QVQLVSGGCVGVQGRSLRLSCAASGFTFSYGMHWROAPGKLEWVAIVYDGSKYY 60

QY 61 ADSYKGRFTISRDNKNTLYLQNMSLRAEDTAVFYCARAPVYIGAFDVGQGTWTVSS 119
DB 61 ADSYKGRFTISRDNKNTLYLQNMSLRAEDTAVFYCARAPVYIGAFDVGQGTWTVSS 119

RESULT 2

US-08-331-397B-46
Sequence 46, Application US/08331397B
Patent No. 5981726

GENERAL INFORMATION:

APPLICANT: Pastan, Ira
APPLICANT: Benhar, Itai
TITLE OF INVENTION: Chimeric and Mutationally Stabilized Tumor-
TITLE OF INVENTION: Specific Antibody Fragments, Fusion Proteins, and Uses
NUMBER OF SEQUENCES: 68
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew
STREET: One Market Plaza, Steuart Street Plaza
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94105-1492

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/331,397B
FILING DATE: 28-OCT-1994
CLASSIFICATION: 435

PRIORITY APPLICATION DATA:

APPLICATION NUMBER: US 07/767,331
FILING DATE: 30-SEP-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/596,289
FILING DATE: 12-OCT-1990

ATTORNEY/AGENT INFORMATION:

NAME: Hunter, Tom
REGISTRATION NUMBER: 38,498
REFERENCE/DOCKET NUMBER: 015280-126120US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 543-9600
TELEFAX: (415) 543-5043

INFORMATION FOR SEQ ID NO: 46:

SEQUENCE CHARACTERISTICS:
LENGTH: 119 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURE:

NAME/KEY: Protein
LOCATION: 1..119
OTHER INFORMATION: /note="Human fetal immunoglobulin
OTHER INFORMATION: 56p1/CL Variable Heavy chain (V-H)"
US-08-331-397B-46

Query Match 86.7%; Score 549; DB 2; Length 119;
Best Local Similarity 89.1%; Pred. No. 4e-49;
Matches 106; Conservative 3; Mismatches 10; Indels 0; Gaps 0;

QY 1 QVQLVSGGCVGVQGRSLRLSCAASGFTFSYGMHWROAPGKLEWVAIVYDGSKYY 60
DB 1 QVQLVSGGCVGVQGRSLRLSCAASGFTFSYGMHWROAPGKLEWVAIVYDGSKYY 60

QY 61 ADSYKGRFTISRDNKNTLYLQNMSLRAEDTAVFYCARAPVYIGAFDVGQGTWTVSS 119
DB 61 ADSYKGRFTISRDNKNTLYLQNMSLRAEDTAVFYCARAPVYIGAFDVGQGTWTVSS 119

RESULT 3

US-08-759-804A-46
Sequence 46, Application US/08759804A
Patent No. 5990296

GENERAL INFORMATION:

APPLICANT: Pastan, Ira
APPLICANT: Willingham, Mark
APPLICANT: Fitzgerald, David J.
APPLICANT: Brinkmann, Ulrich
APPLICANT: Pal, Lee
TITLE OF INVENTION: Tumor-Specific Antibody Fragments,
TITLE OF INVENTION: Fusion Proteins, and Uses Thereof
NUMBER OF SEQUENCES: 68
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/759,804A
FILING DATE: 03-DEC-1996
CLASSIFICATION: 536

PRIORITY APPLICATION DATA:

APPLICATION NUMBER: US 08/331,398
FILING DATE: 28-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/767,331
FILING DATE: 30-SEP-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/596,289
FILING DATE: 12-OCT-1990

ATTORNEY/AGENT INFORMATION:

NAME: Weber, Ellen L.
REGISTRATION NUMBER: 32,762
REFERENCE/DOCKET NUMBER: 015280-126140US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300

INFORMATION FOR SEQ ID NO: 46:

SEQUENCE CHARACTERISTICS:
LENGTH: 119 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURE:

NAME/KEY: Protein
LOCATION: 1..119
OTHER INFORMATION: /note="Human fetal immunoglobulin
OTHER INFORMATION: 56p1/CL Variable Heavy chain (V-H)"
US-08-759-804A-46

Query Match 86.7%; Score 549; DB 2; Length 119;

Best Local Similarity 89.1%; Pred. No. 4e-49;
Matches 106; Conservative 3; Mismatches 10; Indels 0; Gaps 0;

QY 1 QVQLVSGGCVVQPGKSLRLSCAASGFTSSYGMHWROAPGKGLEWYAVIWDGSKNTKY 60
DB 1 QVELVESGGGVVQPGKSLRLSCAASGFTSSYGMHWROAPGKGLEWYAVIWDGSKNTKY 60
QY 61 ADSVGRFTISRDNKNTLYIQMNSLRADDTAVFYCARAPNYIGAPDWGQGTMTVSS 119
DB 61 ADSVGRFTISRDNKNTLYIQMNSLRADDTAVFYCARAPNYIGAPDWGQGTMTVSS 119

RESULT 4

US-09-227-693-46
Sequence 46, Application US/09227693
Patent No. 6287562

GENERAL INFORMATION:
APPLICANT: PASTAN, Ira
APPLICANT: BENHAR, Itai
APPLICANT: PADLAN, Eduardo A.
APPLICANT: JUNG, Sun-Hee
APPLICANT: LEE, Byungkook
TITLE OF INVENTION: HUMANIZED TUMOR-SPECIFIC ANTIBODY
TITLE OF INVENTION: FRAGMENTS, FUSION PROTEINS, AND USES THEREOF
NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
ADDRESSER: Townsend and Townsend Kourie and Crew
STREET: Stewart Street Tower, One Market Plaza
CITY: San Francisco
STATE: California
COUNTRY: US
ZIP: 94105-1493
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/227,693
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/331,396
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/767,331
FILING DATE: 30-SEP-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/596,289
FILING DATE: 12-OCT-1990
ATTORNEY/AGENT INFORMATION:
NAME: Weber, Ellen Lauver
REGISTRATION NUMBER: 32,762
REFERENCE/DOCKET NUMBER: 15280-126-1-3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 543-9600
TELEFAX: (415) 543-5043
INFORMATION FOR SEQ ID NO: 46:
SEQUENCE CHARACTERISTICS:
LENGTH: 119 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Protein
LOCATION: 1..119
OTHER INFORMATION: /note="Human fetal immunoglobulin
OTHER INFORMATION: 56Pl CL VH region"

US-09-227-693-46
Query Match 86.7%; Score 549; DB 4; Length 119;
Best Local Similarity 89.1%; Pred. No. 4e-49;
Matches 106; Conservative 3; Mismatches 10; Indels 0; Gaps 0;

QY 1 QVQLVSGGCVVQPGKSLRLSCAASGFTSSYGMHWROAPGKGLEWYAVIWDGSKNTKY 60
DB 1 QVELVESGGGVVQPGKSLRLSCAASGFTSSYGMHWROAPGKGLEWYAVIWDGSKNTKY 60
QY 61 ADSVGRFTISRDNKNTLYIQMNSLRADDTAVFYCARAPNYIGAPDWGQGTMTVSS 119
DB 61 ADSVGRFTISRDNKNTLYIQMNSLRADDTAVFYCARAPNYIGAPDWGQGTMTVSS 119

RESULT 5

US-09-240-274-8
Sequence 8, Application US/09240274
Patent No. 6255455

GENERAL INFORMATION:
APPLICANT: Siegel, Donald L.
TITLE OF INVENTION: RH(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
FILE REFERENCE: 09596-4202
CURRENT APPLICATION NUMBER: US/09/240,274
CURRENT FILING DATE: 1999-01-29
EARLIER APPLICATION NUMBER: 60/081,380
EARLIER FILING DATE: 1998-04-10
EARLIER APPLICATION NUMBER: 60/028,550
EARLIER FILING DATE: 1996-10-11
NUMBER OF SEQ ID NOS: 224
SOFTWARE: Patent In Ver. 2.0
SEQ ID NO 8
LENGTH: 125
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: anti-Rh(D) chain D01

US-09-240-274-8
Query Match 86.7%; Score 549; DB 4; Length 125;
Best Local Similarity 82.4%; Pred. No. 4.2e-49;
Matches 103; Conservative 8; Mismatches 8; Indels 6; Gaps 1;

QY 1 QVQLVSGGCVVQPGKSLRLSCAASGFTSSYGMHWROAPGKGLEWYAVIWDGSKNTKY 60
DB 1 QVELVESGGGVVQPGKSLRLSCAASGFTSSYGMHWROAPGKGLEWYAVIWDGSKNTKY 60
QY 61 ADSVGRFTISRDNKNTLYIQMNSLRADDTAVFYCARA-----PNYIGAPDWGQGTMTV 114
DB 61 ADSVGRFTISRDNKNTLYIQMNSLRADDTAVFYCARAENQIKLSRYLYFDYWGQGTLT 120
QY 115 VTSS 119
DB 121 VTSS 125

RESULT 6

US-09-240-274-20
Sequence 20, Application US/09240274
Patent No. 6255455

GENERAL INFORMATION:
APPLICANT: Siegel, Donald L.
TITLE OF INVENTION: RH(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
FILE REFERENCE: 09596-4202
CURRENT APPLICATION NUMBER: US/09/240,274
CURRENT FILING DATE: 1999-01-29
EARLIER APPLICATION NUMBER: 60/081,380
EARLIER FILING DATE: 1998-04-10
EARLIER APPLICATION NUMBER: 60/028,550
EARLIER FILING DATE: 1996-10-11
NUMBER OF SEQ ID NOS: 224
SOFTWARE: Patent In Ver. 2.0
SEQ ID NO 20
LENGTH: 125
TYPE: PRT
ORGANISM: Homo sapiens

FEATURE:
OTHER INFORMATION: anti-Rh(D) chain D15
US-09-240-274-20

Query Match 86.7%; Score 549; DB 4; Length 125;
Best Local Similarity 82.4%; Pred. No. 4.2e-49;
Matches 103; Conservative 8; Mismatches 8; Indels 6; Gaps 1;

QY 1 QVQLVESGGGVVQPGSRSLRLSCAASGFTSSVGMHWYRQAPGKGLEWVAIVYDGSNKYY 60
DB 1 EVQLLESGGAVVQPGSRSLRLSCVSGFTFNNYGMHWYRQAPGKGLEWVAIVYDGSNKYY 60
QY 61 ADSVKGRTISRDNKNTLYIQMNSLRADTAIFYCARA-----PNYIGAPDWGCGTM 114
DB 61 ADSVKGRTISRDNKNTLYIQMNSLRADTAIFYCARAENQIKMSRYLYPDYWGQGLT 120
QY 115 VTWSS 119
DB 121 VTWSS 125

RESULT 7

US-09-240-274-21
Sequence 21, Application US/09240274
Patent No. 6255455
GENERAL INFORMATION:
APPLICANT: Siegel, Donald L.
TITLE OF INVENTION: RH(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
FILE REFERENCE: 09596-4202
CURRENT APPLICATION NUMBER: US/09/240,274
EARLIER FILING DATE: 1999-01-29
EARLIER APPLICATION NUMBER: 60/081,380
EARLIER FILING DATE: 1998-04-10
EARLIER APPLICATION NUMBER: 60/028,550
NUMBER OF SEQ ID NOS: 224
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 21
LENGTH: 125
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: anti-Rh(D) chain D16
US-09-240-274-21

Query Match 86.7%; Score 549; DB 4; Length 125;
Best Local Similarity 82.4%; Pred. No. 4.2e-49;
Matches 103; Conservative 8; Mismatches 8; Indels 6; Gaps 1;

QY 1 QVQLVESGGGVVQPGSRSLRLSCAASGFTSSVGMHWYRQAPGKGLEWVAIVYDGSNKYY 60
DB 1 EVQLLESGGAVVQPGSRSLRLSCVSGFTFNNYGMHWYRQAPGKGLEWVAIVYDGSNKYY 60
QY 61 ADSVKGRTISRDNKNTLYIQMNSLRADTAIFYCARA-----PNYIGAPDWGCGTM 114
DB 61 ADSVKGRTISRDNKNTLYIQMNSLRADTAIFYCARAENQIKMSRYLYPDYWGQGLT 120
QY 115 VTWSS 119
DB 121 VTWSS 125

RESULT 8

US-09-240-274-22
Sequence 22, Application US/09240274
Patent No. 6255455
GENERAL INFORMATION:
APPLICANT: Siegel, Donald L.
TITLE OF INVENTION: RH(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
FILE REFERENCE: 09596-4202
CURRENT APPLICATION NUMBER: US/09/240,274

CURRENT FILING DATE: 1999-01-29
EARLIER APPLICATION NUMBER: 60/081,380
EARLIER FILING DATE: 1998-04-10
EARLIER APPLICATION NUMBER: 60/028,550
EARLIER FILING DATE: 1996-10-11
NUMBER OF SEQ ID NOS: 224
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 22
LENGTH: 125
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: anti-Rh(D) chain D17
US-09-240-274-22

Query Match 86.7%; Score 549; DB 4; Length 125;
Best Local Similarity 82.4%; Pred. No. 4.2e-49;
Matches 103; Conservative 8; Mismatches 8; Indels 6; Gaps 1;

QY 1 QVQLVESGGGVVQPGSRSLRLSCAASGFTSSVGMHWYRQAPGKGLEWVAIVYDGSNKYY 60
DB 1 EVQLLESGGAVVQPGSRSLRLSCVSGFTFNNYGMHWYRQAPGKGLEWVAIVYDGSNKYY 60
QY 61 ADSVKGRTISRDNKNTLYIQMNSLRADTAIFYCARA-----PNYIGAPDWGCGTM 114
DB 61 ADSVKGRTISRDNKNTLYIQMNSLRADTAIFYCARAENQIKMSRYLYPDYWGQGLT 120
QY 115 VTWSS 119
DB 121 VTWSS 125

RESULT 9

US-09-240-274-24
Sequence 24, Application US/09240274
Patent No. 6255455
GENERAL INFORMATION:
APPLICANT: Siegel, Donald L.
TITLE OF INVENTION: RH(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
FILE REFERENCE: 09596-4202
CURRENT APPLICATION NUMBER: US/09/240,274
EARLIER FILING DATE: 1999-01-29
EARLIER APPLICATION NUMBER: 60/081,380
EARLIER FILING DATE: 1998-04-10
EARLIER APPLICATION NUMBER: 60/028,550
NUMBER OF SEQ ID NOS: 224
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 24
LENGTH: 125
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: anti-Rh(D) chain D20
US-09-240-274-24

Query Match 86.3%; Score 546; DB 4; Length 125;
Best Local Similarity 84.0%; Pred. No. 8.5e-49;
Matches 105; Conservative 6; Mismatches 8; Indels 6; Gaps 1;

QY 1 QVQLVESGGGVVQPGSRSLRLSCAASGFTSSVGMHWYRQAPGKGLEWVAIVYDGSNKYY 60
DB 1 EVQLLESGGAVVQPGSRSLRLSCAASGFTFNNYGMHWYRQAPGKGLEWVAIVYDGSNKYY 60
QY 61 ADSVKGRTISRDNKNTLYIQMNSLRADTAIFYCARA-----PNYIGAPDWGCGTM 114
DB 61 ADSVKGRTISRDNKNTLYIQMNSLRADTAIFYCARAENQIKMSRYLYPDYWGQGLT 120
QY 115 VTWSS 119
DB 121 VTWSS 125

RESULT 10
US-09-240-274-9
; Sequence 9, Application US/09240274
; Patent No. 6255455
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; FILE REFERENCE: 09596-4202
; CURRENT APPLICATION NUMBER: US/09/240,274
; EARLIER FILING DATE: 1999-01-29
; EARLIER APPLICATION NUMBER: 60/081,380
; EARLIER FILING DATE: 1998-04-10
; EARLIER APPLICATION NUMBER: 60/028,550
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 9
; LENGTH: 125
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) chain D03
US-09-240-274-9
Query Match 86.1%; Score 545; DB 4; Length 125;
Best Local Similarity 83.2%; Pred. No. 1.1e-48;
Matches 104; Conservative 7; Mismatches 8; Indels 6; Gaps 1;
QY 1 QVQLVESGGGVVQVQPSRLSLSCAASGFTSSVGMHWVROAPKGLRWAVIWDGSKNTY 60
DB 1 EVQLVESGGGVVQVQPSRLSLSCAASGFTSTYGMHWVROAPKGLRWAVIWDGSKNTY 60
QY 61 ADVSKGRFTISRDNKNTLYIQMNSLRADDTAVFYCARAPNYIG-APDVGQGTMTVS 114
DB 61 ADVSKGRFTISRDNKNTLYIQMNSLRADDTAVFYCARAPNYIG-APDVGQGTMTVS 120
QY 115 VTSS 119
DB 121 VTSS 125
RESULT 11
US-07-942-245-35
; Sequence 35, Application US/07942245
; Patent No. 5639641
; GENERAL INFORMATION:
; APPLICANT: PEDERSEN, Jan T.
; APPLICANT: SEARLE, Stephen M.J.
; APPLICANT: REES, Anthony R.
; APPLICANT: ROGUSKA, Michael A.
; APPLICANT: GUILD, Braddon C.
; TITLE OF INVENTION: SURFACE RESIDUE VENERING OF RODENT
; NUMBER OF SEQUENCES: 522
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sughrue, Mion, Zinn, Macpeak & Seas
; STREET: 2100 Pennsylvania Avenue, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: United States
; ZIP: 20037-3202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: HP 9000/700 Workstation
; OPERATING SYSTEM: UNIX
; SOFTWARE: In house
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/942,245
; FILING DATE: 09-SEP-1992
; CLASSIFICATION: 530
; TELECOMMUNICATION INFORMATION:

TELEPHONE: (202) 293-7060
TELEFAX: (202) 293-7860
TELEX: 6491103
; INFORMATION FOR SEQ ID NO: 35:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 120 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-07-942-245-35
Query Match 85.9%; Score 544; DB 1; Length 120;
Best Local Similarity 89.2%; Pred. No. 1.3e-48;
Matches 107; Conservative 2; Mismatches 9; Indels 2; Gaps 1;
QY 1 QVQLVESGGGVVQVQPSRLSLSCAASGFTSSVGMHWVROAPKGLRWAVIWDGSKNTY 60
DB 1 EVQLVESGGGVVQVQPSRLSLSCAASGFTSSVGMHWVROAPKGLRWAVIWDGSKNTY 60
QY 61 ADVSKGRFTISRDNKNTLYIQMNSLRADDTAVFYCARAPNYIG-APDVGQGTMTVS 118
DB 61 ADVSKGRFTISRDNKNTLYIQMNSLRADDTAVFYCARAPNYIG-APDVGQGTMTVS 120
RESULT 12
US-09-240-274-23
; Sequence 23, Application US/09240274
; Patent No. 6255455
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; FILE REFERENCE: 09596-4202
; CURRENT APPLICATION NUMBER: US/09/240,274
; EARLIER FILING DATE: 1999-01-29
; EARLIER APPLICATION NUMBER: 60/081,380
; EARLIER FILING DATE: 1998-04-10
; EARLIER APPLICATION NUMBER: 60/028,550
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 23
; LENGTH: 125
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) chain D18
US-09-240-274-23
Query Match 85.5%; Score 541; DB 4; Length 125;
Best Local Similarity 81.6%; Pred. No. 2.8e-48;
Matches 102; Conservative 8; Mismatches 9; Indels 6; Gaps 1;
QY 1 QVQLVESGGGVVQVQPSRLSLSCAASGFTSSVGMHWVROAPKGLRWAVIWDGSKNTY 60
DB 1 EVQLVESGGGVVQVQPSRLSLSCVSGFTFNNGHWVROAPKGLRWAVIWDGSKNTY 60
QY 61 ADVSKGRFTISRDNKNTLYIQMNSLRADDTAVFYCARAPNYIG-APDVGQGTMTVS 114
DB 61 ADVSKGRFTISRDNKNTLYIQMNSLRADDTAVFYCARAPNYIG-APDVGQGTMTVS 120
QY 115 VTSS 119
DB 121 VTSS 125
RESULT 13
US-09-240-274-149
; Sequence 149, Application US/09240274
; Patent No. 6255455
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 3, 2003, 08:09:29 ; Search time 2.17065 Seconds
(without alignments)
531.460 Million cell updates/sec

Title: US-09-644-668a-25
Perfect score: 52
Sequence: 1 RASQSVSSSFLA 12

Scoring table: BLOSUM62
Gapop 10.0 ; Gapext 0.5

Searched: 283224 .segs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 73:1*
1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	49	94.2	83	2 I30607	Ig kappa chain V-I
2	49	94.2	87	2 S16823	Ig kappa chain V r
3	49	94.2	89	2 S34096	Ig kappa chain V r
4	49	94.2	91	2 S37520	Ig kappa chain V r
5	49	94.2	91	2 S67940	Ig kappa chain V r
6	49	94.2	92	2 S37513	Ig kappa chain V r
7	49	94.2	92	2 S37519	Ig kappa chain V r
8	49	94.2	92	2 S37517	Ig kappa chain V r
9	49	94.2	92	2 S37514	Ig kappa chain V r
10	49	94.2	92	2 S37518	Ig kappa chain V r
11	49	94.2	93	2 S37526	Ig kappa chain V r
12	49	94.2	93	2 S37528	Ig kappa chain V r
13	49	94.2	96	2 A30601	Ig kappa chain V-I
14	49	94.2	100	1 K3HUNG	Ig kappa chain pre
15	49	94.2	104	2 PH0964	Ig kappa chain V r
16	49	94.2	107	2 PH0965	Ig kappa chain V r
17	49	94.2	108	2 C30608	Ig kappa chain V-I
18	49	94.2	108	2 H44151	Ig kappa chain V r
19	49	94.2	109	1 K3HUTI	Ig kappa chain V r
20	49	94.2	109	2 PH0963	Ig kappa chain V-I
21	49	94.2	109	2 B30601	Ig kappa chain V r
22	49	94.2	109	2 A30608	Ig kappa chain V-I
23	49	94.2	109	2 D30601	Ig kappa chain V-I
24	49	94.2	109	2 P30607	Ig kappa chain V-I
25	49	94.2	109	2 C30601	Ig kappa chain V-I
26	49	94.2	109	2 H30601	Ig kappa chain V-I
27	49	94.2	116	2 B27594	Ig kappa chain pre
28	49	94.2	121	2 S40327	Ig kappa chain - h
29	49	94.2	129	1 K3HUMA	Ig kappa chain pre

30	49	94.2	129	1 K3HUTI	Ig kappa chain pre
31	49	94.2	129	2 S45369	Ig light chain var
32	49	94.2	134	2 S38643	Ig kappa chain V r
33	48	92.3	114	2 S46375	Ig kappa chain V-J
34	46	88.5	47	2 B30607	Ig kappa chain V-I
35	46	88.5	62	2 I30601	Ig kappa chain V-I
36	46	88.5	92	2 S37510	Ig kappa chain V r
37	46	88.5	96	2 S45441	Ig kappa chain V r
38	46	88.5	109	1 K3HUTI	Ig kappa chain V-I
39	46	88.5	116	2 C27594	Ig kappa chain pre
40	46	88.5	116	2 S41817	Ig kappa chain V r
41	46	88.5	119	2 S41816	Ig kappa chain V r
42	45	86.5	87	2 S16843	Ig kappa chain V r
43	45	86.5	87	2 S16842	Ig kappa chain V r
44	45	86.5	92	2 S37524	Ig kappa chain V r
45	45	86.5	93	2 S37508	Ig kappa chain V r

ALIGNMENTS

RESULT 1
I30607
Ig kappa chain V-III region (Wei) - human (fragments)
C/Species: Homo sapiens (man)
C/Date: 29-Jun-1989 #sequence_revision 29-Jun-1989 #text_change 09-May-1997
C/Accession: I30607
R/Genl, F.R.; Chen, P.P.; McGinnis, D.; Arjonilla, M.L.; Fernandez, J.; Carson, D.; So, J. Immunol. 142, 3158-3163, 1989
A/Title: Structural and idiotype characterization of the L chains of human Igm autoant
A/Reference number: A30601; MUID:89215279; PMID:2496160
A/Accession: I30607
A/Status: preliminary
A/Molecule type: protein
A/Residues: 1-83 <GON>
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin

Query Match Best Local Similarity 94.2% ; Score 49; DB 2; Length 83;
Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RASQSVSSSFLA 12
|||
DB 24 RASQSVSSSYLA 35

RESULT 2
S16823
Ig kappa chain V region - human (fragment)
C/Species: Homo sapiens (man)
C/Date: 19-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000
C/Accession: S16823
R/Blaisson, G.; Kuntz, J.L.; Pasqualet, J.L.
Burr, J. Immunol. 21, 1221-1227, 1991
A/Title: Molecular analysis of V(kappa)III variable regions of polyclonal rheumatoid fe
A/Reference number: S16823; MUID:91243737; PMID:1903706
A/Accession: S16823
A/Status: preliminary; translation not shown
A/Molecule type: mRNA
A/Residues: 1-87 <BLA>
A/Cross-references: EMBL:X54821
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin
F/7-82/Domain: immunoglobulin homology <IMM>

Query Match Best Local Similarity 94.2% ; Score 49; DB 2; Length 87;
Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RASQSVSSSFLA 12
|||
DB 15 RASQSVSSSYLA 26

RESULT 3

IG kappa chain V region - human
C/Species: Homo sapiens (man)
C/Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 21-Jan-2000
C/Accession: S34096
R/Klein, U.; Kueppers, R.; Rajewsky, K.
submitted to the EMBL Data Library, September 1993
A/Description: Human IGM(+) IgD(+) cells, the major B cell subset in the peripheral blood
A/Reference number: S34076; MUID:93170387; PMID:8436174
A/Accession: S34096
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-89 <WAG>
C/Cross-references: EMBL:X67180
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin
F/9-84/Domain: immunoglobulin homology <IMM>

Query Match 94.2%; Score 49; DB 2; Length 89;
Best Local Similarity 91.7%; Pred. No. 0.0067;
Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RASQSVSSSFLA 12
DB 17 RASQSVSSSYLA 28

RESULT 4

IG kappa chain V region (V-kappa 3) - human (fragment)
C/Species: Homo sapiens (man)
C/Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999
C/Accession: S37520
R/Klein, U.; Kueppers, R.; Rajewsky, K.
submitted to the EMBL Data Library, September 1993
A/Description: Human IGM(+) IgD(+) cells, the major B cell subset in the peripheral blood
A/Reference number: S37501
A/Accession: S37520
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-91 <KLE>
C/Cross-references: EMBL:Z26612; NID:g405682; PIDN:CAA81365.1; PID:g405683
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin

Query Match 94.2%; Score 49; DB 2; Length 91;
Best Local Similarity 91.7%; Pred. No. 0.0068;
Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RASQSVSSSFLA 12
DB 7 RASQSVSSSYLA 18

RESULT 5

IG kappa chain V region, subgroup III (clone MH52) - human (fragment)
C/Species: Homo sapiens (man)
C/Date: 19-Mar-1997 #sequence_revision 09-May-1997 #text_change 20-Mar-1998
C/Accession: S67940
R/Hexham, J.M.; Furmanak, J.; Peggs, C.; Burton, D.R.; Smith, B.R.
Autoimmunity 12, 135-141, 1992
A/Title: Cloning of a human autoimmune response: preparation and sequencing of a human
A/Reference number: S67940; MUID:92314301; PMID:1617110
A/Accession: S67940
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-91 <HEX>
C/Cross-references: EMBL:X73852
C/Superfamily: immunoglobulin V region; immunoglobulin homology

Query Match 94.2%; Score 49; DB 2; Length 91;
Best Local Similarity 91.7%; Pred. No. 0.0068;
Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RASQSVSSSFLA 12
DB 5 RASQSVSSSYLA 16

RESULT 6

IG kappa chain V region (V-kappa 3) - human (fragment)
C/Species: Homo sapiens (man)
C/Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999
C/Accession: S37513
R/Klein, U.; Kueppers, R.; Rajewsky, K.
submitted to the EMBL Data Library, September 1993
A/Description: Human IGM(+) IgD(+) cells, the major B cell subset in the peripheral blood
A/Reference number: S37501
A/Accession: S37513
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-92 <KLE>
C/Cross-references: EMBL:Z26598; NID:g405688; PIDN:CAA81352.1; PID:g405689
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin

Query Match 94.2%; Score 49; DB 2; Length 92;
Best Local Similarity 91.7%; Pred. No. 0.0069;
Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RASQSVSSSFLA 12
DB 7 RASQSVSSSYLA 18

RESULT 7

IG kappa chain V region (V-kappa 3) - human (fragment)
C/Species: Homo sapiens (man)
C/Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999
C/Accession: S37519
R/Klein, U.; Kueppers, R.; Rajewsky, K.
submitted to the EMBL Data Library, September 1993
A/Description: Human IGM(+) IgD(+) cells, the major B cell subset in the peripheral blood
A/Reference number: S37501
A/Accession: S37519
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-92 <KLE>
C/Cross-references: EMBL:Z26613; NID:g405680; PIDN:CAA81366.1; PID:g405681
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin

Query Match 94.2%; Score 49; DB 2; Length 92;
Best Local Similarity 91.7%; Pred. No. 0.0069;
Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RASQSVSSSFLA 12
DB 7 RASQSVSSSYLA 18

RESULT 8

IG kappa chain V region (V-kappa 3) - human (fragment)
C/Species: Homo sapiens (man)
C/Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999
C/Accession: S37517
R/Klein, U.; Kueppers, R.; Rajewsky, K.
submitted to the EMBL Data Library, September 1993
A/Description: Human IGM(+) IgD(+) cells, the major B cell subset in the peripheral blood

A:Reference number: S37501

A:Accession: S37517

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-92 <KLB>

A:Cross-references: EMBL:Z26615; NID:G405676; PIDN:CAA81368.1; PID:G405677

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

Query Match 94.2%; Score 49; DB 2; Length 92;

Best Local Similarity 91.7%; Pred. No. 0.0069;

Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 RASQSVSSSFLA 12

Db 7 RASQSVSSSYLA 18

RESULT 9

S37514

Ig kappa chain V region (V-kappa 3) - human (fragment)

C:Species: Homo sapiens (man)

C>Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999

C:Accession: S37514

R:Klein, U.; Kuipers, R.; Rajewsky, K.

submitted to the EMBL Data Library, September 1993

A:Description: Human IGM(+)IGD(+) cells, the major B cell subset in the peripheral blood

A:Reference number: S37501

A:Accession: S37514

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-92 <KLB>

A:Cross-references: EMBL:Z26597; NID:G405670; PIDN:CAA81351.1; PID:G405671

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

Query Match 94.2%; Score 49; DB 2; Length 92;

Best Local Similarity 91.7%; Pred. No. 0.0069;

Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 RASQSVSSSFLA 12

Db 7 RASQSVSSSYLA 18

RESULT 10

S37518

Ig kappa chain V region (V-kappa 3) - human (fragment)

C:Species: Homo sapiens (man)

C>Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999

C:Accession: S37518

R:Klein, U.; Kuipers, R.; Rajewsky, K.

submitted to the EMBL Data Library, September 1993

A:Description: Human IGM(+)IGD(+) cells, the major B cell subset in the peripheral blood

A:Reference number: S37501

A:Accession: S37518

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-92 <KLB>

A:Cross-references: EMBL:Z26614; NID:G405678; PIDN:CAA81367.1; PID:G405679

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

Query Match 94.2%; Score 49; DB 2; Length 92;

Best Local Similarity 91.7%; Pred. No. 0.0069;

Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 RASQSVSSSFLA 12

Db 7 RASQSVSSSYLA 18

RESULT 11

S37526

Ig kappa chain V region (V-kappa 3) - human (fragment)

C:Species: Homo sapiens (man)

C>Date: 06-Jan-1994 #sequence_revision 26-May-1995 #text_change 23-Jul-1999

C:Accession: S37526

R:Klein, U.; Kuipers, R.; Rajewsky, K.

submitted to the EMBL Data Library, September 1993

A:Description: Human IGM(+)IGD(+) cells, the major B cell subset in the peripheral blood

A:Reference number: S37501

A:Accession: S37526

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-93 <KLB>

A:Cross-references: EMBL:Z26618; NID:G405694; PIDN:CAA81371.1; PID:G405695

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

Query Match 94.2%; Score 49; DB 2; Length 93;

Best Local Similarity 91.7%; Pred. No. 0.007;

Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 RASQSVSSSFLA 12

Db 7 RASQSVSSSYLA 18

RESULT 12

S37528

Ig kappa chain V region (V-kappa 3) - human (fragment)

C:Species: Homo sapiens (man)

C>Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999

C:Accession: S37528

R:Klein, U.; Kuipers, R.; Rajewsky, K.

submitted to the EMBL Data Library, September 1993

A:Description: Human IGM(+)IGD(+) cells, the major B cell subset in the peripheral blood

A:Reference number: S37501

A:Accession: S37528

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-93 <KLB>

A:Cross-references: EMBL:Z26616; NID:G405698; PIDN:CAA81369.1; PID:G405699

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

Query Match 94.2%; Score 49; DB 2; Length 93;

Best Local Similarity 91.7%; Pred. No. 0.007;

Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 RASQSVSSSFLA 12

Db 7 RASQSVSSSYLA 18

RESULT 13

A30601

Ig kappa chain V-III region (KV325) - human (fragment)

C:Species: Homo sapiens (man)

C>Date: 29-Jun-1989 #sequence_revision 29-Jun-1989 #text_change 21-Jan-2000

C:Accession: A30601

R:Goni, F.R.; Chen, P.P.; McGinnis, D.; Arjona, M.L.; Fernandez, J.; Carson, D.; Sol

U.; Immunol. 142, 3158-3163, 1989

A:Title: Structural and idiotypic characterization of the L chains of human IGM autocal

A:Reference number: A30601; MUID:89215279; PMID:2496160

A:Accession: A30601

A:Status: preliminary

A:Molecule type: protein

A:Residues: 1-96 <GDN>

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F/16-91/Domain: immunoglobulin homology <IMM>

Query Match 94.2%; Score 49; DB 2; Length 96;

Best Local Similarity 91.7%; Pred. No. 0.0072;

Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 RASQSVSSSFLA 12
 |||||
 DB 24 RASQSVSSSYLA 35

RESULT 14

K3HUNG
 Ig kappa chain precursor V-III region (NG9) - human (fragment)
 C/Species: Homo sapiens (man)
 C/Date: 03-Aug-1984 #sequence_revision 03-Aug-1984 #text_change 21-Jan-2000
 C/Accession: A01894
 R/Bentley, D. L.
 Nature 307, 77-80, 1984
 A/Title: Most kappa immunoglobulin mRNA in human lymphocytes is homologous to a small fa
 A/Reference number: A01894; MUID:84093600; PMID:6419127
 A/Accession: A01894
 A/Molecule type: DNA
 A/Residues: 1-100 <BEN>
 A/Note: the sequence was determined from the germ-line gene
 C/Comment: This gene was isolated from the NG9/9.1 hybridoma.
 C/Genetics:
 A/Gene: GDB:IGKV3
 A/Cross-references: GDB:136266
 A/Map position: 2p12-2p11
 C/Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kappa) chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into 1a
 C/Superfamily: immunoglobulin V region; immunoglobulin homology
 C/Keywords: heterotetramer; hybridoma; immunoglobulin
 F/1-4/Domain: signal sequence (fragment) #status predicted <SIG>
 F/5-100/Product: Ig kappa chain V-III region (NG9) #status predicted <MAT>
 F/20-95/Domain: immunoglobulin homology <IMM>
 F/27-93/Disulfide bonds: #status predicted

Query Match 94.2%; Score 49; DB 1; Length 100;
 Best Local Similarity 91.7%; Pred. No. 0.0075;
 Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RASQSVSSSFLA 12
 |||||
 DB 28 RASQSVSSSYLA 39

RESULT 15

PH0964
 Ig kappa chain V region (G6+ CIL-SIC) - human (fragment)
 C/Species: Homo sapiens (man)
 C/Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 21-Jan-2000
 C/Accession: PH0964
 R/Martin, T.; Duffy, S.F.; Carson, D.A.; Kipp, T.J.
 J. Exp. Med. 175, 983-991, 1992
 A/Title: Evidence for somatic selection of natural autoantibodies.
 A/Reference number: PH0952; MUID:92202880; PMID:1552291
 A/Accession: PH0964
 A/Status: nucleic acid sequence not shown
 A/Molecule type: DNA
 A/Residues: 1-104 <VAR>
 C/Superfamily: immunoglobulin V region; immunoglobulin homology
 C/Keywords: heterotetramer; immunoglobulin
 F/1-21/Region: framework 1
 F/14-69/Domain: immunoglobulin homology <IMM>
 F/22-32/Region: complementarity-determining 1
 F/33-48/Region: framework 2
 F/49-54/Region: complementarity-determining 2
 F/55-87/Region: framework 3
 F/88-92/Region: complementarity-determining 3

Query Match 94.2%; Score 49; DB 2; Length 104;
 Best Local Similarity 91.7%; Pred. No. 0.0079;
 Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RASQSVSSSFLA 12

DB 22 RASQSVSSSYLA 33
 |||||

Search completed: June 3, 2003, 08:22:40
 Job time: 2.17065 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 3, 2003, 08:02:44 ; Search time 1.1058 Seconds
(without alignments)
450.095 Million cell updates/sec

Title: US-09-644-668a-25
Sequence: 1 RASQSVSSSFLA 12

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues
Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysts of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	49	94.2	100	1	KV3C_HUMAN
2	49	94.2	109	1	KV3D_HUMAN
3	49	94.2	129	1	KV3L_HUMAN
4	49	94.2	129	1	KV3M_HUMAN
5	46	88.5	109	1	KV3B_HUMAN
6	45	86.5	109	1	KV3F_HUMAN
7	45	86.5	116	1	KV3J_HUMAN
8	41	78.8	109	1	KV3E_HUMAN
9	39	75.0	108	1	KV3A_HUMAN
10	35	67.3	108	1	KV3V_MOUSE
11	35	67.3	128	1	KV3K_HUMAN
12	35	67.3	129	1	KV4A_MOUSE
13	34.5	66.3	115	1	KV3I_HUMAN
14	34	65.4	333	1	PSBO_SOLTU
15	34	65.4	447	1	PSBO_LACIA
16	34	65.4	913	1	VGLB_PRTV
17	33	63.5	108	1	KV1H_HUMAN
18	33	63.5	117	1	KV1J_HUMAN
19	33	63.5	433	1	MCRB_METBA
20	32	61.5	129	1	KV3H_HUMAN
21	32	61.5	236	1	CHLH_MESVI
22	32	61.5	438	1	MCRB_MERPE
23	32	61.5	442	1	MCRB_MERTH
24	32	61.5	442	1	MCRB_MERTM
25	32	61.5	449	1	Q43A_DROME
26	32	61.5	4385	1	YF73_CAEEL
27	31	59.6	111	1	KV3R_MOUSE
28	31	59.6	111	1	KV3S_MOUSE
29	31	59.6	111	1	KV3U_MOUSE
30	31	59.6	191	1	SPR6_YEAST
31	31	59.6	329	1	PSBO_TYCES
32	31	59.6	332	1	PSBO_TOBAC
33	31	59.6	344	1	HY6H_HYONI

34	31	59.6	380	1	YMH7_CAEEL	P34474 caenorhabdi
35	31	59.6	449	1	G6PI_STRMU	Q94670 streptococc
36	31	59.6	449	1	G6PI_STRPN	Q97ng0 streptococc
37	31	59.6	449	1	G6PI_STRPY	Q9a11 streptococc
38	31	59.6	897	1	DYHC_HUMAN	Q14204 homo sapien
39	31	59.6	4644	1	DYHC_MOUSE	Q9jhu4 mus musculu
40	31	59.6	4644	1	DYHC_RAT	P38650 rattus norv
41	30	57.7	107	1	KV1D_HUMAN	P01596 homo sapien
42	30	57.7	111	1	YCO4_PARDE	P08304 paracoccuss
43	30	57.7	115	1	KV5I_MOUSE	P01642 mus musculu
44	30	57.7	129	1	KV1W_HUMAN	P04431 homo sapien
45	30	57.7	135	1	ATPZ_PSEPU	P25760 pseudomonas

ALIGNMENTS

RESULT 1	ID	Sequence	Standard	PRT	100 AA
KV3C_HUMAN	KV3C_HUMAN	STANDARD;	PRT;	100 AA.	
AC	P01621;				
DT	21-JUL-1986 (Rel. 01, Created)				
DT	21-JUL-1986 (Rel. 01, Last sequence update)				
DT	15-JUL-1999 (Rel. 38, Last annotation update)				
DE	IG kappa chain V-III region NG9 precursor (Fragment).				
OS	Homo sapiens (Human).				
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;				
CC	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.				
OX	NCBI_Taxid=9606;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=84093600; PubMed=6419127;				
RA	Bentley D.L.;				
RT	"Most kappa immunoglobulin mRNA in human lymphocytes is homologous to a small family of germ-line V genes."				
RL	Nature 307:77-80(1984).				
CC	-I- MISCELLANEOUS: THIS GENE WAS ISOLATED FROM THE NG9/9.1 HYBRIDOMA.				
DR	PIR; A01894; K3HUNG.				
DR	HSSP; P80362; IWTU.				
DR	InterPro; IPR003006; IG_MHC.				
DR	InterPro; IPR003596; IG_V.				
DR	Pfam; PF00047; IG_V.				
DR	SMART; SM00406; IG_V.				
KW	Immunoglobulin V region; Signal; Hydrindoma.				
FT	NON TER				
FT	SIGNAL				
FT	CHAIN				
FT	DISULFID				
FT	NON TER				
SO	SEQUENCE				
Query Match	Score 49; DB 1; Length 100;				
Best Local Similarity	91.7%; Pred. No. 0.0029;				
Matches	11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;				
QY	1 RASQSVSSSFLA 12				
DB	28 RASQSVSSSFLA 39				
RESULT 2					
ID	KV3D_HUMAN	STANDARD;	PRT;	109 AA.	
AC	P01622;				
DT	21-JUL-1986 (Rel. 01, Created)				
DT	21-JUL-1986 (Rel. 01, Last sequence update)				
DT	15-JUL-1999 (Rel. 38, Last annotation update)				
DE	IG kappa chain V-III region TI.				
OS	Homo sapiens (Human).				
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;				
CC	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.				
OX	NCBI_Taxid=9606;				
RN	[1]				

RP SEQUENCE.
 RX MEDLINE=72188439; PubMed=5027703;
 RA Suter L, Barnikol H.U., Matanabe S., Hilschmann N.,
 RT "Role of antibody structure. The primary structure of a monoclonal
 RT immunoglobulin L-chain of kappa-type, subgroup 3 (Bence-Jones protein
 RT T1). IV. The complete amino acid sequence and its significance for
 RT the mechanism of antibody production."
 RL Hoppe-Seyler's Z. Physiol. Chem. 353:189-208(1972).
 CC -1- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
 CC -1- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.
 DR PIR; A01895; K3HUT1.
 DR HSSP; P80362; 1WTL.
 DR InterPro; IPR003006; IG_MHC.
 DR InterPro; IPR003596; IG_V.
 DR Pfam; PF00047; Ig_1.
 DR SMART; SM00406; IgV_1.
 KW Immunoglobulin V region; Bence-Jones protein.
 FT DISULFID 23 89
 FT NON TER 109 109 BY SIMILARITY.
 SQ SEQUENCE 109 AA; 11788 MW; 8C35058CDCT749BC CRC64;

Query Match 94.2%; Score 49; DB 1; Length 109;
 Best Local Similarity 91.7%; Pred. No. 0.0032;
 Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Oy 1 RASQSVSSSFLA 12
 Db 24 RASQSVSSSFLA 35

RESULT 3
 ID KV3B_HUMAN STANDARD; PRT; 129 AA.
 AC P18135;
 DT 01-NOV-1990 (Rel. 16, Created)
 DT 01-NOV-1990 (Rel. 16, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DR Ig kappa chain V-III region HAH precursor.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_Taxid=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=88171307; PubMed=3127527;
 RA Kipps T.J., Tomhave E., Chen P.P., Carson D.A.,
 RT "Autoantibody-associated kappa light chain variable region gene
 RT expressed in chronic lymphocytic leukemia with little or no somatic
 RT mutation. Implications for etiology and immunotherapy."
 RL J. Exp. Med. 167:840-852(1988)
 CC -1- DISEASE: THE PROTEIN IS ONE OF THE SURFACE IMMUNOGLOBULIN M
 CC AUTANTIBODIES EXPRESSED IN PATIENTS WITH CHRONIC LYMPHOCYTIC
 CC LEUKEMIA.
 DR PIR; P10022; K3HUT1.
 DR HSSP; P80362; 1WTL.
 DR InterPro; IPR003006; IG_MHC.
 DR InterPro; IPR003596; IG_V.
 DR Pfam; PF00047; Ig_1.
 DR SMART; SM00406; IgV_1.
 KW Immunoglobulin V region; Signal.
 FT SIGNAL 1 20
 FT CHAIN 21 129 IG KAPPA CHAIN V-III REGION HAH.
 FT DOMAIN 21 43 FRAMEWORK-1.
 FT DOMAIN 44 55 COMPLEMENTARITY-DETERMINING-1.
 FT DOMAIN 56 70 FRAMEWORK-2.
 FT DOMAIN 71 77 COMPLEMENTARITY-DETERMINING-2.
 FT DOMAIN 78 109 FRAMEWORK-3.
 FT DOMAIN 110 118 COMPLEMENTARITY-DETERMINING-3.
 FT DOMAIN 119 129 JKL SEGMENT.
 FT DISULFID 43 109 BY SIMILARITY.
 FT NON TER 129 129
 SQ SEQUENCE 129 AA; 14073 MW; D3C55292772774D0 CRC64;

Query Match 94.2%; Score 49; DB 1; Length 129;
 Best Local Similarity 91.7%; Pred. No. 0.0032;
 Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 Oy 1 RASQSVSSSFLA 12
 Db 44 RASQSVSSSYLA 55

RESULT 4
 ID KV3B_HUMAN STANDARD; PRT; 129 AA.
 AC P18136;
 DT 01-NOV-1990 (Rel. 16, Created)
 DT 01-NOV-1990 (Rel. 16, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Ig kappa chain V-III region HIC precursor.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_Taxid=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=88171307; PubMed=3127527;
 RA Kipps T.J., Tomhave E., Chen P.P., Carson D.A.,
 RT "Autoantibody-associated kappa light chain variable region gene
 RT expressed in chronic lymphocytic leukemia with little or no somatic
 RT mutation. Implications for etiology and immunotherapy."
 RL J. Exp. Med. 167:840-852(1988)
 CC -1- DISEASE: THE PROTEIN IS ONE OF THE SURFACE IMMUNOGLOBULIN M
 CC AUTANTIBODIES EXPRESSED IN PATIENTS WITH CHRONIC LYMPHOCYTIC
 CC LEUKEMIA.
 DR PIR; P10021; K3HUT1.
 DR HSSP; P80362; 1WTL.
 DR InterPro; IPR003006; IG_MHC.
 DR InterPro; IPR003596; IG_V.
 DR Pfam; PF00047; Ig_1.
 DR SMART; SM00406; IgV_1.
 KW Immunoglobulin V region; Signal.
 FT SIGNAL 1 20
 FT CHAIN 21 129 IG KAPPA CHAIN V-III REGION HIC.
 FT DOMAIN 21 43 FRAMEWORK-1.
 FT DOMAIN 44 55 COMPLEMENTARITY-DETERMINING-1.
 FT DOMAIN 56 70 FRAMEWORK-2.
 FT DOMAIN 71 77 COMPLEMENTARITY-DETERMINING-2.
 FT DOMAIN 78 109 FRAMEWORK-3.
 FT DOMAIN 110 118 COMPLEMENTARITY-DETERMINING-3.
 FT DOMAIN 119 129 JKL SEGMENT.
 FT DISULFID 43 109 BY SIMILARITY.
 FT NON TER 129 129
 SQ SEQUENCE 129 AA; 7395528EA2B74D6 CRC64;

Query Match 94.2%; Score 49; DB 1; Length 129;
 Best Local Similarity 91.7%; Pred. No. 0.0032;
 Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 Oy 1 RASQSVSSSFLA 12
 Db 44 RASQSVSSSYLA 55

RESULT 5
 ID KV3B_HUMAN STANDARD; PRT; 109 AA.
 AC P01620;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Ig kappa chain V-III region SIE.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_Taxid=9606;

```

RN [1]
RX MEDLINE=82046598; PubMed=6794615;
RA Andrews D.W., Capra J.D.;
RT "Amino acid sequence of the variable regions of light chains from two
RT idiotypically cross-reactive human IGM anti-gamma-globulins of the Wa
RT group."
RL Biocenter 20:5816-5822(1981).
CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGM WITH ANTI-GAMMA
CC GLOBULIN ACTIVITY.
CC PIR: A01892; K3HUSI.
DR HSSP; P80362; 1WTL.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF00047; Ig_1.
DR SMART; SM00406; IGV; 1.
KM Immunoglobulin V region.
FT DISULFID 23 89
FT NON_TER 109 109
SQ SEQUENCE 109 AA; 11775 MW; 7689C3ECD646FFB4 CRC64;

Query Match 88.5%; Score 46; DB 1; Length 109;
Best Local Similarity 83.3%; Pred. No. 0.013;
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 RASOSVSSSFLA 12
DB 24 RASOSVSSSYLA 35

RESULT 6
KV3F HUMAN STANDARD; PRT; 109 AA.
ID KV3F HUMAN
AC P01623;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE IG kappa chain V-III region POM.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
NCBI_Taxid=9606;
RX MEDLINE=76276460; PubMed=60899;
RA Klapper D.G., Capra J.D.;
RT "The amino acid sequence of the variable regions of the light chains
RT from two idiotypically cross reactive IGM anti-gamma globulins."
RL Ann. Immunol. (Paris) 127C:261-271(1976).
CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGM WITH ANTI-GAMMA
CC GLOBULIN ACTIVITY.
CC PIR: A01897; K3HUPM.
DR HSSP; P80362; 1WTL.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF00047; Ig_1.
DR SMART; SM00406; IGV; 1.
KM Immunoglobulin V region.
FT DISULFID 23 89
FT NON_TER 109 109
SQ SEQUENCE 109 AA; 11922 MW; 62821DDC6A8ABA86 CRC64;

Query Match 86.5%; Score 45; DB 1; Length 109;
Best Local Similarity 75.0%; Pred. No. 0.022;
Matches 9; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

OY 1 RASOSVSSSFLA 12
DB 24 RASOSVSSSYLA 35

RESULT 7
KV3J HUMAN

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ID KV3J HUMAN STANDARD; PRT; 116 AA.
AC P04434;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG kappa chain V-III region VH precursor (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
NCBI_Taxid=9606;
RX MEDLINE=85087932; PubMed=6440122;
RA Peck M., Zachau H.G.;
RT "Immunoglobulin genes of different subgroups are interdigitated
RT within the VK locus."
RL Nucleic Acids Res. 12:923-9236(1984).
CC -----
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CC or send an email to license@ebi.ac.uk).
CC -----
CC EMBL; X02725; -; NOT_ANNOTATED_CDS.
DR PIR; A01901; K3HUVH.
DR HSSP; P80362; 1WTL.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF00047; Ig_1.
DR SMART; SM00406; IGV; 1.
KM Immunoglobulin V region; Signal.
FT SIGNAL 1 20
FT CHAIN 21 >116 IG KAPPA CHAIN V-III REGION VH.
FT DOMAIN 21 43 FRAMEWORK-1.
FT DOMAIN 44 55 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 56 70 FRAMEWORK-2.
FT DOMAIN 71 77 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 78 109 FRAMEWORK-3.
FT DOMAIN 110 116 COMPLEMENTARITY-DETERMINING-3.
FT DISULFID 43 109 BY SIMILARITY.
FT NON_TER 116 116
SQ SEQUENCE 116 AA; 12757 MW; 51CDS5BA53B21929 CRC64;

Query Match 86.5%; Score 45; DB 1; Length 116;
Best Local Similarity 90.9%; Pred. No. 0.023;
Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 RASOSVSSSFL 11
DB 44 RASOSVSSSYL 54

RESULT 8
KV3E HUMAN STANDARD; PRT; 109 AA.
ID KV3E HUMAN
AC P01623;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG kappa chain V-III region WOL.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
NCBI_Taxid=9606;
RX MEDLINE=82046598; PubMed=6794615;
RA Andrews D.W., Capra J.D.;
RT "Amino acid sequence of the variable regions of light chains from two
RT idiotypically cross-reactive human IGM anti-gamma-globulins of the Wa

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RT group.
RL Biochemistry 20:5816-5822(1981).
CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGM WITH ANTI-GAMMA
CC GLOBULIN ACTIVITY.
DR PIR: A01896; K3HDWL.
DR HSSP: P80362; 1MTL.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_v.
DR Pfam: PF00047; Ig_1.
DR SMART: SM00406; IgV_1.
KW Immunoglobulin V region.
FT DISULFID 23
FT NON_TER 109
SQ SEQUENCE 109 AA; 11746 MW; 566C115E6B9CBEEB CRC64;

Query Match
Best Local Similarity 81.8%; Score 41; DB 1; Length 109;
Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 RASQSVSSSFL 11
DB 24 RASQSVSSGYL 34

RESULT 9
KV3A HUMAN STANDARD; PRT; 108 AA.
AC P01619;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-II region B6.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_Taxid=9606;
RN [1]
RP SEQUENCE.
RA Milstein C.;
RT "The basic sequences of immunoglobulin kappa chains: sequence studies
RT of Bence Jones proteins Rad, F4 and B6."
RL FEBS Lett. 2:301-304(1969).
CC -1- MISCELLANEOUS: THIS IS A BENICE-JONES PROTEIN.
DR PIR: A01891; K3HDB6.
DR HSSP: P80362; 1MTL.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_v.
DR Pfam: PF00047; Ig_1.
DR SMART: SM00406; IgV_1.
KW Immunoglobulin V region; Bence-Jones protein.
FT DISULFID 23
FT NON_TER 108
SQ SEQUENCE 108 AA; 11635 MW; 8BC14F07A19E3D CRC64;

Query Match
Best Local Similarity 75.0%; Score 39; DB 1; Length 108;
Matches 8; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 RASQSVSSSFL 12
DB 24 RASQSVSSGYL 35

RESULT 10
KV3V MOUSE STANDARD; PRT; 108 AA.
AC P01674;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-II region PC 2154.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

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OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_Taxid=10090;
RN [1]
RP SEQUENCE.
RX MEDLINE=79073152; PubMed=103003;
RA Weigert M., Gacmaitan L., Loh E., Schilling J., Hood L.E.;
RT "Rearrangement of genetic information may produce immunoglobulin
RT diversity."
RL Nature 276:785-790(1978).
DR PIR: A01940; KVM554.
DR HSSP: P80362; 1MTL.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_v.
DR Pfam: PF00047; IgV_1.
DR SMART: SM00406; IgV_1.
KW Immunoglobulin V region.
FT DOMAIN 1 23
FT DOMAIN 24 38
FT DOMAIN 39 53
FT DOMAIN 54 60
FT DOMAIN 61 92
FT DOMAIN 93 101
FT DOMAIN 102 108
FT DISULFID 23
FT NON_TER 108
SQ SEQUENCE 108 AA; 11639 MW; D40921D18DACB9E CRC64;

Query Match
Best Local Similarity 67.3%; Score 35; DB 1; Length 108;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RASQSVSSS 9
DB 24 RASQSVSS 32

RESULT 11
KV3K HUMAN STANDARD; PRT; 128 AA.
AC P06311;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-II region IARC/BL4 precursor.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_Taxid=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=86041852; PubMed=2997711;
RA Klobbeck H.G., Weindl A., Combiato G., Solomon A., Zachau H.G.;
RT "Human immunoglobulin kappa light chain genes of subgroups II and
RT III."
RL Nucleic Acids Res. 13:6499-6513(1985).
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CC -----
DR EMBL: Z00021; CAAT7316.1; -
DR PIR: A01899; K3HD41.
DR HSSP: P01607; 1REI.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_v.
DR Pfam: PF00047; Ig_1.
DR SMART: SM00406; IgV_1.
KW Immunoglobulin V region; signal.
FT SIGNAL 1 20

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FT CHAIN 21 128 IG KAPPA CHAIN V-III REGION IARC/BL41.
FT DOMAIN 21 43 FRAMEWORK-1.
FT DOMAIN 44 54 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 55 69 FRAMEWORK-2.
FT DOMAIN 70 76 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 77 108 FRAMEWORK-3.
FT DOMAIN 109 117 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 118 128 JK1 SEGMENT.
FT DISULFID 43 108 BY SIMILARITY.
FT NON TER 128 128
SQ SEQUENCE 128 AA; 14070 MW; CC8957F0FE3B9012 CRC64;

Query Match 67.3%; Score 35; DB 1; Length 128;
Best Local Similarity 88.9%; Pred. No. 3;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RASQSVSSS 9
44 RASQSVSSN 52

RESULT 12
KV4A MOUSE STANDARD; PRT; 129 AA.
ID KV4A MOUSE STANDARD; PRT; 129 AA.
AC P01680;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-IV region S107B precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=82115300; PubMed=679208;
RX Kwan S.-P., Max E.E., Seidman J.G., Leder P., Scharff M.D.;
RT "Two kappa immunoglobulin genes are expressed in the myeloma S107.";
RL Cell 26:57-66(1981).
CC -1- MISCELLANEOUS: THIS PROTEIN, IN WHICH THERE IS A DELETION OF TWO
CC AMINO ACIDS AT THE V-J RECOMBINATION SITE (AFTER POSITION 118), IS
CC SYNTHESIZED BUT NOT SECRETED IN CELLS THAT EXPRESS AND SECRETE THE
CC NORMAL KAPPA CHAIN S107.
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CC -----
DR EMBL; J00577; AAA8780.1; -
DR EMBL; V00780; CAA24157.1; -
DR PIR; A01943; KVMG7B.
DR HSSP; P01679; 2FBU.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR Immunoglobulin V region; Signal.
FT CHAIN 1 22
FT SIGNAL 1 22
FT CHAIN 23 129 IG KAPPA CHAIN V-IV REGION S107B.
FT DOMAIN 23 45 FRAMEWORK-1.
FT DOMAIN 46 57 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 58 72 FRAMEWORK-2.
FT DOMAIN 73 79 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 80 111 FRAMEWORK-3.
FT DOMAIN 112 118 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 119 128 FRAMEWORK-4.
FT DISULFID 45 111 BY SIMILARITY.
FT NON TER 129 129
SQ SEQUENCE 129 AA; 13893 MW; E4BB73072DCFB8B4 CRC64;

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Query Match 67.3%; Score 35; DB 1; Length 129;
Best Local Similarity 80.0%; Pred. No. 3;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 ASQSVSSSFL 11
47 ASSSVSSSYL 56

RESULT 13
KV31 HUMAN STANDARD; PRT; 115 AA.
ID KV31 HUMAN STANDARD; PRT; 115 AA.
AC P04433;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-III region VG precursor (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=85087932; PubMed=6440122;
RX Pech M., Zachau H.G.;
RT "Immunoglobulin genes of different subgroups are interdigitated
RT within the VK locus."
RL Nucleic Acids Res. 12:9229-9236(1984).
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CC -----
DR EMBL; X01668; -; NOT_ANNOTATED_CDS.
DR PIR; A01900; K3HUVG.
DR HSSP; P80362; 1WTL.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR Immunoglobulin V region; Signal.
FT CHAIN 1 20
FT SIGNAL 1 20
FT CHAIN 21 >115 IG KAPPA CHAIN V-III REGION VG.
FT DOMAIN 21 43 FRAMEWORK-1.
FT DOMAIN 44 54 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 55 69 FRAMEWORK-2.
FT DOMAIN 70 76 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 77 108 FRAMEWORK-3.
FT DOMAIN 109 115 COMPLEMENTARITY-DETERMINING-3.
FT DISULFID 43 108 BY SIMILARITY.
FT NON TER 115 115
SQ SEQUENCE 115 AA; 12575 MW; 2DE47CDA3A17D555 CRC64;

Query Match 66.3%; Score 34.5; DB 1; Length 115;
Best Local Similarity 83.3%; Pred. No. 3.4;
Matches 10; Conservative 1; Mismatches 0; Indels 1; Gaps 1;

QY 1 RASQSVSSSFLA 12
44 RASQSV-SSYLA 54

RESULT 14
PSBO SOLTU STANDARD; PRT; 333 AA.
ID PSBO SOLTU STANDARD; PRT; 333 AA.
AC P26320;
DT 01-MAY-1992 (Rel. 22, Created)
DT 01-MAY-1992 (Rel. 22, Last sequence update)

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DE 16-OCT-2001 (Rel. 40, Last annotation update)
DE Oxygen-evolving enhancer protein 1, chloroplast precursor (OE1) (33
DE kDa subunit of oxygen evolving system of photosystem II) (OEC 33 kDa
DE subunit) (33 kDa thylakoid membrane protein).
GN PSBO.
OS Solanum tuberosum (Potato).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; euasterids I; Solanales; Solanaceae; Solanum.
OK NCBI_TaxID=4113;
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Bintje; Tissue=leaf;
RX MEDLINE=91329725; PubMed=1840688;
RA van Spanne W., Dirkse W.G., Nap J.P., Stiekema W.J.;
RT "Isolation and analysis of cDNA encoding the 33 kDa precursor protein
RT of the oxygen-evolving complex of potato."
RL Plant Mol. Biol. 17:157-160(1991).
CC -1- FUNCTION: STABILIZES THE MANGANESE CLUSTER WHICH IS THE PRIMARY
CC SITE OF WATER SPLITTING (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Chloroplast thylakoid membrane; associated
CC with the photosystem II complex.
CC -1- SIMILARITY: BELONGS TO THE PSBO FAMILY.
CC -----
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CC -----
DR EMBL: X11578; CAA35601.1; ALT_SEQ.
DR PIR: S16586; S16586.
DR InterPro: IPR002628; PSI1_MSP.
DR Pfam: PF01716; MSP. 1.
DR K01716; MSP. 1.
KM Photosynthesis; Photosystem II; Chloroplast; Transit peptide;
KM Thylakoid; Membrane; Manganese.
FT TRANSIT 1 85 CHLOROPLAST.
FT CHAIN 86 333 OXYGEN-EVOLVING ENHANCER PROTEIN 1.
SQ SEQUENCE 333 AA; 35389 MW; 77751D20D4620519 CRC64;

Query Match 65.4%; Score 34; DB 1; Length 333;
Best Local Similarity 70.0%; Pred. No. 14;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 RASQSVSSSF 10
DB 29 RRSQSVSKAF 38

RESULT 15
ID 66PI_LACIA STANDARD; PRT; 447 AA.
AC P811B1;
DT 15-JUL-1998 (Rel. 35, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Glucose-6-phosphate isomerase (EC 5.3.1.9) (GPI) (Phosphoglucose
DE isomerase) (PGI) (Phosphohexose isomerase) (PHI).
GN PGI OR PGI OR IL2168.
OS Lactococcus lactis (subsp. lactis) (Streptococcus lactis).
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae; Lactococcus.
OK NCBI_TaxID=1360;
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN=IL1403;
RX MEDLINE=2135186; PubMed=11337471;
RA Bolotin A., Wincker P., Manger S., Jallion O., Malarme K.,
RA Weisbach J., Ehrlich S.D., Sorokin A.;
RT "The complete genome sequence of the lactic acid bacterium Lactococcus
RT lactis ssp. lactis IL1403."
RL Genome Res. 11:731-753(2001).

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RN [2]
RP SEQUENCE OF 1-19.
RX MEDLINE=9732580; PubMed=9169021;
RA Nomura M., Nakajima I., Matsuzaki M., Kimoto H., Suzuki I., Aso H.;
RT "The N-terminal sequence of Lactococcus lactis phosphoglucose
RT isomerase purified by affinity chromatography differs from the other
RT species."
RL Arch. Biochem. Biophys. 341:315-320(1997).
CC -1- CATALYTIC ACTIVITY: D-glucose 6-phosphate = D-fructose 6-
CC phosphate.
CC -1- PATHWAY: Involved in glycolysis and in gluconeogenesis.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC -1- SIMILARITY: BELONGS TO THE GPI FAMILY.
CC -----
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CC -----
DR EMBL: AB006445; AK06266.1; -.
DR HSSP: P13376; 2PGI.
DR InterPro: IPR001672; G6P_Isomerase.
DR Pfam: PF00342; PGI. 1.
DR PRINTS: PR00662; G6PISOMERASE.
DR PROSITE: PS00765; P_GLUCOSE_ISOMERASE_1; 1.
DR PROSITE: PS00174; P_GLUCOSE_ISOMERASE_2; 1.
KM Isomerase; Gluconeogenesis; Glycolysis; Complete proteome.
FT INIT MET 0 0
FT ACT SITE 310 310 BY SIMILARITY.
FT ACT SITE 424 424 BY SIMILARITY.
SQ SEQUENCE 447 AA; 49463 MW; 40DD4FC7D106FD29 CRC64;

Query Match 65.4%; Score 34; DB 1; Length 447;
Best Local Similarity 63.6%; Pred. No. 20;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 RASQSVSSFLA 12
DB 115 AGNSISSSYLA 125

Search completed: June 3, 2003, 08:15:46
Job time : 2.1058 secs

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OM protein - protein search, using SW model

Run on: June 3, 2003, 08:07:54 / Search time 5.97952 Seconds
(without alignments)
413.506 Million cell updates/sec

Title: US-09-644-668a-25
Perfect score: 52
Sequence: 1 RASQSVSSSFLA 12

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database:

SPTREMBL_21:*

- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mmc:*
- 8: sp_organelle:*
- 9: sp_phage:*
- 10: sp_plant:*
- 11: sp_rodent:*
- 12: sp_virus:*
- 13: sp_vertebrate:*
- 14: sp_unclassified:*
- 15: sp_virus:*
- 16: sp_bacteriap:*
- 17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	49	94.2	109	4 Q9UL86	Q9UL86 homo sapien
2	49	94.2	109	4 Q9UL78	Q9UL78 homo sapien
3	36	69.2	525	10 Q9UL87	Q9UL87 arabidopsis
4	35	67.3	108	4 Q9UL83	Q9UL83 homo sapien
5	35	67.3	815	5 Q44897	Q44897 caenorhabdi
6	34	65.4	157	16 Q34692	Q34692 bacillus su
7	34	65.4	218	12 Q69105	Q69105 herpes simp
8	34	65.4	238	10 Q94DH3	Q94DH3 oryza sativ
9	34	65.4	317	11 Q8VGS8	Q8VGS8 mus musculu
10	34	65.4	333	17 Q8ZSP5	Q8ZSP5 pyrobaculum
11	34	65.4	349	10 Q9ZU00	Q9ZU00 arabidopsis
12	34	65.4	353	12 Q9PZ28	Q9PZ28 xestia c-ni
13	34	65.4	510	16 Q9WWR2	Q9WWR2 braphylococ
14	34	65.4	906	12 Q91WR3	Q91WR3 pseudoradie
15	34	65.4	1003	5 Q8WQL8	Q8WQL8 caenorhabdi
16	34	65.4	1171	5 Q18820	Q18820 caenorhabdi

17	34	65.4	1857	5 Q9VLM3	Q9VLM3 drosophila
18	33	63.5	101	11 Q9DAQ2	Q9DAQ2 mus musculu
19	33	63.5	107	4 Q96SA9	Q96SA9 homo sapien
20	33	63.5	108	4 Q9UL77	Q9UL77 homo sapien
21	33	63.5	197	16 Q9JVD7	Q9JVD7 neisseria m
22	33	63.5	234	10 Q24088	Q24088 medicago cr
23	33	63.5	338	5 Q02336	Q02336 caenorhabdi
24	33	63.5	363	16 Q8XK57	Q8XK57 clostridium
25	33	63.5	379	5 Q8T3D8	Q8T3D8 caenorhabdi
26	33	63.5	388	10 Q944H1	Q944H1 arabidopsis
27	33	63.5	398	10 Q9ZSA5	Q9ZSA5 arabidopsis
28	33	63.5	434	17 Q8THG7	Q8THG7 methanobarc
29	33	63.5	459	5 Q21054	Q21054 caenorhabdi
30	33	63.5	470	5 Q9B183	Q9B183 caenorhabdi
31	33	63.5	536	11 Q9QZFB	Q9QZFB rattus norv
32	33	63.5	613	5 Q9VC38	Q9VC38 drosophila
33	33	63.5	840	16 Q8USY9	Q8USY9 agrobacteri
34	33	63.5	841	2 Q9R6B6	Q9R6B6 agrobacteri
35	33	63.5	878	2 Q52603	Q52603 agrobacteri
36	33	63.5	1214	12 Q9E3V8	Q9E3V8 grass carp
37	33	63.5	1214	12 Q9E3I67	Q9E3I67 grass carp
38	33	63.5	1737	5 Q9TW28	Q9TW28 dictyostelli
39	33	63.5	2311	5 Q9BLB1	Q9BLB1 leishmania
40	32	61.5	262	16 Q97M94	Q97M94 clostridium
41	32	61.5	343	17 Q97AH1	Q97AH1 thermoplasma
42	32	61.5	431	10 Q9SJM5	Q9SJM5 arabidopsis
43	32	61.5	449	5 Q9VAK2	Q9VAK2 drosophila
44	32	61.5	457	5 Q9NFO1	Q9NFO1 caenorhabdi
45	32	61.5	457	16 P71898	P71898 mycobacteri

ALIGNMENTS

RESULT 1

Q9UL86 PRELIMINARY; PRT; 109 AA.
ID Q9UL86
AC Q9UL86;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE Myosin-reactive immunoglobulin kappa chain variable region (Fragment).
DE OS Homo sapiens (Human).
DE CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
DE CC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
DE CC NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalle N.N., Berney S.M.,
RA Young D.C.,
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RT Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035028; AAD56264.1; -
DR HSSP; P80362; IWTL.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF00047; IG_1.
DR SMART; SM00406; IGv_1.
FT NON_TER 1
FT NON_TER 109
SEQUENCE 109 AA; 11928 MW; 243325F72C7DAC83 CRC64;

Query Match 94.2%; Score 49; DB 4; Length 109;
Best Local Similarity 91.7%; Pred. No. 0.01;
Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RASQSVSSSFLA 12
|||
Db 24 RASQSVSSSYLA 35

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RESULT 2
ID 09UL78 PRELIMINARY; PRT; 109 AA.
AC 09UL78;
DT 01-MAY-2000 (TREMblrel. 13, Created)
DT 01-MAY-2000 (TREMblrel. 13, Last sequence update)
DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)
DE Myosin-reactive immunoglobulin light chain variable region
   (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN 11
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
   fetus."
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035036; AAD56272.1; -.
DR HSSP; P80362; 1WTL.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF00047; IG; 1.
DR SMART; SM00406; IGV; 1.
FT NON TER
FT NON TER
SQ SEQUENCE 109 AA; 11646 MW; 5F675C52ECTEB197 CRC64;

Query Match
Best Local Similarity 94.2%; Score 49; DB 4; Length 109;
Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RASQSVSSFLA 12
DB 24 RASQSVSSSYLA 35

RESULT 3
ID 09LR07 PRELIMINARY; PRT; 525 AA.
AC 09LR07;
DT 01-OCT-2000 (TREMblrel. 15, Created)
DT 01-OCT-2000 (TREMblrel. 15, Last sequence update)
DT 01-MAR-2002 (TREMblrel. 20, Last annotation update)
DE F10A5.13 (Hypochemical 57.9 kDa protein).
GN F10A5.13.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC Eurosidae II; Brassicales; Brassicaceae; Arabidopsids.
OX NCBI_TaxID=3702;
RN 11
RP SEQUENCE FROM N.A.
RX Khan S., Shinn P., Brooks S., Buehler E., Chao Q., Johnson-Hopson C.,
RA Khan S., Kim C., Altafi H., Bei B., Chin C., Chou J., Choi E.,
RA Conn L., Conway A., Gonzalez A., Hansen N., Howing B., Koo T., Lam B.,
RA Lee J., Lenz C., Li J., Liu A., Liu J., Liu S., Mukharzky N.,
RA Nguyen M., Palm C., Pham P., Sakano H., Schwartz J., Southwick A.,
RA Thaveri A., Toriumi M., Vayberg M., Yu G., Davis R., Federspiel N.,
RA Theologis A., Ecker J.;
RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
RN 12
RP SEQUENCE FROM N.A.
RX Cheuk R., Shinn P., Brooks S., Buehler E., Chao Q., Johnson-Hopson C.,
RA Khan S., Kim C., Altafi H., Bei B., Chin C., Chou J., Choi E.,
RA Conn L., Conway A., Gonzalez A., Hansen N., Howing B., Koo T., Lam B.,
RA Lee J., Lenz C., Li J., Liu A., Liu J., Liu S., Mukharzky N.,
RA Nguyen M., Palm C., Pham P., Sakano H., Schwartz J., Southwick A.,
RA Thaveri A., Toriumi M., Vayberg M., Yu G., Davis R., Federspiel N.,

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RA Theologis A., Ecker J.;
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
RN 13
RP SEQUENCE FROM N.A.
RX Yamada K., Liu S.X., Sakano H., Pham P.K., Banh J., Chung M.K.,
RA Dale J.M., Gibson H.A., Goldsmith A.D., Jiang P.X., Lee J.M.,
RA Quach H.L., Tang C., Toriumi M., Yu G., Bowser L., Carlini P.,
RA Chen H., Cheuk R., Hayaishizaki Y., Ishida J., Jones T., Kamiya A.,
RA Kerlin-Neumann G., Kawai J., Kim C., Koesema E., Lam B., Lin J.,
RA Meyers M.C., Miranda M., Narusaka M., Nguyen M., Palm C.J.,
RA Sakurai T., Satou M., Seki M., Shinn P., Southwick A., Tracy S.E.,
RA Shinzaki K., Davis R.W., Ecker J.R., Theologis A.;
RT "Full length cDNA of gene F10A5.13 (GI:9369363)."
RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AC006434; AA87112.1; -.
DR EMBL; AF039938; AAK64042.1; -.
DR HSSP; P6221; 1TF4.
DR InterPro; IPR001701; GH_9.
DR Pfam; PF00759; Glyco_hydro_9; 1.
DR PROSITE; PS00592; GLYCOSYL_HYDROL_F9_1; 1.
KV Hypothetical protein
SQ SEQUENCE 525 AA; 57868 MW; FBC3704F4BB8B71 CRC64;

Query Match
Best Local Similarity 69.2%; Score 36; DB 10; Length 525;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 QSVSSSFLA 12
DB 373 QSVSSAFLA 381

RESULT 4
ID 09UL83 PRELIMINARY; PRT; 108 AA.
AC 09UL83;
DT 01-MAY-2000 (TREMblrel. 13, Created)
DT 01-MAY-2000 (TREMblrel. 13, Last sequence update)
DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)
DE Myosin-reactive immunoglobulin light chain variable region
   (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN 11
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
   fetus."
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035031; AAD56267.1; -.
DR HSSP; P80362; 1WTL.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF00047; IG; 1.
DR SMART; SM00406; IGV; 1.
FT NON TER
FT NON TER
SQ SEQUENCE 108 AA; 11834 MW; 9F9C5A92BBA96EEA CRC64;

Query Match
Best Local Similarity 67.3%; Score 35; DB 4; Length 108;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RASQSVSS 9
DB 24 RASQSVSSN 32

RESULT 5

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044897 ID 044897 PRELIMINARY; PRT: 815 AA.
 AC 044897;
 DT 01-JUN-1998 (TREMblrel. 06, Created)
 DT 01-JUN-2001 (TREMblrel. 17, Last sequence update)
 DT 01-JUN-2002 (TREMblrel. 21, Last annotation update)
 DE ZK484.2 protein.
 GN ZK484.2
 OS Caenorhabditis elegans.
 CC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
 OC Rhabditidae; Peloderinae; Caenorhabditis.
 NCBI_TaxID=6239;
 RN [1]
 RA SEQUENCE FROM N.A.
 RC STRAIN=BRISTOL N2;
 RX MEDLINE=99069613; PubMed=9851916;
 RT None;
 RL "Genome sequence of the nematode C. elegans: a platform for
 investigating biology. The C. elegans Sequencing Consortium.";
 RL Science 282:2012-2018(1998).
 RN [2]
 RA SEQUENCE FROM N.A.
 RC STRAIN=BRISTOL N2;
 RX Murray J., Wohlmann P.;
 RT "The sequence of C. elegans cosmid ZK484";
 RL Submitted (JUN-1998) to the EMBL/Genbank/DBJ databases.
 RN [3]
 RA SEQUENCE FROM N.A.
 RC STRAIN=BRISTOL N2;
 RX Waterston R.;
 RL Submitted (APR-2001) to the EMBL/Genbank/DBJ databases.
 DR EMBL; AF040659; AAK39394.1.-.
 DR InterPro; IPR003593; AAA_ATPase.
 DR InterPro; IPR001440; ABCtransporter.
 DR InterPro; IPR003439; ABC transporter.
 DR InterPro; IPR005293; Ag transporter.
 DR InterPro; IPR003662; sub transporter.
 DR Pfam; PF00664; ABC_membrane; 1.
 DR Pfam; PF00005; ABC_tran; 1.
 DR ProDom; PD000006; ABC_transporter; 1.
 DR SMART; SM00382; AAA; 1.
 DR TIGRFAMs; TIGR00958; 3a01208; 1.
 DR PROSITE; PS00211; ABC_TRANSPORTER; 1.
 DR PROSITE; PS00217; SUGAR_TRANSPORT_2; UNKNOWN; 1.
 KW ATP-binding.
 SQ SEQUENCE 815 AA; 90793 MW; 71119D4C438D06C CRC64;
 Query Match 67.3%; Score 35; DB 5; Length 815;
 Best Local Similarity .88.9%; Pred. No. 93;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 3 SOSVSSSFL 11
 Db 798 SOSVSSSFL 806
 RESULT 6
 ID 034692 PRELIMINARY; PRT: 157 AA.
 AC 034692;
 DT 01-JAN-1998 (TREMblrel. 05, Created)
 DT 01-JAN-1998 (TREMblrel. 05, Last sequence update)
 DT 01-MAR-2002 (TREMblrel. 20, Last annotation update)
 DE YVNA.
 GN YVNA.
 OS Bacillus subtilis.
 CC Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillales;
 OC Bacillaceae; Bacillus.
 NCBI_TaxID=1423;
 RN [1]
 RA SEQUENCE FROM N.A.
 RP Lazarovic V., Soldo B., Rivolta C., Reynolds S., Manuel C.,
 RA Karamata D.;

RL Submitted (NOV-1997) to the EMBL/Genbank/DBJ databases.
 RN [2]
 RA SEQUENCE FROM N.A.
 RC STRAIN=168;
 RX MEDLINE=98044033; PubMed=9384377;
 RA Kunst F., Ogasawara N., Moser I., Albertini A.M., Alloni G.,
 RA Azevedo V., Bertero M.G., Bessieres P., Bojoltin A., Borchert S.,
 RA Borriess R., Bourrier L., Brans A., Braun M., Brigelli S.C., Bron S.,
 RA Brouillet S., Brusch C.V., Caldwell B., Capuano V., Carter N.M.,
 RA Choi S.K., Codan J.J., Connerion I.F., Cummings N.J., Daniel R.A.,
 RA Denzot F., Devine K.M., Dusterhoft A., Ehrlich S.D., Emerson P.T.,
 RA Entian K.D., Errington J., Fabret C., Ferrari E., Foulger D.,
 RA Fritz C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galleron N.,
 RA Ghim S.Y., Glaser P., Goffeau A., Golligly E.J., Grandi G.,
 RA Guisepi G., Guy B.J., Haga K., Haleth U., Harwood C.R., Henaut A.,
 RA Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,
 RA Joris B., Karamata D., Kasahara Y., Klaerr-Blanchard M., Klein C.,
 RA Kobayashi Y., Koeltter P., Koningsstein G., Krogh S., Kumano M.,
 RA Kurita K., Lapidus A., Lardinois S., Lauber J., Lazarevic V.,
 RA Lee S.M., Levine A., Liu H., Masuda S., Manuel C., Medigue C.,
 RA Medina N., Mellado R.P., Mizuno M., Mostl D., Nakai S., Nodack M.,
 RA Noone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H.,
 RA Parro V., Pohl T.M., Portetelle D., Porwollik S., Prescott A.M.,
 RA Pressecan E., Pujic P., Purnelle B., Rapoport G., Rey M., Reynolds S.,
 RA Rieger M., Rivolta C., Roche B., Roche B., Rose M., Sadate Y.,
 RA Sato T., Scanlan E., Schleich S., Schroeter R., Scoffone F.,
 RA Sekiguchi J., Sekowska A., Sefor S.J., Serron P., Shin B.S., Soldo B.,
 RA Sorokin A., Tacconi E., Takagi T., Takahashi H., Takemaru K.,
 RA Takeuchi A., Tanaka T., Terpetra P., Tognoni A.,
 RA Toasto V., Uchiyama S., Vandenbol M., Vannier F., Vaasartot A.,
 RA Viari A., Wambut R., Wedler H., Wedler H., Weitzneger T.,
 RA Winters P., Wipat A., Yamamoto H., Yamane K., Yasumoto K., Yata K.,
 RA Yoshida K., Yoshikawa H.F., Zumbstein E., Yoshikawa H., Danchin A.,
 RT "The complete genome sequence of the gram-positive bacterium Bacillus
 subtilis";
 RL Nature 390:249-256(1997).
 RN [3]
 RA SEQUENCE FROM N.A.
 RC STRAIN=168;
 RA Kunst F., Ogasawara N., Yoshikawa H., Danchin A.;
 RL Submitted (NOV-1997) to the EMBL/Genbank/DBJ databases.
 CC -1- SIMILARITY: BELONGS TO THE MARR FAMILY OF TRANSCRIPTIONAL
 CC REGULATORS.
 DR EMBL; AF017113; AAC67281.1.-.
 DR EMBL; Z99122; CAB15522.1.-.
 DR EMBL; Z99121; CAB15510.1.-.
 DR InterPro; IPR000835; HTH_Marr.
 DR Pfam; PF01047; Marr; 1.
 DR SMART; SM00347; HTH_MARR; 1.
 KW DNA-binding; Transcription regulation; Complete proteome.
 SQ SEQUENCE 157 AA; 18244 MW; 7E39E94723596A53 CRC64;
 Query Match 65.4%; Score 34; DB 16; Length 157;
 Best Local Similarity 70.0%; Pred. No. 25;
 Matches 7; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
 QY 3 SOSVSSSFL 12
 Db 61 SOSVSSSFL 70
 RESULT 7
 ID 069105 PRELIMINARY; PRT: 218 AA.
 AC 069105;
 DT 01-NOV-1996 (TREMblrel. 01, Created)
 DT 01-NOV-1996 (TREMblrel. 01, Last sequence update)
 DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)
 DE LAT protein.
 GN LAT.
 OS Herpes simplex virus (type 2).
 CC Viruses; dsDNA viruses; no RNA stage; Herpesviridae;
 OC Alphaherpesvirinae; Simplexvirus.

OK NCBI_TaxID=10310;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=91374627; PubMed=1654458;
 RA Krause P.R., Ostrove J.M., Straub S.E.,
 RT "The nucleotide sequence, 5' end, promoter domain, and kinetics of
 RT latency-associated transcript."
 RL J. Virol. 65:5619-5623 (1991).
 DR EMBL/ M69065; AAA45850.1;
 SQ SEQUENCE 218 AA; 22514 MW; 0D94D0847F45FBCA CRC64;

Query Match 65.4%; Score 34; DB 12; Length 218;
 Best Local Similarity 72.7%; Pred. No. 36;
 Matches 8; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 RASQSVSSSFL 11
 Db 3 RVSSSSSSSFL 13

RESULT 8

Q94DH3 PRELIMINARY; PRT; 238 AA.
 AC Q94DH3;
 DT 01-DEC-2001 (TRENBLrel. 19, Created)
 DT 01-DEC-2001 (TRENBLrel. 19, Last sequence update)
 DT 01-DEC-2001 (TRENBLrel. 19, Last annotation update)
 DE P0518C01.13 protein.
 GN P0518C01.13.
 OS Oryza sativa (Rice).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC Ehrhartoideae; Oryzae; Oryza.
 OK NCBI_TaxID=4530;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CV. NIPPONBARE;
 RA Sasaki T., Matsumoto T., Yamamoto K.,
 RT "Oryza sativa nipponbare (GA3) genomic DNA, chromosome 1, PAC
 RT clone: P0518C01."
 RL Submited (FEB-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL/ AB003277; BAB63676.1;
 SQ SEQUENCE 238 AA; 25617 MW; 2360194B496C2974 CRC64;

Query Match 65.4%; Score 34; DB 10; Length 238;
 Best Local Similarity 75.0%; Pred. No. 39;
 Matches 9; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 RASQSVSSSFLA 12
 Db 74 RASSSSSSSSFLA 85

RESULT 9

Q8VGJ8 PRELIMINARY; PRT; 317 AA.
 AC Q8VGJ8;
 DT 01-MAR-2002 (TRENBLrel. 20, Created)
 DT 01-MAR-2002 (TRENBLrel. 20, Last sequence update)
 DT 01-JUN-2002 (TRENBLrel. 21, Last annotation update)
 DE Olfactory receptor MOR127-4.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OK NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Zhang X., Firestein S.J.,
 RT "The olfactory receptor gene superfamily of the mouse."
 RL Nat. Neurosci. 0:0-012002).
 RN [2]
 RP SEQUENCE FROM N.A.

RA Adams M.,
 RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL/ AY073149; AL60812.1;
 DR InterPro; IPR000276; GPCR_Rhodopsin.
 DR Pfam; PF00001; 7tm.1; 1.
 DR PRINTS; PR00237; GPCRHHODOPS.
 DR PROSITE; PS00237; G_PROTEIN_RECPT_F1_1; UNKNOWN_1.
 DR PROSITE; PS50262; G_PROTEIN_RECPT_F1_2; 1.
 KW Receptor.
 SQ SEQUENCE 317 AA; 34949 MW; CFA22359EC72A3DF CRC64;

Query Match 65.4%; Score 34; DB 11; Length 317;
 Best Local Similarity 63.6%; Pred. No. 54;
 Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 RASQSVSSSFL 11
 Db 6 RVNQSVASDPL 16

RESULT 10

Q8ZSP5 PRELIMINARY; PRT; 333 AA.
 AC Q8ZSP5;
 DT 01-MAR-2002 (TRENBLrel. 20, Created)
 DT 01-MAR-2002 (TRENBLrel. 20, Last sequence update)
 DT 01-MAR-2002 (TRENBLrel. 20, Last annotation update)
 DE Hypothetical protein PAE3644.
 GN PAE3644.
 OS Pyrobaculum aerophilum.
 OC Archaea; Crenarchaeota; Thermoprotei; Thermoproteales;
 OC Thermoproteaceae; Pyrobaculum.
 OK NCBI_TaxID=13773;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=IM2 / ATCC 51768 / DSM 7523;
 RX PubMed=11792869;
 RA Fitz-Gibbon S.T., Ladner H., Kim U.-J., Stetter K.O., Simon M.I.,
 RA Miller J.H.,
 RT "Genome sequence of the hyperthermophilic crenarchaeon Pyrobaculum
 RT aerophilum."
 RL Proc. Natl. Acad. Sci. U.S.A. 99:984-989 (2002).
 DR EMBL/ AB009943; AAL65068.1;
 KW Hypothetical protein; Complete proteome.
 SQ SEQUENCE 333 AA; 36031 MW; 3F88123A09021BB8 CRC64;

Query Match 65.4%; Score 34; DB 17; Length 333;
 Best Local Similarity 80.0%; Pred. No. 57;
 Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 3 SOSVSSSFLA 12
 Db 167 SPSVSTSTFLA 176

RESULT 11

Q9ZU0 PRELIMINARY; PRT; 349 AA.
 AC Q9ZU0;
 DT 01-MAY-1999 (TRENBLrel. 10, Created)
 DT 01-MAY-1999 (TRENBLrel. 10, Last sequence update)
 DT 01-DEC-2001 (TRENBLrel. 19, Last annotation update)
 DE Putative WRKY-type DNA-binding protein (WRKY transcription factor
 DE 44).
 GN ATG37260 OR WRKY44.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC Eurosid II; Brassicales; Brassicaceae; Arabidopsis.
 OK NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CV. COLUMBIA;

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RX MEDLINE=20083487; PubMed=10611797;
RA Lin X., Kaul S., Rounsley S.D., Shea T.P., Bentico M.-I., Town C.D.,
RA Fujii C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldblum T.V.,
RA Buell C.R., Ketchum K.A., Lee J.J., Roming C.M., Koo H., Motlat K.S.,
RA Cronin L.A., Shen M., Vanaken S.E., Unayam L., Tallon L.J., Gill J.E.,
RA Adams M.D., Carreira A.J., Creasy T.H., Goodman H.M., Somerville C.R.,
RA Copenhaver G.P., Preuss D., Niernan W.C., White O., Eelen J.A.,
RA Salzberg S.L., Fraser C.M., Venter J.C.;
RT "Sequence and analysis of chromosome 2 of the plant Arabidopsis
thaliana.";
RL Nature 402:761-768 (1999).
RN
RP SEQUENCE FROM N.A.
RC STRAIN=CV. COLUMBIA;
RA Lin X.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN
RP SEQUENCE FROM N.A.
RC TISSUE=INFLORESCENCE;
RA Ulker B., Kuehnir S., Somasich I.;
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AC005896; AAC98047.1; -
DR EMBL; AF040862; AAC96200.1; -
DR InterPro; IPR003657; WRKY.
DR Pfam; PF03106; WRKY; 2.
KM DNA-binding.
SQ SEQUENCE 349 AA; 38673 MW; 386FF8932676CA93 CRC64;

Query Match
Best Local Similarity 70.0%; Score 34; DB 10; Length 349;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 RASOSVSSSF 10
DB 150 RASSSISGCF 159

RESULT 12
O9P228 PRELIMINARY; PRT; 353 AA.
AC O9P228;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE ORF15.
OS Xestia c-nigrum granulosis virus (XngV) (Xestia c-nigrum
OS granulovirus).
OC Viruses; dsDNA viruses, no RNA stage; Baculoviridae; Granulovirus.
CX NCBI_TaxID=51677;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=99434230; PubMed=10502508;
RA Hayakawa T., Ko R., Okano K., Seong S.I., Goto C., Maeda S.;
RT "Sequence analysis of the Xestia c-nigrum granulovirus genome.";
RL Virology 262:277-297 (1999).
DR EMBL; AF162221; AAF05129.1; -
SQ SEQUENCE 353 AA; 38606 MW; 344CG9CE5466F1BD CRC64;

Query Match
Best Local Similarity 65.4%; Score 34; DB 12; Length 353;
Matches 7; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

OY 2 ASQSVSSSFL 11
DB 316 SSQSVSNFL 325

RESULT 13
O99WR2 PRELIMINARY; PRT; 510 AA.
AC O99WR2;
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)

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DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE Hypothetical protein SAV0314.
GN SAV0314 OR SA0303.
OS Staphylococcus aureus (strain Mu50 / ATCC 700699), and
OS Staphylococcus aureus (strain N315).
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillales;
OC Staphylococcus.
CX NCBI_TaxID=158878, 158879;
RN
RP SEQUENCE FROM N.A.
RC SPECIES=S.aureus (strain Mu50), and S.aureus (strain N315);
RX MEDLINE=21311952; PubMed=11418146;
RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
RA Cui L., Oguchi A., Aoki K.-I., Nagai Y., Iino J.-Q., Ito T.,
RA Kanamori M., Matsumaru H., Murakami A., Murakami H., Hosoyama A.,
RA Mizutani Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
RA Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,
RA Kanehisa M., Yamashita A., Oshida K., Puruya K., Yoshino C., Shiba T.,
RA Hattori M., Ogasawara N., Hayashi H., Hiratsuka K.;
RT "Whole genome sequencing of methicillin-resistant Staphylococcus
aureus.";
RL Lancet 357:1225-1240 (2001).
DR EMBL; AP003359; BAB56476.1; -
DR EMBL; AP003110; BAB1527.1; -
DR InterPro; IPR001734; Na_soluc_symport.
DR Pfam; PF00474; SSF; 1.
DR TIGRFAMs; TIGR00813; sss; 1.
DR PROSITE; PS50283; NA_SOLUT_SYMP_3; 1.
KM Hypothetical protein; Complete proteome.
SQ SEQUENCE 510 AA; 55889 MW; D98E7657FF2F0CC0 CRC64;

Query Match
Best Local Similarity 66.7%; Score 34; DB 16; Length 510;
Matches 8; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 1 RASOSVSSSFLA 12
DB 31 RASOSTNSFFTA 42

RESULT 14
O91WV3 PRELIMINARY; PRT; 906 AA.
AC O91WV3;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE Glycoprotein B GII (Fragment).
OS GB.
OS Pseudorabies virus.
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC Alphaherpesvirinae; Varicellovirus.
CX NCBI_TaxID=10345;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=EA;
RA Hong W., Chen H., Xiao S., He Q., Fang L.;
RT "Clone and sequence analysis of gb gene of Pseudorabies Virus Ea
strain.";
RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF257079; AAF68982.1; -
DR InterPro; IPR000234; Glycoprot_B.
DR Pfam; PF00606; Glycoprotein B; 1.
DR ProDom; PD000693; Glycoprot_B; 1.
FT NON TER 906
SQ SEQUENCE 906 AA; 99474 MW; C4D2E8687CD58725 CRC64;

Query Match
Best Local Similarity 65.4%; Score 34; DB 12; Length 906;
Matches 7; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

OY 1 RASOSVSSSFL 11

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Db 346 RASSVTRNFL 356

RESULT 15

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O8WOL8      PRELIMINARY;      PRT; 1003 AA.
ID O8WOL8
AC O8WOL8;
DT 01-MAR-2002 (TREMBlrel. 20, Created)
DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)
DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
DE Insulin receptor substrate-like protein.
GN ISt-1.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RA Wojkow C., Hu P., Tewari M., Vidal M., Ruvkun G.;
RT "IRS and p55 orthologous adaptor proteins function in the C. elegans
RT daf-2/insulin-like signaling pathway.";
RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY064245; AAL40865.1; -.
KW Receptor.
SQ SEQUENCE 1003 AA; 113562 MW; F06FCE030D0836A0 CRC64;

Query March 65.4%; Score 34; DB 5; Length 1003;
Best Local Similarity 72.7%; Pred. No. 1.9e+02;
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 ASOSVSSSFLA 12
Db 677 ASPSASSNPLA 687

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Search completed: June 3, 2003, 08:20:50
 Job time : 7.97952 secs

XX	RESULT 1
DR	AAB67498
XX	ID AAB67498 standard; peptide; 12 AA.
XX	AC AAB67498;
XX	DT 29-MAY-2001 (first entry)
DE	Human light chain complementarity determining region 1 (CDRL).
KM	Complementarity determining region; CDR; immune response; antibody;
KM	Cytotoxic T lymphocyte associated antigen-4; CTLA-4; B7 ligand; cancer;
KM	autoimmune disease; infectious disease; inflammation; allergy;
KM	rheumatoid arthritis; myasthenia gravis; lupus erythematosus;
KM	multipple sclerosis; insulin-dependent diabetes mellitus; inflammation;
KM	transplant rejection; graft versus host disease.
OS	Homo sapiens.
XX	MO20011424-A2.
PN	XX
PD	01-MAR-2001.
XX	XX
PF	24-AUG-2000; 2000MO-US23356.
PR	XX
XX	24-AUG-1999; 99US-0150452.
PA	(MEDA-) MEDAREX INC.
PI	Korman AJ, Halk EL, Lonberg N;
WFI	2001-202933/20.

PT Novel human sequence antibody that binds to human cytotoxic T
 PT lymphocyte associated antigen-4, useful for inducing, augmenting or
 PT prolonging immune response to antigen or for suppressing immune
 PT response in patient
 PS Claim 31; Page 100; 127pp; English.
 XX
 CC AAB67490-99 and AAB67501-06 represents complementarily determining
 CC regions (CDRs) of human antibodies. The antibodies specifically bind to
 CC human cytotoxic T lymphocyte associated antigen-4 (CTLA-4). Such
 CC antibodies are used in methods for inducing, augmenting or prolonging
 CC an immune response to an antigen in a patient, where the antibodies
 CC block binding of human CTLA-4 to human B7 ligands. The antibodies are
 CC also useful for treating autoimmune disease in a subject caused or
 CC exacerbated by increased activity of T cells and for treating prostate
 CC cancer, melanoma or epithelial cancer. A polyvalent or polyclonal
 CC antibody preparation comprising two antibodies of the invention are
 CC useful for suppressing an immune response in a patient. They are used for
 CC treating cancer, infectious diseases and promoting beneficial autoimmune
 CC reactions for the treatment of diseases with inflammatory or allergic
 CC components. The polyvalent or polyclonal preparations are useful for
 CC treating autoimmune diseases such as rheumatoid arthritis, myasthenia
 CC gravis and lupus erythematosus, multiple sclerosis, insulin-dependent
 CC diabetes mellitus, transplant rejection, and inflammation, graft versus
 CC host disease.
 CC
 SQ Sequence 12 AA;
 Query Match 100.0%; Score 52; DB 22; Length 12;
 Best Local Similarity 100.0%; Pred. No. 0.00056;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 RASQSVSSSFLA 12
 DB 1 RASQSVSSSFLA 12
 RESULT 2
 ID AAY93702 standard; Protein; 235 AA.
 XX
 AC AAY93702;
 XX
 DT 03-OCT-2000 (first entry)
 XX
 DE The kappa chain of immunoglobulin clone 4.1.1.
 XX
 KM Cytotoxic T-lymphocyte antigen-4; CTLA-4; antibody; immune system;
 KM hyperimmunity disorder; autoimmune disease; diabetes; graft rejection;
 KM proliferative disorder; cancer; immunodeficient disorder.
 XX
 OS Homo sapiens.
 XX
 PN MO200037504-A2.
 XX
 PD 29-JUN-2000.
 XX
 PF 23-DEC-1999; 99WO-US30895.
 XX
 PR 23-DEC-1998; 98US-0113647.
 XX
 PA (PF12) PRIZER INC.
 PA (ABGE-) ABGENIX INC.
 XX
 PI Hanson DC, Neveu MJ, Mueller EE, Hanke JH, Gilman SC, Davis CG;
 PI Corvalan JR;
 XX
 DR WPI; 2000-442647/38.
 DR N-PSDB; AAA46865.
 XX
 PT Novel antibodies capable of binding cytotoxic T-lymphocyte antigen
 PT (CTLA)-4 containing specified heavy and light chain sequences, useful
 PT for treating, e.g. immune disorders

XX
 PS Claim 3; Fig 1A; 157pp; English.
 XX
 CC The present sequence represents a kappa chain of an antibody of the
 CC invention. The antibody is directed cytotoxic T-lymphocyte antigen
 CC (CTLA)-4. Antibodies of the invention are composed of a heavy chain
 CC variable region, comprising a modified contiguous sequence from a
 CC FRI-FR3 sequence encoded by a human VH3-33 family gene. The
 CC modifications are contained in CDR1, CDR2 and/or framework regions.
 CC The antibodies may be used to inhibit CTLA-4 and down-regulate the
 CC immune system to treat hyperimmunity disorders (e.g. autoimmune
 CC disease, diabetes and graft rejection) and proliferative disorders
 CC (e.g. cancer). CTLA-4 stimulatory agents may be used to up-regulate
 CC immune system to up-regulate immunodeficient disorders.
 CC
 SQ Sequence 235 AA;
 Query Match 98.1%; Score 51; DB 21; Length 235;
 Best Local Similarity 91.7%; Pred. No. 0.026;
 Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 RASQSVSSSFLA 12
 DB 44 RASQSVSSSFLA 55
 RESULT 3
 ID AAY93729 standard; Protein; 235 AA.
 XX
 AC AAY93729;
 XX
 DT 03-OCT-2000 (first entry)
 XX
 DE The kappa chain of immunoglobulin clone 4.1.1.
 XX
 KM Cytotoxic T-lymphocyte antigen-4; CTLA-4; antibody; immune system;
 KM hyperimmunity disorder; autoimmune disease; diabetes; graft rejection;
 KM proliferative disorder; cancer; immunodeficient disorder.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Peptide 1..20
 FT /note= "signal peptide"
 XX
 PN MO200037504-A2.
 XX
 PD 29-JUN-2000.
 XX
 PF 23-DEC-1999; 99WO-US30895.
 XX
 PR 23-DEC-1998; 98US-0113647.
 XX
 PA (PF12) PRIZER INC.
 PA (ABGE-) ABGENIX INC.
 XX
 PI Hanson DC, Neveu MJ, Mueller EE, Hanke JH, Gilman SC, Davis CG;
 PI Corvalan JR;
 XX
 DR WPI; 2000-442647/38.
 DR N-PSDB; AAA46893.
 XX
 PT Novel antibodies capable of binding cytotoxic T-lymphocyte antigen
 PT (CTLA)-4 containing specified heavy and light chain sequences, useful
 PT for treating, e.g. immune disorders
 XX
 PS Claim 3; Fig 22g; 157pp; English.
 XX
 CC The present sequence represents a kappa chain of an antibody of the
 CC invention. The antibody is directed cytotoxic T-lymphocyte antigen
 CC (CTLA)-4. Antibodies of the invention are composed of a heavy chain
 CC variable region, comprising a modified contiguous sequence from a

CC FRI-FR3 sequence encoded by a human VH3-33 family gene. The
 CC modifications are contained in CDR1, CDR2 and/or framework regions.
 CC The antibodies may be used to inhibit CTLA-4 and down-regulate the
 CC immune system to treat hyperimmunity disorders (e.g. autoimmune
 CC disease, diabetes and graft rejection) and proliferative disorders
 CC (e.g. cancer). CTLA-4 stimulatory agents may be used to up-regulate
 CC immune system to up-regulate immunodeficient disorders.

XX Sequence 235 AA;

Query Match 98.1%; Score 51; DB 21; Length 235;

Best Local Similarity 91.7%; Pred. No. 0.026;

Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RASQSVSSSFLA 12
 |||||
 DB 44 RASQSVSSSFLA 55

RESULT 4

AA15375

AC AA15375;

DT 05-MAR-1992 (first entry)

DE IGM-RF G10.

XX Rheumatoid factor; RF; antigen; CDR; IGM.

XX Synthetic.

PN US068177-A.

PD 26-NOV-1991.

PF 05-AUG-1985; 85US-0762698.

PR 05-AUG-1985; 85US-0762698.

PR 28-DEC-1983; 83US-0566172.

PA (SCRI-) SCRIPPS CLINIC RES.

PI Carson DA, Fong S, Chen PP;

DR WPI; 1991-368612/50.

PT Synthetic polypeptide(s) for inducing anti-idiotypic antibodies -

PT useful for treating auto immune-, endocrine- and

PT rheumatic-diseases and myasthenia gravis

PS Claim 10; Page 42; 4pp; English.

XX Three rabbits were inoculated with two s.c. injections of PGL1

XX (synthetic peptide) conjugated to KdH as an immunogen, and their

XX sera were analysed for anti-peptide antibody activity by ELISA.

XX All three immunised rabbits produced anti-PGL1 antibody. Antisera

XX drawn from a rabbit on two different days reacted significantly with

XX the corresp. intact IGM-RF G10.

XX See also AA15365-74 and AA15375.

XX Sequence 12 AA;

Query Match 94.2%; Score 49; DB 12; Length 12;

Best Local Similarity 91.7%; Pred. No. 0.0023;

Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RASQSVSSSFLA 12
 |||||
 DB 1 RASQSVSSSFLA 12

RESULT 5
 AA083718
 ID AA083718 standard; Peptide; 12 AA.

XX AA083718;

DT 08-MAY-2002 (first entry)

XX MS-GPC-6 light chain variable region CDR1 sequence.

DE Human; antibody-based antigen; HLA-DR; CDR; antibody;

XX human leukocyte antigen; cell proliferative disorder; lymphoma;

XX MHC class II antigen disorder; lymphoma; B cell lymphoma; leukemia;

XX acute myeloid leukemia; rheumatoid arthritis; multiple sclerosis;

XX Grave's disease; insulin-dependent diabetes; transplant rejection;

XX systemic lupus erythematosus; graft vs. host disease; myasthenia gravis;

XX irritable bowel disease; Sjogren's syndrome; interleukin-2 secretion;

XX IL-2; MS-GPC; complementarity determining region.

XX Homo sapiens.

XX WO200187337-A1.

XX 22-NOV-2001.

XX 14-MAY-2001; 2001MO-US15625.

XX 12-MAY-2000; 2000EP-0110065.

XX 06-OCT-2000; 2000US-238492P.

XX (GPCB-) GPC BIOTECH AG.

XX (MORP-) MORPHOSYS AG.

XX Nagy Z, Brunner C, Tesar M, Thomassen-Wolf E;

XX WPI; 2002-075288/10.

XX Polypeptide compositions which bind to cell surface epitopes, which in

XX multivalent form kills lymphoid tumor cells and in monovalent form

XX causes immunosuppression or inhibits activation of lymphocytes

XX Example 4; Page 66; 150pp; English.

XX The invention relates to a composition which includes a polypeptide

XX or a multivalent polypeptide comprising one or more

XX antibody-based antigen-binding domain of human composition

XX with binding specificity for an antigen expressed on surface of a

XX human cell, especially HLA-DR (human leukocyte antigen DR), where

XX treating cells expressing HLA-DR with the multivalent polypeptide causes

XX or leads to killing of cells without need of cytotoxic entities or

XX immunological mechanisms. Also included are the nucleic acid

XX encoding the polypeptide, a vector comprising the nucleic acid and a host

XX cell harbouring vector or nucleic acid. The polypeptide (optionally

XX linked to cytotoxic or immunogenic agent), the nucleic acid and the host

XX cell are useful for preparing a pharmaceutical preparation for the

XX treatment of cell proliferative disorders, disorders involving

XX transformed cells expressing MHC class II antigens, B cell non-Hodgkin's

XX lymphoma, B cell lymphoma, B cell acute lymphoid leukemia, Burkitt's

XX lymphoma, Hodgkin's lymphoma, hairy cell leukemia, acute myeloid

XX leukemia, T cell lymphoma, T cell non-Hodgkin's lymphoma, chronic

XX myeloid leukemia, chronic lymphoid leukemia or multiple myeloid

XX leukemia, disorders involving unwanted activation of the cells of the

XX immune system, such as lymphoid cells expressing MHC class II, rheumatoid

XX arthritis, juvenile arthritis, multiple sclerosis, Grave's disease,

XX insulin-dependent diabetes, narcolepsy, psoriasis, systemic lupus

XX erythematosus, ankylosing spondylitis, transplant rejection, graft vs.

XX host disease, Hashimoto's disease, myasthenia gravis, pemphigus

XX vulgaris, glomerulonephritis, thyroiditis, pancreatitis, insulin's

XX primary biliary cirrhosis, irritable bowel disease and Sjogren's

XX syndrome in humans. The antigen is useful for suppressing activation or

XX proliferation of a cell of the immune system, suppressing interleukin-2

XX (IL-2) secretion by a cell of the immune system, such as expressing

XX HLA-DR, the interaction of the cell of the immune system with another

cell, immunosuppressing a patient and for killing a cell expressing an antigen, HLA-DR on the surface of the cell, where neither cytotoxic enzymes nor immunological mechanisms are needed to cause or lead to the killing. The killing is dependent on the action of non-caspase proteases and/or cannot be inhibited by zVAD-fmk or zDEVD-fmk. The present sequence is a complementarity determining region (CDR) based on the human antigen binding polypeptides of the invention MS-GPC-1, 6, 8 and 10. The CDRs are either the native sequence or have been optimized/mutated to alter their antigen binding capabilities.

Sequence 12 AA;

Query Match 94.2%; Score 49; DB 23; Length 12;
Best Local Similarity 91.7%; Pred. No. 0.0023;
Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

1 RASQSVSSSFLA 12
1 RASQSVSSSYLA 12

RESULT 6
ABB57469

ABB57469 standard; Peptide; 12 AA.

ABB57469;

18-MAR-2002 (first entry)

HLA-DR-specific protein VL-CDRI-Sequence MS-GPC-2.

Immunomodulatory human MHC class II antigen-binding protein; HLA; human leukocyte antigen; immune system; immunosuppression; antibody; major histocompatibility complex; antirheumatic; antiarthritic; neuroprotective; antiinflammatory; antidiabetic; antipsoriatic; immunosuppressive; dermatological; antithyroid; nephrotropic; psoriasis; thyromimetic; hepatotropic; immune response suppressor; narcolepsy; rheumatoid arthritis; juvenile arthritis; multiple sclerosis; insulin; Grave's disease; insulin-dependent diabetes; Hashimoto's disease; systemic lupus erythematosus; ankylosing spondylitis; myasthenia gravis; transplant rejection; graft versus host disease; pemphigus vulgaris; glomerulonephritis; thyroiditis; pancreatitis; primary biliary cirrhosis; irritable bowel disease; Sjogren's syndrome.

Homo sapiens.
Synthetic.

WO200187338-A1.

22-NOV-2001.

14-MAY-2001; 2001WO-US15626.

12-MAY-2000; 2000EP-0110063.

06-OCT-2000; 2000US-238762P.

(GPCB-) GPC BIOTECH AG.
(MORP-) MORPHOSYS AG.

Nagy Z, Tesar M, Thomassen-Wolf E;

WPI; 2002-075289/10.

Composition for suppressing immune response, treating diseases of immune system, has polypeptide comprising antibody-based antigen-binding domain of human composition, which binds antigen expressed on a cell surface.

Example; Page 60; 139pp; English.

The present invention describes a composition (1), comprising a polypeptide comprising an antibody-based antigen-binding domain of human composition with binding specificity for an antigen expressed on the

surface of a cell, where treating cells expressing the antigen with the polypeptide leads to suppression of an immune response, and the IC50 for the suppression of immune response is 1 microm or less. (1) has antithematic, antiarthritic, neuroprotective, antiinflammatory, antidiabetic, antipsoriatic, immunosuppressive, dermatological, antithyroid, nephrotropic, thyromimetic and hepatotropic activities, and can be used as a suppressor of immune response. (1) is useful for suppressing activation or proliferation of a cell of the immune system, suppressing IL-2 secretion by a cell, the interaction of a cell of the immune system with another cell, immunosuppressing a patient and for killing a cell expressing an antigen, human leukocyte antigen (HLA)-DR on the surface of the cell, where neither cytotoxic enzymes nor immunological mechanisms are needed to cause or lead to the killing. (1) (optionally linked to cytotoxic or immunogenic agent) is useful for preparing a pharmaceutical preparation for the treatment of rheumatoid arthritis, juvenile arthritis, multiple sclerosis, Grave's disease, insulin-dependent diabetes, narcolepsy, psoriasis, systemic lupus erythematosus, ankylosing spondylitis, transplant rejection, graft versus host disease, Hashimoto's disease, myasthenia gravis, pemphigus vulgaris, glomerulonephritis, thyroiditis, pancreatitis, insulinitis, primary biliary cirrhosis, irritable bowel disease and Sjogren's syndrome in humans. ABA92469 to ABA92474 and ABB57457 to ABB57590 represent sequence used in the exemplification of the present invention.

Sequence 12 AA;

Query Match 94.2%; Score 49; DB 23; Length 12;
Best Local Similarity 91.7%; Pred. No. 0.0023;
Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

1 RASQSVSSSFLA 12
1 RASQSVSSSYLA 12

RESULT 7
ABB57472

ABB57472 standard; Peptide; 12 AA.

ABB57472;

18-MAR-2002 (first entry)

HLA-DR-specific protein VL-CDRI-Sequence MS-GPC-3.

Immunomodulatory human MHC class II antigen-binding protein; HLA; human leukocyte antigen; immune system; immunosuppression; antibody; major histocompatibility complex; antirheumatic; antiarthritic; neuroprotective; antiinflammatory; antidiabetic; antipsoriatic; immunosuppressive; dermatological; antithyroid; nephrotropic; psoriasis; thyromimetic; hepatotropic; immune response suppressor; narcolepsy; rheumatoid arthritis; juvenile arthritis; multiple sclerosis; insulin; Grave's disease; insulin-dependent diabetes; Hashimoto's disease; systemic lupus erythematosus; ankylosing spondylitis; myasthenia gravis; transplant rejection; graft versus host disease; pemphigus vulgaris; glomerulonephritis; thyroiditis; pancreatitis; primary biliary cirrhosis; irritable bowel disease; Sjogren's syndrome.

Homo sapiens.
Synthetic.

WO200187338-A1.

22-NOV-2001.

14-MAY-2001; 2001WO-US15626.

12-MAY-2000; 2000EP-0110063.

06-OCT-2000; 2000US-238762P.

(GPCB-) GPC BIOTECH AG.
(MORP-) MORPHOSYS AG.

PI Nagy Z, Tesar M, Thomassen-Wolf E;
 XX WPI; 2002-075289/10.
 DR
 XX
 XX
 XX
 PT Composition for suppressing immune response, treating diseases of
 PT immune system, has polypeptide comprising antibody-based
 PT antigen-binding domain of human composition, which binds antigen
 PT expressed on a cell surface
 XX
 PS Example; Page 60; 139pp; English.
 CC The present invention describes a composition (I), comprising a
 CC polypeptide comprising an antibody-based antigen-binding domain of human
 CC composition with binding specificity for an antigen expressed on the
 CC surface of a cell, where treating cells expressing the antigen with the
 CC polypeptides leads to suppression of an immune response, and the IC50 for
 CC the suppression of immune response is 1 microm or less. (I) has
 CC antirheumatic, antiarthritic, neuroprotective, antiinflammatory,
 CC antidiabetic, antiparalytic, immunosuppressive, dermatological,
 CC antithyroid, nephroretropic, thyromimetic and hepatotropic activities, and
 CC can be used as a suppressor of immune response. (I) is useful for
 CC suppressing activation or proliferation of a cell of the immune system,
 CC suppressing IL-2 secretion by a cell, the interaction of a cell of the
 CC immune system with another cell, immunosuppressing a patient and for
 CC killing a cell expressing an antigen, human leukocyte antigen (HLA)-DR
 CC on the surface of the cell, where neither cytotoxic entities nor
 CC immunological mechanisms are needed to cause or lead to the killing.
 CC (I) (optionally linked to cytotoxic or immunogenic agent) is useful for
 CC preparing a pharmaceutical preparation for the treatment of rheumatoid
 CC arthritis, juvenile arthritis, multiple sclerosis, Grave's disease,
 CC insulin-dependent diabetes, narcolepsy, psoriasis, systemic lupus
 CC erythematosus, Hashimoto's disease, myasthenia gravis, pemphigus vulgaris,
 CC glomerulonephritis, thyroditis, pancreatitis, insulinitis, primary biliary
 CC cirrhosis, irritable bowel disease and Sjogren's syndrome in humans.
 CC ABA92469 to ABA92474 and ABB57457 to ABB57590 represent sequence used in
 CC the exemplification of the present invention.
 XX
 SQ Sequence 12 AA;
 Query Match 94.2%; Score 49; DB 23; Length 12;
 Best Local Similarity 91.7%; Pred. No. 0.0023;
 Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 RASOSVSSSFLA 12
 |||||
 1 RASOSVSSSYLA 12
 Db
 RESULT 8
 ABB57475
 ID ABB57475 standard; Peptide: 12 AA.
 XX
 AC ABB57475;
 XX
 XX 18-MAR-2002 (first entry)
 DT
 XX
 DE HLA-DR-specific protein VL-CDRI-Sequence MS-GPC-4.
 XX
 XX Immunomodulatory human MHC class II antigen-binding protein; HLA;
 XX human leukocyte antigen; immune system; immunosuppression; antibody;
 XX major histocompatibility complex; antirheumatic; antiarthritic;
 XX neuroprotective; antiinflammatory; antidiabetic; antipsoriatic;
 XX immunosuppressive; dermatological; antithyroid; nephroretropic; psoriasis;
 XX thyromimetic; hepatotropic; immune response suppressor; narcolepsy;
 XX rheumatoid arthritis; juvenile arthritis; multiple sclerosis; insulinitis;
 XX Grave's disease; insulin-dependent diabetes; Hashimoto's disease;
 XX systemic lupus erythematosus; ankylosing spondylitis; myasthenia gravis;
 XX transplant rejection; graft versus host disease; pemphigus vulgaris;
 XX glomerulonephritis; thyroditis; pancreatitis; primary biliary cirrhosis;
 XX irritable bowel disease; Sjogren's syndrome.
 XX
 OS Homo sapiens.

OS Synthetic.
 XX
 XX W0200187338-A1.
 XX
 XX 22-NOV-2001.
 PD
 XX
 XX 14-MAY-2001; 2001WO-US15626.
 PF
 XX 12-MAY-2000; 2000EP-0110663.
 PR 06-OCT-2000; 2000US-238762P.
 XX
 PA (GPCB-) GPC BIOTEC AG.
 PA (MORP-) MORPHOSYS AG.
 PI Nagy Z, Tesar M, Thomassen-Wolf E;
 XX WPI; 2002-075289/10.
 DR
 XX
 XX
 PT Composition for suppressing immune response, treating diseases of
 PT immune system, has polypeptide comprising antibody-based
 PT antigen-binding domain of human composition, which binds antigen
 PT expressed on a cell surface
 XX
 PS Example; Page 60; 139pp; English.
 CC The present invention describes a composition (I), comprising a
 CC polypeptide comprising an antibody-based antigen-binding domain of human
 CC composition with binding specificity for an antigen expressed on the
 CC surface of a cell, where treating cells expressing the antigen with the
 CC polypeptides leads to suppression of an immune response, and the IC50 for
 CC the suppression of immune response is 1 microm or less. (I) has
 CC antirheumatic, antiarthritic, neuroprotective, antiinflammatory,
 CC antidiabetic, antiparalytic, immunosuppressive, dermatological,
 CC antithyroid, nephroretropic, thyromimetic and hepatotropic activities, and
 CC can be used as a suppressor of immune response. (I) is useful for
 CC suppressing activation or proliferation of a cell of the immune system,
 CC suppressing IL-2 secretion by a cell, the interaction of a cell of the
 CC immune system with another cell, immunosuppressing a patient and for
 CC killing a cell expressing an antigen, human leukocyte antigen (HLA)-DR
 CC on the surface of the cell, where neither cytotoxic entities nor
 CC immunological mechanisms are needed to cause or lead to the killing.
 CC (I) (optionally linked to cytotoxic or immunogenic agent) is useful for
 CC preparing a pharmaceutical preparation for the treatment of rheumatoid
 CC arthritis, juvenile arthritis, multiple sclerosis, Grave's disease,
 CC insulin-dependent diabetes, narcolepsy, psoriasis, systemic lupus
 CC erythematosus, ankylosing spondylitis, transplant rejection, graft versus
 CC host disease, Hashimoto's disease, myasthenia gravis, pemphigus vulgaris,
 CC glomerulonephritis, thyroditis, pancreatitis, insulinitis, primary biliary
 CC cirrhosis, irritable bowel disease and Sjogren's syndrome in humans.
 CC ABA92469 to ABA92474 and ABB57457 to ABB57590 represent sequence used in
 CC the exemplification of the present invention.
 XX
 SQ Sequence 12 AA;
 Query Match 94.2%; Score 49; DB 23; Length 12;
 Best Local Similarity 91.7%; Pred. No. 0.0023;
 Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 RASOSVSSSFLA 12
 |||||
 1 RASOSVSSSYLA 12
 Db
 RESULT 9
 ABB57480
 ID ABB57480 standard; Peptide: 12 AA.
 XX
 XX ABB57480;
 XX
 XX 18-MAR-2002 (first entry)
 DT
 XX
 DE HLA-DR-specific protein VL-CDRI-Sequence MS-GPC-6.
 XX
 XX Homo sapiens.

KW Immunomodulatory human MHC class II antigen-binding protein; HLA;
 KW human leukocyte antigen; immune system; immunosuppression; antibody;
 KW major histocompatibility complex; antirheumatic; antiarthritic;
 KW neuroprotective; antiinflammatory; antidiabetic; antipsoriatic;
 KW immunosuppressive; dermatological; antichryoid; nephrotropic; psoriasis;
 KW chryomelic; hepatotropic; immune response suppressor; narcolepsy;
 KW rheumatoid arthritis; juvenile arthritis; multiple sclerosis; insulinitis;
 KW Grave's disease; insulin-dependent diabetes; Hashimoto's disease;
 KW systemic lupus erythematosus; ankylosing spondylitis; myasthenia gravis;
 KW transplant rejection; graft versus host disease; pemphigus vulgaris;
 KW glomerulonephritis; thyroiditis; pancreatitis; primary biliary cirrhosis;
 KW irritable bowel disease; Sjogren's syndrome.
 OS Homo sapiens.
 OS Synthetic.
 XX WO200187338-A1.
 XX 22-NOV-2001.
 XX 14-MAY-2001; 2001WO-US15626.
 XX 12-MAY-2000; 2000EP-0110063.
 XX 06-OCT-2000; 2000US-238762P.
 XX (GRCB-) GPC BIOTECH AG.
 XX (MORP-) MORPHOSYS AG.
 PI Nagy Z, Tesar M, Thomassen-Wolf E;
 XX WPI; 2002-075289/10.
 DR Composition for suppressing immune response, treating diseases of
 XX immune system, has polypeptide comprising antibody-based
 PT antigen-binding domain of human composition, which binds antigen
 PT expressed on a cell surface -
 XX Example; Page 60; 139pp; English.
 PS The present invention describes a composition (I), comprising a
 XX polypeptide comprising an antibody-based antigen-binding domain of human
 CC composition with binding specificity for an antigen expressed on the
 CC surface of a cell, where treating cells expressing the antigen with the
 CC polypeptides leads to suppression of an immune response, and the IC50 for
 CC the suppression of immune response is 1 microm or less. (I) has
 CC antineumatic, antiarthritic, neuroprotective, antinflammatory,
 CC antidiabetic, antipsoriatic, immunosuppressive, dermatological,
 CC antichryoid, nephrotropic, thyromelic and hepatotropic activities, and
 CC can be used as a suppressor of immune response. (I) is useful for
 CC suppressing activation or proliferation of a cell of the immune system,
 CC immune system with another cell, the interaction of a cell of the
 CC killing a cell expressing an antigen, human leukocyte antigen (HLA)-DR
 CC on the surface of the cell, where neither cytotoxic entities nor
 CC immunological mechanisms are needed to cause or lead to the killing.
 CC (I) optionally linked to cytotoxic or immunogenic agent is useful for
 CC preparing a pharmaceutical preparation for the treatment of rheumatoid
 CC arthritis, juvenile arthritis, multiple sclerosis, Grave's disease,
 CC insulin-dependent diabetes, narcolepsy, psoriasis, systemic lupus
 CC erythematosus, ankylosing spondylitis, transplant rejection, graft versus
 CC host disease, Hashimoto's disease, myasthenia gravis, pemphigus vulgaris,
 CC glomerulonephritis, thyroiditis, pancreatitis, insulinitis, primary biliary
 CC cirrhosis, irritable bowel disease, and Sjogren's syndrome in humans.
 CC ABA94469 to ABA92474 and ABB57457 to ABB57590 represent sequence used in
 CC the exemplification of the present invention.
 XX Sequence 12 AA;
 SO Query Match 94.2%; Score 49; DB 23; Length 12;
 Best Local Similarity 91.7%; Pred. No. 0.0023;
 Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 1 RASQSVSSSFLA 12

DB 1 RASQSVSSSYLA 12
 RESULT 10
 ID AAU70331 standard; Peptide: 12 AA.
 AC AAU70331;
 XX 14-FEB-2002 (first entry)
 DT Human Kappa III light chain CDR1.
 DE Immunoglobulin; antibody; light chain; heavy chain; CDR; FR;
 KW complementarity determining region; framework region; IGBP;
 KW transgenic plant; immunoglobulin binding protein array;
 KW IGM; IGA; IGD; IGE; IGY; IGM; kappa; lambda; CHBP.
 XX Homo sapiens.
 OS WO200183806-A1.
 XX 08-NOV-2001.
 XX 02-MAY-2001; 2001WO-US14349.
 XX 02-MAY-2000; 2000US-0563222.
 XX (EPIC-) EPICYTE PHARM INC.
 PA Hiatt AC, Hein MB;
 PI WPI; 2002-055482/07.
 DR Preparing immunoglobulin binding protein array in plant cells by
 XX transforming the cells with different polynucleotides encoding binding
 PT protein polypeptides specific to ligand, selecting plant cells for
 PT preparing array -
 XX Disclosure; Page 14; 129pp; English.
 PS The invention relates to transforming a population of cells (e.g. plant
 CC cells), comprising using a library of two different polynucleotides
 CC encoding different immunoglobulin binding protein (IGBP) polypeptides
 CC that specifically bind to a ligand or form one or more disulphide bonds
 CC with polypeptides in transfected cells, to generate an IGBP that
 CC binds to a ligand, and transformed plant cells are selected, and
 CC preparing an IGBP array in plant cells. At least one peptide sequence has
 CC at least 75% sequence identity to a framework region (FR) of a native
 CC IGM, IGA, IGD, IGE, IGY, kappa or lambda immunoglobulin molecule.
 CC The method is useful for preparing an immunoglobulin binding protein
 CC array, preferably heavy chain binding protein (CHBP) array in eukaryotic
 CC cells especially plant cells (e.g. Agrobacterium tumefaciens or maize)
 CC or other eukaryotic cells (e.g. insect cells or mammalian cells). The
 CC CHBP is useful for discovery of e.g. screening assays of IGBPs having
 CC desired characteristics. The present sequence is a mammalian
 CC immunoglobulin derived peptide that may be incorporated into an IGBP of
 CC the invention.
 XX Sequence 12 AA;
 SO Query Match 94.2%; Score 49; DB 23; Length 12;
 Best Local Similarity 91.7%; Pred. No. 0.0023;
 Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 1 RASQSVSSSYLA 12
 RESULT 11
 ABB07181

ID ABB07181 standard; Protein; 101 AA.
 AC ABB07181;
 DT 13-MAR-2002 (first entry)
 DE CB2IE12 kappa chain variable region.
 KM Neuromodulatory; central nervous system; CNS; eHIGM22; LYM 22; AKR4;
 KM eBVH1GM Me119D10; eBV H1GM CB2DG8; CB2IE12; MS119E5; virucide;
 KM antiParkinsonian; neuroprotective; nootropic; vulnerary.
 OS Homo sapiens.
 XX MO200185797-A1.
 XX
 XX PD 15-NOV-2001.
 XX PF 30-MAY-2000; 2000MO-US14902.
 XX PR 10-MAY-2000; 2000US-0568351.
 XX
 XX (MAYO-) MAYO FOUND MEDICAL EDUCATION RES.
 XX
 XX PI Rodriguez M, Miller DJ, Pease LR;
 XX WPI; 2002-066596/09.
 XX N-PSDB; ABA94228.
 XX
 XX Novel neuromodulatory agent (a human IGM monoclonal antibody),
 PT promoting neurite outgrowth, regeneration, remyelination and
 PT post-infectious encephalomyelitis -
 XX
 XX Claim 24; Fig 40; 219pp; English.
 XX
 CC The invention provides a neuromodulatory agent (I) capable of promoting
 CC neurite outgrowth, regeneration, remyelination and neuroprotection in
 CC central nervous system (CNS). (I) is capable of inducing remyelination,
 CC promoting cellular proliferation of glial cells, and promoting Ca2+
 CC signaling with oligodendrocytes. An humanized antibody to (I) can be
 CC selected from antibody SHIGM22 (LYM 22), eBVH1GM Me119D10, eBV H1GM
 CC CB2DG8, AKR4, CB2IE12, CB2IE7 or MS119E5. (I) is useful for stimulating
 CC remyelination of CNS axons, stimulating proliferation of glial cells in
 CC CNS axons, or treating demyelinating disease of CNS in a mammal in need
 CC of such therapy. (I) is capable of binding to structures and cells within
 CC CNS. (I) is preferably useful for treating a demyelinating disease of CNS
 CC of a mouse infected with Strain DA of Theiler's murine encephalomyelitis
 CC (TMEV) or for treating a human being having multiple sclerosis, or a
 CC human or domestic animal with a viral demyelinating disease, or a post-
 CC neural disease of CNS. (I) is also useful for an in vitro method of
 CC stimulating the proliferation of glial cells from mixed cell culture.
 CC (I) is also useful for stimulating remyelination of CNS axons. The
 CC antibodies are useful for preventing infection by a bacterium, virus or
 CC like pathogen that causes demyelination or other neurodegenerative
 CC condition in a subject. Methods where (I) is administered to a patient
 CC are useful for treating multiple sclerosis, Parkinson's disease,
 CC Alzheimer's disease, amyotrophic lateral sclerosis (ALS), a viral
 CC demyelinating disease, CNS diseases, and other conditions in the CNS
 CC where nerves are damaged as by trauma. The present sequence represents
 CC the CB2IE12 kappa chain variable region.
 XX
 XX SQ Sequence 101 AA;

Query Match 94.2%; Score 49; DB 23; Length 101;
 Best Local Similarity 91.7%; Pred. No. 0.025; 0; Indels 0; Gaps 0;
 Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 RASQSVSSSFLA 12
 |||||
 DB 24 RASQSVSSSYLA 35

RESULT 12
 ID AAR54314
 AC AAR54314 standard; Protein; 105 AA.
 XX
 XX AC AAR54314;
 XX
 XX DT 10-NOV-1994 (first entry)
 XX
 DE Anti-HIV gp120 immunoglobulin light chain variable region 55.
 KM Human immunodeficiency virus; HIV1; glycoprotein gp120; epitope;
 KM neutralisation; monoclonal antibody; kappa light chain;
 KM variable region; framework; complementarity determining region.
 XX
 XX OS Homo sapiens.
 XX
 XX Key Location/Qualifiers
 XX FH 1..18
 XX FT Region /label= FR1
 XX FT 19..30 /label= CDR1
 XX FT Region 31..45 /label= FR2
 XX FT 46..52 /label= CDR2
 XX FT Region 53..84 /label= FR3
 XX FT 85..94 /label= CDR3
 XX FT Region 95..105 /label= FR4
 XX
 XX W09407922-A.
 XX
 XX PD 14-APR-1994.
 XX
 XX PF 30-SEP-1993; 93MO-US09328.
 XX PR 30-SEP-1992; 92US-0954148.
 XX PA (SCRI) SCRIPPS RES INST.
 XX PI Barbas CF, Burton DR, Lerner RA;
 XX WPI; 1994-135516/16.
 XX
 XX New human monoclonal antibodies neutralising HIV - react with
 XX gp120 or gp41 and nucleic acid encoding them, useful for in vivo
 XX or in vitro diagnosis and for passive immuno-therapy
 XX
 XX Example; Page 182; 248pp; English.
 XX
 CC Lymphocyte mRNA was converted to cDNA and subjected to PCR
 CC amplification using primers specific for heavy and light chain
 CC variable regions. The amplification products were inserted into a
 CC dicistronic vector to produce a library of fragments. E.coli XL1
 CC blue cells were transformed with the library. Filamentous phage were
 CC produced which expressed the Mab regions on their surface. Panning
 CC with gp120 and gp41 resulted in the recovery of immunoreactive
 CC clones. The light chain VK region sequence AAR54314 is from a gp120-
 CC specific clone.
 XX
 XX SQ Sequence 105 AA;

Query Match 94.2%; Score 49; DB 15; Length 105;
 Best Local Similarity 91.7%; Pred. No. 0.027; 0; Indels 0; Gaps 0;
 Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 RASQSVSSSFLA 12
 |||||
 DB 19 RASQSLSSSFLA 30

RESULT 13

AAW01272 standard; Protein; 105 AA.

XX AAW01272;

XX 28-JAN-1997 (first entry)

XX VL region of HIV neutralising Mab, clone s5.

XX Heavy chain, light chain, variable region; VH; monoclonal antibody;
 KW Mab; HIV; human immunodeficiency virus; glycoprotein; gp120; clone;
 KM virus infectivity assay; precursor gp160; immunocompetence; human;
 XX anti-HIV antibody; detection; HIV infection.

OS Homo sapiens.

XX Key Location/Qualifiers

XX Region 1..18 /label= FR1

XX Region 19..30 /label= FR1

XX Region 31..45 /label= CDRI

XX Region 46..52 /label= FR2

XX Region 53..84 /label= CDR2

XX Region 85..94 /label= FR3

XX Region 95..105 /label= CDR3

XX Region /label= FR4

XX W09602273-A1.

XX 01-FEB-1996.

XX 11-JUL-1995; 95WO-US08743.

XX 18-JUL-1994; 94US-0276852.

XX (SCRI) SCRIPPS RES INST.

XX Barbas CF, Burton DR, Lerner RA;

XX MPI; 1996-179601/18.

XX Monoclonal antibody binding to VI/V2 loop of HIV gp120 - used in

XX passive immunotherapy and detection of HIV infection.

XX Example; Fig 11; 366pp; English.

XX The sequences given in AAW01261-92 represent the light chain variable
 CC regions (VL) of a series of monoclonal antibodies (Mab's) which are
 CC immunoreactive with HIV glycoprotein gp120 and are capable of
 CC neutralising HIV. This sequence represents the sequence of the JX2
 CC gene clone, s5. A Mab containing this VL sequence has the capacity
 CC to reduce HIV infectivity titre in an in vivo virus infectivity assay
 CC by 50 % at a concentration of less than 700 ng of antibody/ml, and
 CC binds mature gp120 preferentially over the precursor gp160. The Mab
 CC may be used for determining immunocompetence of a human anti-HIV
 CC antibody and in the detection of HIV infection.

XX Sequence 105 AA;

XX Query Match 94.2%; Score 49; DB 17; Length 105;

XX Best Local Similarity 91.7%; Pred. No. 0.027; Mismatches 0; Indels 0; Gaps 0;

XX Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

XX 1 RASQVSSSFLA 12

XX 19 RASQSLSSSFLA 30

RESULT 14

AAV95124 standard; Protein; 105 AA.

XX AAV95124;

XX 30-JUN-2000 (first entry)

XX Anti-gp120 antibody light chain variable region from clone s5.

XX Anti-human immunodeficiency virus type 1 antibody; HIV-1; neutralise;
 KW reduce HIV infection; diagnosis; immunotherapy; HIV induced disease;
 KM glycoprotein 120; gp120; glycoprotein 41; gp41; monoclonal antibody.

OS Homo sapiens.

XX Key Location/Qualifiers

XX Region 1..18 /label= FR1

XX Region 19..30 /label= FR1

XX Region 31..45 /label= CDRI

XX Region 46..52 /label= FR2

XX Region 53..84 /label= CDR2

XX Region 85..94 /label= FR3

XX Region 95..105 /label= CDR3

XX Region /label= FR4

XX WPI; 2000-293393/26.

XX 16-SEP-1999; 99AU-0048756.

XX 16-SEP-1999; 99AU-0048756.

XX (SCRI) SCRIPPS RES INST.

XX Burton DR, Barbas CF, Lerner RA;

XX MPI; 2000-293393/26.

XX Novel human monoclonal antibodies which immunoreact with and neutralise

XX human immunodeficiency virus useful for treating HIV infections

XX Example 9; Figure 11; 366pp; English.

XX The present sequence represents a fragment of an anti-human
 CC immunodeficiency virus type 1 (HIV-1) antibody. The invention relates to
 CC a human whole immunoglobulin (Ig) molecule which immunoreacts with HIV
 CC mature glycoprotein gp120 preferentially over HIV precursor glycoprotein
 CC gp160 and neutralises HIV and which reduces HIV infectivity titre in an
 CC in vitro virus infectivity assay by 50%, at a concentration of less than
 CC 700 ng/ml. The antibodies are used as reagents for the diagnosis and
 CC immunotherapy of HIV induced disease. They are useful as neutralising
 CC field isolates and provide useful information regarding the
 CC immunocompetence of an immune response in HIV infected patients. The
 CC monoclonal antibodies are useful for producing anti-idiotypic antibodies
 CC which can be used to screen human monoclonal antibodies to identify
 CC whether the antibody has the same binding specificity as the antibodies
 CC of the invention. The neutralising antibodies define new epitopes on the
 CC HIV gp120 and gp41 glycoproteins, thus increasing the availability of new
 CC immunotherapeutic human monoclonal antibodies. A major advantage of the
 CC monoclonal antibodies derives from the fact that they are encoded by a
 CC human polynucleotide sequence. Thus in vivo use of the monoclonal
 CC antibodies for diagnosis and immunotherapy of HIV induced disease greatly
 CC reduces the problems of significant host immune response to the passively
 CC administered antibodies which is a problem commonly encountered when
 CC monoclonal antibodies of xenogeneic or chimeric derivation are utilized.
 CC An additional major advantage of the monoclonal antibodies described
 CC derives from the fact that they immunoreact with a unique determinant
 CC present on mature HIV glycoprotein gp120. This class of antibodies is
 CC particularly effective at neutralising field isolates of HIV.

XX Sequence 105 AA;

XX Query Match 94.2%; Score 49; DB 21; Length 105;

XX Best Local Similarity 91.7%; Pred. No. 0.027; Mismatches 0; Indels 0; Gaps 0;

XX Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

XX 1 RASQVSSSFLA 12

XX 19 RASQSLSSSFLA 30

RESULT 15
AA98233 ID AAY98233 standard. Protein; 105 AA.
AC AAY98233;
DT 04-JUL-2000 (first entry)
DE Anti-gp120 antibody light chain variable region from clone 85.
KW Antibody; anti-HIV monoclonal antibody; glycoprotein-120;
KW human immunodeficiency virus type 1; HIV-1; infectivity titre;
KW passive immunotherapy; reduce severity; HIV-induced disease;
KW immunocompetence; active immunisation.
OS Homo sapiens.
PN AU9948754-A.
PD 17-FEB-2000.
PF 16-SEP-1999; 99AU-0048754.
PR 16-SEP-1999; 99AU-0048754.
RA (SCRI) SCRIPPS RES INST.
PI Burton DR, Barbas CF, Lerner RA;
PI WFI, 2000-246867/22.
PT Human neutralizing monoclonal antibodies to human immunodeficiency
PT virus (HIV) used for providing passive immunotherapy to HIV are
PT specific for glycoprotein-120 -
PS Example 9; Figure 11; 374pp; English.
XX This sequence represents a fragment of the antibodies of the invention.
XX The invention relates to the production of an anti-HIV (human
XX immunodeficiency virus) glycoprotein (gp)-120 monoclonal antibody
XX capable of reducing an HIV infectivity titre in an in vitro virus
XX infectivity assay by 50% at a concentration of less than 70 ng/ml. The
XX method for the production of the antibody comprises:
XX (a) providing a first polynucleotide encoding a heavy chain
XX immunoglobulin amino acid sequence (which does not comprise the sequence
XX represented by AAY98206) and a second polynucleotide encoding a light
XX chain immunoglobulin amino acid sequence;
XX (b) inserting the first and second polynucleotide sequences into a host
XX cell;
XX (c) maintaining the host cell in conditions which allow the amino acid
XX sequences encoded by the polynucleotides to be expressed in the host
XX cell; and
XX (d) isolating the antibody comprising the heavy and light chain
XX immunoglobulin amino acid sequences from the host cell.
XX The anti-HIV gp-120 monoclonal antibody is used for providing passive
XX immunotherapy to HIV in a human. They can be administered to high-risk
XX patients to reduce the likelihood and/or severity of HIV-induced disease
XX and to patients who are already HIV-infected. The antibodies are used
XX for neutralising field isolates which provides information about the
XX immunocompetence of an immune response in HIV patients, for detecting
XX HIV in a biological fluid or tissue sample e.g. by radioimmunoassay, for
XX producing anti-idiotypic antibodies which can be used for active
XX immunisation and to screen human monoclonal antibodies to identify those
XX with the same binding specificity and to monitor the course of HIV
XX disease therapy by measuring the changes in concentration of HIV present
XX in the body or in body fluids by immunoassay. The anti-HIV gp-120
XX monoclonal antibodies are encoded by a human polynucleotide sequence and
XX when used in vivo for diagnosis and immunotherapy of HIV-induced disease
XX reduce the problems of significant host immune response to the
XX antibodies associated with monoclonal antibodies of xenogeneic or
XX chimeric derivation.

SQ Sequence 105 AA;
Query Match 94.2%; Score 49; DB 21; Length 105;
Best Local Similarity 91.7%; Pred. No. 0.027;
Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 RASQSVSSSFLA 12
|||:|||||
DB 19 RASQSVSSSFLA 30
Search completed: June 3, 2003, 08:14:49
Job time : 6.40614 secs

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OM protein - protein search, using sw model

Run on: June 3, 2003, 08:21:07 ; Search time 2.84642 Seconds

(without alignments)
426.742 Million cell updates/sec

Title: US-09-644-668a-25

Perfect score: 52

Sequence: 1 RASQSVSSFLA 12

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 383519 seqs, 101223694 residues

Total number of hits satisfying chosen parameters: 383519

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:*

- 1: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
- 2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
- 4: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
- 5: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
- 6: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
- 7: /cgn2_6/ptodata/1/pubpaa/PCTIS_PUBCOMB.pep.*
- 8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
- 9: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
- 10: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep.*
- 11: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
- 12: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep.*
- 13: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
- 14: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	51	98.1	141	9	US-10-153-382-23
2	51	98.1	235	9	US-10-153-382-7
3	49	94.2	12	9	US-10-001-934-62
4	49	94.2	12	9	US-09-563-222-11
5	49	94.2	12	10	US-09-828-708-38
6	49	94.2	12	10	US-09-828-708-40
7	49	94.2	12	10	US-09-828-708-41
8	49	94.2	12	10	US-09-828-708-42
9	49	94.2	74	9	US-10-125-687-23
10	49	94.2	96	9	US-10-025-687-23
11	49	94.2	96	9	US-10-153-382-22
12	49	94.2	104	10	US-09-828-708-6
13	49	94.2	104	10	US-09-828-708-5
14	49	94.2	105	10	US-09-828-708-7
15	49	94.2	105	10	US-09-828-708-8
16	49	94.2	108	9	US-09-300-425B-11
17	49	94.2	109	9	US-10-125-687-10
18	49	94.2	109	9	US-10-073-644C-8

20	49	94.2	109	12	US-10-025-687-10	Sequence 10, Appl
21	49	94.2	110	9	US-10-001-934-40	Sequence 40, Appl
22	49	94.2	150	9	US-09-782-397-5	Sequence 5, Appl
23	49	94.2	224	9	US-09-453-234-40	Sequence 40, Appl
24	49	94.2	224	9	US-09-453-234-52	Sequence 52, Appl
25	49	94.2	224	9	US-09-453-234-76	Sequence 76, Appl
26	49	94.2	226	9	US-09-453-234-38	Sequence 38, Appl
27	49	94.2	226	9	US-09-453-234-42	Sequence 42, Appl
28	49	94.2	226	9	US-09-453-234-50	Sequence 50, Appl
29	49	94.2	226	9	US-09-453-234-80	Sequence 80, Appl
30	49	94.2	226	9	US-09-453-234-86	Sequence 86, Appl
31	49	94.2	241	9	US-09-880-748-1264	Sequence 1264, Ap
32	49	94.2	251	9	US-09-880-748-1219	Sequence 1219, Ap
33	49	94.2	252	9	US-09-880-748-1534	Sequence 1534, Ap
34	49	94.2	287	9	US-09-782-397-17	Sequence 17, Appl
35	49	94.2	304	9	US-09-782-397-14	Sequence 14, Appl
36	48	92.3	108	9	US-09-848-798-178	Sequence 178, Appl
37	48	92.3	142	9	US-10-153-382-27	Sequence 27, Appl
38	46	88.5	96	9	US-10-194-975-88	Sequence 88, Appl
39	46	88.5	107	8	US-08-844-215-8	Sequence 8, Appl
40	46	88.5	224	9	US-09-453-234-44	Sequence 44, Appl
41	46	88.5	224	9	US-09-453-234-78	Sequence 78, Appl
42	46	88.5	249	9	US-09-880-748-1035	Sequence 1035, Ap
43	45	86.5	226	9	US-09-453-234-72	Sequence 72, Appl
44	45	86.5	226	9	US-09-453-234-74	Sequence 74, Appl
45	44	84.6	96	9	US-10-194-975-83	Sequence 83, Appl

ALIGNMENTS

RESULT 1
US-10-153-382-23
; Sequence 23, Application US/10153382
; Publication No. US20030086930A1
; GENERAL INFORMATION:
; APPLICANT: PRIZER PRODUCTS INC.
; TITLE OF INVENTION: USES OF ANTI-CTLA-4 ANTIBODIES
; FILE REFERENCE: PC23019A
; CURRENT APPLICATION NUMBER: US/10/153,382
; CURRENT FILING DATE: 2002-05-22
; PRIOR APPLICATION NUMBER: 60/293042
; PRIOR FILING DATE: 2001-05-23
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 23
; LENGTH: 141
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-153-382-23

Query Match 98.1%, Score 51, DB 9, Length 141,
Best Local Similarity 91.7%, Pred. No. 0.035,
Matches 11, Conservative 1, Mismatches 0, Indels 0, Gaps 0;

QY 1 RASQSVSSFLA 12
|||||
Db 19 RASQSVSSFLA 30

RESULT 2
US-10-153-382-7
; Sequence 7, Application US/10153382
; Publication No. US20030086930A1
; GENERAL INFORMATION:
; APPLICANT: PRIZER PRODUCTS INC.
; TITLE OF INVENTION: USES OF ANTI-CTLA-4 ANTIBODIES
; FILE REFERENCE: PC23019A
; CURRENT APPLICATION NUMBER: US/10/153,382
; CURRENT FILING DATE: 2002-05-22
; PRIOR APPLICATION NUMBER: 60/293042
; PRIOR FILING DATE: 2001-05-23
; NUMBER OF SEQ ID NOS: 39

SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 7
LENGTH: 235
TYPE: PRT
ORGANISM: Homo sapiens
US-10-153-382-7

Query Match
Best Local Similarity 98.1%; Score 51; DB 9; Length 235;
Best Local Similarity 91.7%; Pred. No. 0.059;
Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RASQSVSSSFLA 12
|||||:
Db 44 RASQSVSSSFLA 55

RESULT 3
US-10-001-934-62
Sequence 62, Application US/10001934
Publication No. US20030032782A1
GENERAL INFORMATION:
APPLICANT: NAGY, ZOLTAN
TITLE OF INVENTION: HUMAN PEPTIDES/PROTEINS CAUSING OR LEADING TO THE
KILLING OF CELLS INCLUDING LYMPHOID TUMOR CELLS
FILE REFERENCE: GPCG-P01-003
CURRENT APPLICATION NUMBER: US/10/001,934
CURRENT FILING DATE: 2001-11-15
NUMBER OF SEQ ID NOS: 63
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 62
LENGTH: 12
TYPE: PRT
ORGANISM: Homo sapiens
US-10-001-934-62

Query Match
Best Local Similarity 94.2%; Score 49; DB 9; Length 12;
Best Local Similarity 91.7%; Pred. No. 0.0059;
Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RASQSVSSSFLA 12
|||||:
Db 1 RASQSVSSSFLA 12

RESULT 4
US-09-563-222-11
Sequence 11, Application US/09563222
Publication No. US20030079253A1
GENERAL INFORMATION:
APPLICANT: Hehn, Mich B.
TITLE OF INVENTION: IMMUNOGLOBULIN BINDING PROTEIN ARRAYS IN
FILE REFERENCE: 31038.406
CURRENT APPLICATION NUMBER: US/09/563,222
CURRENT FILING DATE: 2000-05-02
NUMBER OF SEQ ID NOS: 197
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 11
LENGTH: 12
TYPE: PRT
ORGANISM: Homo sapiens
US-09-563-222-11

Query Match
Best Local Similarity 94.2%; Score 49; DB 9; Length 12;
Best Local Similarity 91.7%; Pred. No. 0.0059;
Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RASQSVSSSFLA 12
|||||:
Db 1 RASQSVSSSFLA 12

RESULT 5
US-09-828-708-38
Sequence 38, Application US/09828708
Patent No. US20020146753A1
GENERAL INFORMATION:
APPLICANT: Ditzel, H.
APPLICANT: Burton, D.
APPLICANT: Schaller, M.
TITLE OF INVENTION: Autoantibodies to glucose-6-phosphate isomerase and their pa
FILE REFERENCE: 1361.005051
CURRENT APPLICATION NUMBER: US/09/828,708
CURRENT FILING DATE: 2001-09-24
NUMBER OF SEQ ID NOS: 123
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 38
LENGTH: 12
TYPE: PRT
ORGANISM: Homo sapiens
US-09-828-708-38

Query Match
Best Local Similarity 94.2%; Score 49; DB 10; Length 12;
Best Local Similarity 91.7%; Pred. No. 0.0059;
Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RASQSVSSSFLA 12
|||||:
Db 1 RASQSVSSSFLA 12

RESULT 6
US-09-828-708-40
Sequence 40, Application US/09828708
Patent No. US20020146753A1
GENERAL INFORMATION:
APPLICANT: Ditzel, H.
APPLICANT: Burton, D.
APPLICANT: Schaller, M.
TITLE OF INVENTION: Autoantibodies to glucose-6-phosphate isomerase and their pa
FILE REFERENCE: 1361.005051
CURRENT APPLICATION NUMBER: US/09/828,708
CURRENT FILING DATE: 2001-09-24
NUMBER OF SEQ ID NOS: 123
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 40
LENGTH: 12
TYPE: PRT
ORGANISM: Homo sapiens
US-09-828-708-40

Query Match
Best Local Similarity 94.2%; Score 49; DB 10; Length 12;
Best Local Similarity 91.7%; Pred. No. 0.0059;
Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RASQSVSSSFLA 12
|||||:
Db 1 RASQSVSSSFLA 12

RESULT 7
US-09-828-708-41
Sequence 41, Application US/09828708
Patent No. US20020146753A1
GENERAL INFORMATION:
APPLICANT: Ditzel, H.
APPLICANT: Burton, D.
APPLICANT: Schaller, M.
TITLE OF INVENTION: Autoantibodies to glucose-6-phosphate isomerase and their pa
FILE REFERENCE: 1361.005051
CURRENT APPLICATION NUMBER: US/09/828,708
CURRENT FILING DATE: 2001-09-24

NUMBER OF SEQ ID NOS: 123
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 41
LENGTH: 12
TYPE: PRT
ORGANISM: Homo sapiens
US-09-828-708-41

Query Match 94.2%; Score 49; DB 10; Length 12;
Best Local Similarity 91.7%; Pred. No. 0.0059;
Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RASQSVSSFLA 12
|||
1 RASQSVSSSTYLA 12

RESULT 8

US-09-828-708-42
Sequence 42, Application US/09828708
Patent No. US20020146753A1
GENERAL INFORMATION:
APPLICANT: Dizziel, H.
APPLICANT: Burton, D.
APPLICANT: Schaller, M.

TITLE OF INVENTION: Autoantibodies to glucose-6-phosphate isomerase and their particl
FILE REFERENCE: 1361.005051
CURRENT APPLICATION NUMBER: US/09/828,708
CURRENT FILING DATE: 2001-09-24
NUMBER OF SEQ ID NOS: 123
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 42
LENGTH: 12
TYPE: PRT
ORGANISM: Homo sapiens
US-09-828-708-42

Query Match 94.2%; Score 49; DB 10; Length 12;
Best Local Similarity 91.7%; Pred. No. 0.0059;
Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RASQSVSSFLA 12
|||
1 RASQSVSSSTYLA 12

RESULT 9

US-10-125-687-23
Sequence 23, Application US/10125687
Publication No. US20030054407A1
GENERAL INFORMATION:
APPLICANT: Luo, Peter

TITLE OF INVENTION: STRUCTURE-BASED CONSTRUCTION OF HUMAN ANTIBODY LIBRARY
FILE REFERENCE: 26050-705
CURRENT APPLICATION NUMBER: US/10/125,687
CURRENT FILING DATE: 2002-04-17
NUMBER OF SEQ ID NOS: 28
SOFTWARE: PatentIn version 3.1
SEQ ID NO 23
LENGTH: 74
TYPE: PRT
ORGANISM: Homo sapiens
US-10-125-687-23

Query Match 94.2%; Score 49; DB 9; Length 74;
Best Local Similarity 91.7%; Pred. No. 0.041;
Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RASQSVSSFLA 12
|||
17 RASQSVSSSTYLA 28

RESULT 10
US-10-025-687-23
Sequence 23, Application US/10025687
Patent No. US20020142255A1
GENERAL INFORMATION:
APPLICANT: Luo, Peter

TITLE OF INVENTION: STRUCTURE-BASED CONSTRUCTION OF HUMAN ANTIBODY LIBRARY
FILE REFERENCE: 26050-705
CURRENT APPLICATION NUMBER: US/10/025,687
CURRENT FILING DATE: 2002-04-17
NUMBER OF SEQ ID NOS: 28
SOFTWARE: PatentIn version 3.1
SEQ ID NO 23
LENGTH: 74
TYPE: PRT
ORGANISM: Homo sapiens
US-10-025-687-23

Query Match 94.2%; Score 49; DB 12; Length 74;
Best Local Similarity 91.7%; Pred. No. 0.041;
Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RASQSVSSFLA 12
|||
17 RASQSVSSSTYLA 28

RESULT 11

US-10-194-975-82
Sequence 82, Application US/10194975
Publication No. US2003039649A1
GENERAL INFORMATION:
APPLICANT: Foote, Jefferson

TITLE OF INVENTION: Super Humanized Antibodies
FILE REFERENCE: 501231.01
CURRENT APPLICATION NUMBER: US/10/194,975
CURRENT FILING DATE: 2002-10-10
PRIOR APPLICATION NUMBER: US 60/305,111
PRIOR FILING DATE: 2001-07-12
NUMBER OF SEQ ID NOS: 122
SOFTWARE: PatentIn version 3.1
SEQ ID NO 82
LENGTH: 96
TYPE: PRT
ORGANISM: Homo sapiens
US-10-194-975-82

Query Match 94.2%; Score 49; DB 9; Length 96;
Best Local Similarity 91.7%; Pred. No. 0.054;
Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RASQSVSSFLA 12
|||
24 RASQSVSSSTYLA 35

RESULT 12

US-10-153-382-22
Sequence 22, Application US/10153382
Publication No. US20030086930A1
GENERAL INFORMATION:
APPLICANT: Pfizer Products Inc.

TITLE OF INVENTION: USES OF ANTI-CTLA-4 ANTIBODIES
FILE REFERENCE: PC23019A
CURRENT APPLICATION NUMBER: US/10/153,382
CURRENT FILING DATE: 2002-05-22
PRIOR APPLICATION NUMBER: 60/293042
PRIOR FILING DATE: 2001-05-23
NUMBER OF SEQ ID NOS: 39
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 22
LENGTH: 96

Query Match 94.2%; Score 49; DB 9; Length 96;
Best Local Similarity 91.7%; Pred. No. 0.054;
Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

TYPE: PRT
ORGANISM: Homo sapiens
US-10-153-382-22

Query Match: 94.2% Score 49; DB 9; Length 96;
Best Local Similarity 91.7% Pred. No. 0.054;
Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RASQSVSSSFLA 12
|||||:
Db 24 RASQSVSSSYLA 35

RESULT 13
US-09-828-708-6
Sequence 6, Application US/09828708
Patent No. US20020146753A1
GENERAL INFORMATION:
APPLICANT: Ditzel, H.
APPLICANT: Burton, D.
APPLICANT: Schaller, M.
TITLE OF INVENTION: Autoantibodies to glucose-6-phosphate isomerase and their particl
FILE REFERENCE: 1361.005US1
CURRENT APPLICATION NUMBER: US/09/828,708
CURRENT FILING DATE: 2001-09-24
NUMBER OF SEQ ID NOS: 123
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 6
LENGTH: 104
TYPE: PRT
ORGANISM: Homo sapiens
US-09-828-708-6

Query Match: 94.2% Score 49; DB 10; Length 104;
Best Local Similarity 91.7% Pred. No. 0.058;
Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RASQSVSSSFLA 12
|||||:
Db 17 RASQSVSSSYLA 28

RESULT 14
US-09-828-708-3
Sequence 3, Application US/09828708
Patent No. US20020146753A1
GENERAL INFORMATION:
APPLICANT: Ditzel, H.
APPLICANT: Burton, D.
APPLICANT: Schaller, M.
TITLE OF INVENTION: Autoantibodies to glucose-6-phosphate isomerase and their particl
FILE REFERENCE: 1361.005US1
CURRENT APPLICATION NUMBER: US/09/828,708
CURRENT FILING DATE: 2001-09-24
NUMBER OF SEQ ID NOS: 123
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 3
LENGTH: 105
TYPE: PRT
ORGANISM: Homo sapiens
US-09-828-708-3

Query Match: 94.2% Score 49; DB 10; Length 105;
Best Local Similarity 91.7% Pred. No. 0.059;
Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RASQSVSSSFLA 12
|||||:
Db 17 RASQSVSSSYLA 28

RESULT 15
US-09-828-708-5
Sequence 5, Application US/09828708
Patent No. US20020146753A1
GENERAL INFORMATION:
APPLICANT: Ditzel, H.
APPLICANT: Burton, D.
APPLICANT: Schaller, M.
TITLE OF INVENTION: Autoantibodies to glucose-6-phosphate isomerase and their pa
FILE REFERENCE: 1361.005US1
CURRENT APPLICATION NUMBER: US/09/828,708
CURRENT FILING DATE: 2001-09-24
NUMBER OF SEQ ID NOS: 123
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 5
LENGTH: 105
TYPE: PRT
ORGANISM: Homo sapiens
US-09-828-708-5

Query Match: 94.2% Score 49; DB 10; Length 105;
Best Local Similarity 91.7% Pred. No. 0.059;
Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RASQSVSSSFLA 12
|||||:
Db 17 RASQSVSSSYLA 28

Search completed: June 3, 2003, 08:52:54
Job time : 2.84642 secs

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OM protein - protein search, using sw model

Run on: June 3, 2003, 08:10:19 ; Search time 1.8253 Seconds
(without alignments)
193.728 Million cell updates/sec

Title: US-09-644-668A-25
Perfect score: 52
Sequence: 1 RASQSVSSFLA 12

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: Issued Patents AA:
1: /cgn2_6/ptodata/1/1aa/5A.COMB.pep:*
2: /cgn2_6/ptodata/1/1aa/5B.COMB.pep:*
3: /cgn2_6/ptodata/1/1aa/6A.COMB.pep:*
4: /cgn2_6/ptodata/1/1aa/6B.COMB.pep:*
5: /cgn2_6/ptodata/1/1aa/PCTUS.COMB.pep:*
6: /cgn2_6/ptodata/1/1aa/backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	49	94.2	105	1	US-08-276-852-93
2	49	94.2	105	1	US-08-899-575-93
3	49	94.2	105	1	US-08-899-575-93
4	49	94.2	105	5	PCT-US95-08743-93
5	49	94.2	107	2	US-08-652-558-49
6	49	94.2	108	1	US-08-488-113B-150
7	49	94.2	108	1	US-08-477-484B-150
8	49	94.2	108	2	US-08-646-360-150
9	49	94.2	108	2	US-08-232-081B-42
10	49	94.2	108	4	US-08-839-765-150
11	49	94.2	108	4	US-09-136-389-150
12	49	94.2	108	4	US-09-610-838-150
13	49	94.2	108	4	US-09-025-769B-16
14	49	94.2	110	4	US-09-025-769B-30
15	49	94.2	110	4	US-09-025-769B-47
16	49	94.2	116	1	US-08-053-131-183
17	49	94.2	116	2	US-08-096-762-183
18	49	94.2	116	2	US-09-042-353-46
19	49	94.2	116	4	US-08-758-417A-311
20	49	94.2	150	4	US-08-862-124-5
21	49	94.2	287	4	US-08-862-124-17
22	49	94.2	304	4	US-08-862-124-14
23	49	94.2	304	4	US-09-240-274-178
24	49	94.2	304	4	US-08-276-852-147
25	49	94.2	304	4	US-08-899-575-147
26	49	94.2	304	4	US-08-899-575-147
27	49	94.2	304	4	PCT-US95-08743-147

28	45	86.5	112	1	US-08-276-852-151	Sequence 151, App
29	45	86.5	112	1	US-08-899-575-151	Sequence 151, App
30	45	86.5	112	1	US-08-899-575-151	Sequence 151, App
31	45	86.5	112	5	PCT-US95-08743-151	Sequence 151, App
32	44	84.6	104	1	US-08-276-852-94	Sequence 94, App1
33	44	84.6	104	1	US-08-899-575-94	Sequence 94, App1
34	44	84.6	104	1	US-08-899-575-94	Sequence 94, App1
35	44	84.6	104	5	PCT-US95-08743-94	Sequence 94, App1
36	44	84.6	129	2	US-08-480-774A-4	Sequence 4, App1
37	43	82.7	107	1	US-08-276-852-87	Sequence 87, App1
38	43	82.7	107	1	US-08-899-575-87	Sequence 87, App1
39	43	82.7	107	1	US-08-899-575-87	Sequence 87, App1
40	43	82.7	107	5	PCT-US95-08743-87	Sequence 87, App1
41	43	82.7	214	2	US-08-480-753-6	Sequence 6, App1
42	43	82.7	214	3	US-09-041-889-11	Sequence 11, App1
43	43	82.7	214	3	US-08-837-058-11	Sequence 11, App1
44	42	80.8	57	1	US-08-162-102C-38	Sequence 38, App1
45	42	80.8	109	1	US-08-162-102C-23	Sequence 23, App1

ALIGNMENTS

RESULT 1
US-08-276-852-93
Sequence 93, Application US/08276852
Patent No. 5652138
GENERAL INFORMATION:
APPLICANT: Burton, Dennis R
APPLICANT: Barbas, Carlos F
APPLICANT: Lerner, Richard A
TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
NUMBER OF SEQUENCES: 170
CORRESPONDENCE ADDRESS:
ADDRESS: The Scripps Research Institute, Office of
STREET: 10666 No. 5652138th Torrey Pines Road, Suite 220,
STREET: Mail Drop TPC8
CITY: La Jolla
STATE: CA
COUNTRY: USA
ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/276,852
FILING DATE: 18-JUL-1994
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/178,302
FILING DATE: 30-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/954,148
FILING DATE: 30-SEP-1992
ATTORNEY/AGENT INFORMATION:
NAME: Fitting, Thomas
REGISTRATION NUMBER: 34,163
REFERENCE/DOCKET NUMBER: SCRI452P
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-554-2937
TELEFAX: 619-554-6312
INFORMATION FOR SEQ ID NO: 93:
SEQUENCE CHARACTERISTICS:
LENGTH: 105 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-276-852-93

Query Match 94.2%; Score 49; DB 1; Length 105;
Best Local Similarity 91.7%; Pred. No. 0.014;
Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RASQSVSSSFLA 12
||||:|||||
DB 19 RASQSLSSSFLA 30

RESULT 2
US-08-899-575-93
Sequence 93, Application US/08899575
Patent No. 570440
GENERAL INFORMATION:
APPLICANT: Burton, Dennis R
APPLICANT: Bardas, Carlos F
APPLICANT: Lerner, Richard A
TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
NUMBER OF SEQUENCES: 170
CORRESPONDENCE ADDRESS:
ADDRESSEE: The Scripps Research Institute, Office of
ADDRESSEE: Patent Counsel
STREET: 10666 No. 570440th Torrey Pines Road, Suite 220,
STREET: Mail Drop TPC8
CITY: La Jolla
STATE: CA
COUNTRY: USA
ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/899,575
FILING DATE: 24-JUL-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/276,852
FILING DATE: 18-JUL-1994
APPLICATION NUMBER: US 08/178,302
FILING DATE: 30-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/954,148
FILING DATE: 30-SEP-1992
ATTORNEY/AGENT INFORMATION:
NAME: Fitting, Thomas
REGISTRATION NUMBER: 34,163
REFERENCE/DOCKET NUMBER: SCRI452P
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-554-2937
TELEFAX: 619-554-6312
INFORMATION FOR SEQ ID NO: 93:
SEQUENCE CHARACTERISTICS:
LENGTH: 105 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-899-575-93

Query Match 94.2%; Score 49; DB 1; Length 105;
Best Local Similarity 91.7%; Pred. No. 0.014;
Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RASQSVSSSFLA 12
||||:|||||
DB 19 RASQSLSSSFLA 30

RESULT 3
US-08-899-575-93
Sequence 93, Application US/08899575

Patent No. 5804440
GENERAL INFORMATION:
APPLICANT: Burton, Dennis R
APPLICANT: Bardas, Carlos F
APPLICANT: Lerner, Richard A
TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
NUMBER OF SEQUENCES: 170
CORRESPONDENCE ADDRESS:
ADDRESSEE: The Scripps Research Institute, Office of
ADDRESSEE: Patent Counsel
STREET: 10666 No. 580440th Torrey Pines Road, Suite 220,
STREET: Mail Drop TPC8
CITY: La Jolla
STATE: CA
COUNTRY: USA
ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/899,575
FILING DATE: 24-JUL-1997
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/276,852
FILING DATE: 18-JUL-1994
APPLICATION NUMBER: US 08/178,302
FILING DATE: 30-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/954,148
FILING DATE: 30-SEP-1992
ATTORNEY/AGENT INFORMATION:
NAME: Fitting, Thomas
REGISTRATION NUMBER: 34,163
REFERENCE/DOCKET NUMBER: SCRI452P
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-554-2937
TELEFAX: 619-554-6312
INFORMATION FOR SEQ ID NO: 93:
SEQUENCE CHARACTERISTICS:
LENGTH: 105 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-899-575-93

Query Match 94.2%; Score 49; DB 1; Length 105;
Best Local Similarity 91.7%; Pred. No. 0.014;
Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RASQSVSSSFLA 12
||||:|||||
DB 19 RASQSLSSSFLA 30

RESULT 4
PCT-US95-08743-93
Sequence 93, Application PC/TUS9508743
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
NUMBER OF SEQUENCES: 170
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/08743

FILING DATE: 11-JUL-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/276,852
FILING DATE: 18-JUL-1994
INFORMATION FOR SEQ ID NO: 93:
SEQUENCE CHARACTERISTICS:
LENGTH: 105 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US95-08743-93

Query Match 94.2%; Score 49; DB 5; Length 105;
Best Local Similarity 91.7%; Pred. No. 0.014;
Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RASQSVSSSFLA 12
|||:|||||
Db 19 RASQSVSSSFLA 30

RESULT 5
US-08-652-558-49
Sequence 49, Application US/08652558
Patent No. 5861155
GENERAL INFORMATION:
APPLICANT: LIN, AUGUSTINE YEE-THARN
TITLE OF INVENTION: HUMANIZED ANTIBODIES AND USES
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
ADDRESSEE: BANNER & WITCOFF
STREET: 75 STATE STREET, 23RD FLOOR
CITY: BOSTON
STATE: MASSACHUSETTS
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch diskette, 1.4 Mb storage
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect 6.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/652,558
FILING DATE: JUNE 6, 1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/IB94/00387
FILING DATE: NOVEMBER 21, 1994
ATTORNEY/AGENT INFORMATION:
NAME: YANKWICH, LEON R.
REGISTRATION NUMBER: 30,237
REFERENCE/DOCKET NUMBER: 95,497-L
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-345-9100
TELEFAX: 617-345-9111
INFORMATION FOR SEQ ID NO: 49:
SEQUENCE CHARACTERISTICS:
LENGTH: 107 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-652-558-49

Query Match 94.2%; Score 49; DB 2; Length 107;
Best Local Similarity 91.7%; Pred. No. 0.014;
Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RASQSVSSSFLA 12
|||:|||||
Db 24 RASQSVSSSFLA 35

RESULT 6
US-08-488-113B-150
Sequence 150, Application US/08488113B
Patent No. 5744580
GENERAL INFORMATION:
APPLICANT: Better, Marc D.
APPLICANT: Carroll, Stephen F.
APPLICANT: Studilka, Gary M.
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
NUMBER OF SEQUENCES: 169
CORRESPONDENCE ADDRESS:
ADDRESSEE: McAndrews, Held & Malloy, Ltd.
STREET: 500 West Madison Street, 34th floor
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60661

COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/488,113B
FILING DATE: 07-JUN-1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/425,336
FILING DATE: 18-APR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/064,691
FILING DATE: 12-MAY-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/988,430
FILING DATE: 09-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/901,707
FILING DATE: 19-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/787,567
FILING DATE: 04-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: McNicholas, Janet M.
REGISTRATION NUMBER: 32,918
REFERENCE/DOCKET NUMBER: 11022US07/200-70.P3.C2A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/707-8889
TELEFAX: 312/707-9155
TELEX: 650 388-1248
INFORMATION FOR SEQ ID NO: 150:
SEQUENCE CHARACTERISTICS:
LENGTH: 108 amino acids
TYPE: amino acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-488-113B-150

Query Match 94.2%; Score 49; DB 1; Length 108;
Best Local Similarity 91.7%; Pred. No. 0.015;
Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RASQSVSSSFLA 12
|||:|||||
Db 24 RASQSVSSSFLA 35

RESULT 7
US-08-477-484B-150
Sequence 150, Application US/08477484B
Patent No. 5756699
GENERAL INFORMATION:

APPLICANT: Better, Marc D.
APPLICANT: Carroll, Stephen F.
APPLICANT: Studnika, Gary M.
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
TITLE OF INVENTION: Proteins
NUMBER OF SEQUENCES: 169
CORRESPONDENCE ADDRESS:
ADDRESSEE: McAndrews, Held & Malloy, Ltd.
STREET: 500 West Madison Street, 34th floor
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60661
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/477,484B
FILING DATE: 07-JUN-1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/425,336
FILING DATE: 18-APR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/064,691
FILING DATE: 12-MAY-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/988,430
FILING DATE: 09-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/901,707
FILING DATE: 19-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/787,567
FILING DATE: 04-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: McNicholas, Janet M.
REGISTRATION NUMBER: 32,918
REFERENCE/DOCKET NUMBER: 11022US07/200-70.P3.C2A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/707-8889
TELEFAX: 312/707-9155
TELEX: 650 388-1248
INFORMATION FOR SEQ ID NO: 150:
SEQUENCE CHARACTERISTICS:
LENGTH: 108 amino acids
TYPE: amino acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-477-484B-150

Query Match 94.2%; Score 49; DB 1; Length 108;
Best Local Similarity 91.7%; Pred. No. 0.015;
Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RASQSVSSFLA 12
DB 24 RASQSVSSSYLA 35

RESULT 8
US-08-646-360-150
Sequence 150, Application US/08646360
Patent No. 5837491
GENERAL INFORMATION:
APPLICANT: Better, Marc D.
APPLICANT: Carroll, Stephen F.
APPLICANT: Studnika, Gary M.
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
TITLE OF INVENTION: Proteins

NUMBER OF SEQUENCES: 173
CORRESPONDENCE ADDRESS:
ADDRESSEE: McAndrews, Held & Malloy, Ltd.
STREET: 500 West Madison Street, 34th floor
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60661
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/646,360
FILING DATE: 13-MAY-1996
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/05348
FILING DATE: 12-MAY-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/064,691
FILING DATE: 12-MAY-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/988,430
FILING DATE: 09-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/901,707
FILING DATE: 19-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/787,567
FILING DATE: 04-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: McNicholas, Janet M.
REGISTRATION NUMBER: 32,918
REFERENCE/DOCKET NUMBER: 200-70.P4
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/707-8889
TELEFAX: 312/707-9155
TELEX: 650 388-1248
INFORMATION FOR SEQ ID NO: 150:
SEQUENCE CHARACTERISTICS:
LENGTH: 108 amino acids
TYPE: amino acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-646-360-150

Query Match 94.2%; Score 49; DB 2; Length 108;
Best Local Similarity 91.7%; Pred. No. 0.015;
Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RASQSVSSFLA 12
DB 24 RASQSVSSSYLA 35

RESULT 9
US-08-232-081B-42
Sequence 42, Application US/08232081B
Patent No. 5886152
GENERAL INFORMATION:
APPLICANT: NAKATANI, TOMOYUKI
APPLICANT: GOMI, HIDEYUKI
APPLICANT: WIDENES, JOHN
APPLICANT: NOGUCHI, HIROSHI
TITLE OF INVENTION: HUMANIZED B-B10
NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
ADDRESSEE: BIRCH, STEWART, KOLASCH AND BIRCH
STREET: PO BOX 747
CITY: FALLS CHURCH

STATE: VA
COUNTRY: USA
ZIP: 22040-0747
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,081B
FILING DATE:
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: SVENSSON, LEONARD R
REGISTRATION NUMBER: 30,330
REFERENCE/DOCKET NUMBER: 20-3484
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 205-8000
TELEFAX: (703) 205-8050
INFORMATION FOR SEQ ID NO: 42:
SEQUENCE CHARACTERISTICS:
LENGTH: 108 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-232-081B-42

Query Match 94.2% Score 49; DB 2; Length 108;
Best Local Similarity: 91.7%; Pred. No. 0.015;
Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RASQSVSSSFLA 12
Db 24 RASQSVSSSYLA 35

RESULT 10
US-08-839-765-150
Sequence 150, Application US/08839765
Patent No. 6146631
GENERAL INFORMATION:
APPLICANT: Better, Marc D.
APPLICANT: Carroll, Stephen F.
APPLICANT: Studnika, Gary M.
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
NUMBER OF SEQUENCES: 169
CORRESPONDENCE ADDRESS:
ADDRESSEE: McAndrews, Held & Malloy, Ltd.
STREET: 500 West Madison Street, 34th floor
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60661
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/839,765
FILING DATE: 15-APR-1997
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/425,336
FILING DATE: 18-APR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/064,691
FILING DATE: 12-MAY-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/988,430
FILING DATE: 09-DEC-1992

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/901,707
FILING DATE: 19-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/787,567
FILING DATE: 04-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: McNicholas, Janet M.
REGISTRATION NUMBER: 32,918
REFERENCE/DOCKET NUMBER: 11022US09/200-70.P3.C3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/707-8889
TELEFAX: 312/707-9155
TELEX: 650 388-1248
INFORMATION FOR SEQ ID NO: 150:
SEQUENCE CHARACTERISTICS:
LENGTH: 108 amino acids
TYPE: amino acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-839-765-150

Query Match 94.2% Score 49; DB 4; Length 108;
Best Local Similarity: 91.7%; Pred. No. 0.015;
Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RASQSVSSSFLA 12
Db 24 RASQSVSSSYLA 35

RESULT 11
US-09-136-389-150
Sequence 150, Application US/09136389
Patent No. 6146850
GENERAL INFORMATION:
APPLICANT: Better, Marc D.
APPLICANT: Carroll, Stephen F.
APPLICANT: Studnika, Gary M.
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
NUMBER OF SEQUENCES: 173
CORRESPONDENCE ADDRESS:
ADDRESSEE: McAndrews, Held & Malloy, Ltd.
STREET: 500 West Madison Street, 34th floor
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60661
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/136,389
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/646,360
FILING DATE: 13-MAY-1996
APPLICATION NUMBER: PCT/US94/05348
FILING DATE: 12-MAY-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/064,691
FILING DATE: 12-MAY-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/988,430
FILING DATE: 09-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/901,707
FILING DATE: 19-JUN-1992

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/787,567
FILING DATE: 04-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: McNicholas, Janet M.
REGISTRATION NUMBER: 32,918
REFERENCE/DOCKET NUMBER: 200-70.P4
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/707-8889
TELEFAX: 312/707-9155
TELEX: 650 388-1248
INFORMATION FOR SEQ ID NO: 150:
SEQUENCE CHARACTERISTICS:
LENGTH: 108 amino acids
TYPE: amino acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-136-389-150

Query Match 94.2% Score 49; DB 4; Length 108;
Best Local Similarity 91.7% Pred. No. 0.015;
Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

CY 1 RASQSVSSFLA 12
DB 24 RASQSVSSSYLA 35

RESULT 12

US-09-610-838-150
Sequence 150, Application US/09610838
Patent No. 6376217
GENERAL INFORMATION:
APPLICANT: Better, Marc D.
APPLICANT: Carroll, Stephen P.
APPLICANT: Studnika, Gary M.
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
NUMBER OF SEQUENCES: 173
CORRESPONDENCE ADDRESS:
ADDRESSEE: McAndrews, Held & Malloy, Ltd.
STREET: 500 West Madison Street, 34th floor
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60661
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/610,838
FILING DATE: 06-JUL-2000
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/136,389
FILING DATE: 18-AUG-1998
APPLICATION NUMBER: 08/646,360
FILING DATE: 13-MAY-1996
APPLICATION NUMBER: PCT/US94/05348
FILING DATE: 12-MAY-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/064,651
FILING DATE: 12-MAY-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/988,430
FILING DATE: 09-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/901,707
FILING DATE: 19-JUN-1992
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/787,567
FILING DATE: 04-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: McNicholas, Janet M.
REGISTRATION NUMBER: 32,918
REFERENCE/DOCKET NUMBER: 200-70.P4
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/707-8889
TELEFAX: 312/707-9155
TELEX: 650 388-1248
INFORMATION FOR SEQ ID NO: 150:
SEQUENCE CHARACTERISTICS:
LENGTH: 108 amino acids
TYPE: amino acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-610-838-150

Query Match 94.2% Score 49; DB 4; Length 108;
Best Local Similarity 91.7% Pred. No. 0.015;
Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

CY 1 RASQSVSSFLA 12
DB 24 RASQSVSSSYLA 35

RESULT 13

US-09-025-7698-16
Sequence 16, Application US/090257698
Patent No. 630064
GENERAL INFORMATION:
APPLICANT: Knappik, Achim
APPLICANT: Pack, Peter
APPLICANT: Ilag, Vic
APPLICANT: Ge, Liming
APPLICANT: Moroney, Simon
TITLE OF INVENTION: Protein/(poly)peptide libraries
NUMBER OF SEQUENCES: 373
CORRESPONDENCE ADDRESS:
ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
STREET: 1251 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10021
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/025,7698
FILING DATE: 18-FEB-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: James F. Haley, Jr., Esq.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: MORPHO/5
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)596-9000
TELEFAX: (212)596-9090
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 109 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein

US-09-025-769B-16

Query Match

Best Local Similarity 94.2%; Score 49; DB 4; Length 109;
Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RASQSVSSFLA 12

Db 24 RASQSVSSSYLA 35

RESULT 14

US-09-025-769B-30
Sequence 30, Application US/09025769B
Patent No. 6300064

GENERAL INFORMATION:

APPLICANT: Knappik, Achim
APPLICANT: Pack, PeterAPPLICANT: Ilag, Vic
APPLICANT: Ge, LimingAPPLICANT: Moroney, Simon
APPLICANT: Plueckthun, AndreasTITLE OF INVENTION: Protein/(Poly)peptide libraries
NUMBER OF SEQUENCES: 373

CORRESPONDENCE ADDRESS:

ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
STREET: 1251 Avenue of the Americas
CITY: New YorkSTATE: New York
COUNTRY: USA

ZIP: 10021

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatibleOPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/025,769B

FILING DATE: 18-FEB-1998

PRIORITY APPLICATION DATA:
APPLICATION NUMBER: EP 95 11 3021.0

FILING DATE: 18-AUG-1995

ATTORNEY/AGENT INFORMATION:
NAME: James F. Haley, Jr., Esq.

REGISTRATION NUMBER: 27,794

REFERENCE/DOCKET NUMBER: MORPHO/5

TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)596-9000

TELEFAX: (212)596-9090

INFORMATION FOR SEQ ID NO: 30:
SEQUENCE CHARACTERISTICS:LENGTH: 110 amino acids
TYPE: amino acidSTRANDEDNESS:
TOPOLOGY: linearMOLECULE TYPE: protein
US-09-025-769B-30Query Match 94.2%; Score 49; DB 4; Length 110;
Best Local Similarity 91.7%; Pred. No. 0.015;
Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RASQSVSSFLA 12

Db 24 RASQSVSSSYLA 35

RESULT 15

US-09-025-769B-47
Sequence 47, Application US/09025769B
Patent No. 6300064

GENERAL INFORMATION:

APPLICANT: Knappik, Achim

APPLICANT: Pack, Peter
APPLICANT: Ilag, VicAPPLICANT: Ge, Liming
APPLICANT: Moroney, SimonAPPLICANT: Plueckthun, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries

NUMBER OF SEQUENCES: 373

CORRESPONDENCE ADDRESS:

ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
STREET: 1251 Avenue of the Americas
CITY: New YorkSTATE: New York
COUNTRY: USA

ZIP: 10021

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatibleOPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/025,769B

FILING DATE: 18-FEB-1998

PRIORITY APPLICATION DATA:
APPLICATION NUMBER: EP 95 11 3021.0

FILING DATE: 18-AUG-1995

ATTORNEY/AGENT INFORMATION:
NAME: James F. Haley, Jr., Esq.

REGISTRATION NUMBER: 27,794

REFERENCE/DOCKET NUMBER: MORPHO/5

TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)596-9000

TELEFAX: (212)596-9090

INFORMATION FOR SEQ ID NO: 47:
SEQUENCE CHARACTERISTICS:LENGTH: 110 amino acids
TYPE: amino acidSTRANDEDNESS:
TOPOLOGY: linearMOLECULE TYPE: protein
US-09-025-769B-47Query Match 94.2%; Score 49; DB 4; Length 110;
Best Local Similarity 91.7%; Pred. No. 0.015;
Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RASQSVSSFLA 12

Db 24 RASQSVSSSYLA 35

SEARCH COMPLETED: June 3, 2003, 08:24:19

Job time: 2.82253 secs

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OM protein - protein search, using SW model

Run on: June 3, 2003, 08:09:29 ; Search time 1.26621 Seconds

(without alignments)
531.460 Million cell updates/sec

Title: US-09-644-668A-30

Sequence: 1 GASSRRAT 7

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database: PIR 73: *
1: p1r1: *
2: p1r2: *
3: p1r3: *
4: p1r4: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	32	100.0	34	2 H30607	Ig kappa chain V-I
2	32	100.0	54	2 S40381	Ig kappa chain V-I
3	32	100.0	54	2 A25521	Ig kappa chain V-I
4	32	100.0	62	2 I30601	Ig kappa chain V-I
5	32	100.0	83	2 I30607	Ig kappa chain V-I
6	32	100.0	87	2 S16843	Ig kappa chain V-I
7	32	100.0	87	2 S16823	Ig kappa chain V-I
8	32	100.0	89	2 S34096	Ig kappa chain V-I
9	32	100.0	91	2 S37520	Ig kappa chain V-I
10	32	100.0	91	2 S67940	Ig kappa chain V-I
11	32	100.0	92	2 S37524	Ig kappa chain V-I
12	32	100.0	92	2 S37513	Ig kappa chain V-I
13	32	100.0	92	2 S37519	Ig kappa chain V-I
14	32	100.0	92	2 S37517	Ig kappa chain V-I
15	32	100.0	92	2 S37514	Ig kappa chain V-I
16	32	100.0	92	2 S37510	Ig kappa chain V-I
17	32	100.0	92	2 S37518	Ig kappa chain V-I
18	32	100.0	93	2 S37526	Ig kappa chain V-I
19	32	100.0	93	2 S37528	Ig kappa chain V-I
20	32	100.0	96	2 A30601	Ig kappa chain V-I
21	32	100.0	99	2 JH0429	Ig kappa chain V-I
22	32	100.0	104	2 PH0964	Ig kappa chain V-I
23	32	100.0	107	2 PH0965	Ig kappa chain V-I
24	32	100.0	108	2 C30608	Ig kappa chain V-I
25	32	100.0	108	2 H44151	Ig kappa chain V-I
26	32	100.0	109	1 K3HUCI	Ig kappa chain V-I
27	32	100.0	109	1 K3HUCO	Ig kappa chain V-I
28	32	100.0	109	1 K3HUCI	Ig kappa chain V-I
29	32	100.0	109	2 PH0963	Ig kappa chain V-I

30	32	100.0	109	2 G30601	Ig kappa chain V-I
31	32	100.0	109	2 B30601	Ig kappa chain V-I
32	32	100.0	109	2 A30608	Ig kappa chain V-I
33	32	100.0	109	2 D30601	Ig kappa chain V-I
34	32	100.0	109	2 R30607	Ig kappa chain V-I
35	32	100.0	109	2 C30601	Ig kappa chain V-I
36	32	100.0	109	2 F30601	Ig kappa chain V-I
37	32	100.0	109	2 G30607	Ig kappa chain V-I
38	32	100.0	109	2 H30601	Ig kappa chain V-I
39	32	100.0	109	2 F44151	Ig kappa chain V-I
40	32	100.0	109	2 S47181	Ig kappa chain V-I
41	32	100.0	110	2 S20635	Ig kappa chain V-I
42	32	100.0	110	2 E30607	Ig kappa chain V-I
43	32	100.0	110	2 S44120	Ig kappa chain V-I
44	32	100.0	114	2 S46375	Ig kappa chain V-I
45	32	100.0	116	2 B27594	Ig kappa chain V-I

ALIGNMENTS

RESULT 1
Ig kappa chain V-III region (Bla) - human (fragment)
C/Species: Homo sapiens (man)
C/Date: 29-Jun-1989 #sequence_revision 29-Jun-1989 #text_change 30-May-1997
C/Accession: H30607
R/Goni, F.R.; Chen, P.P.; McGinnis, D.; Arjona, M.L.; Fernandez, J.; Carson, D.; So
U. Immunol. 142, 3158-3163, 1989
A/Title: Structural and idiotype characterization of the L chains of human IgM autoca
A/Reference number: A30601; MUID:99215279; PMID:2496160
A/Accession: H30607
A/Status: Preliminary
A/Molecule type: protein
A/Residues: 1-34 <GON>
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin

Query Match Best Local Similarity 100.0%; Score 32; DB 2; Length 34;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GASSRRAT 7
DB 4 GASSRRAT 10

RESULT 2

S40381
Ig kappa chain V-III region - human (fragment)

C/Species: Homo sapiens (man)
C/Date: 06-Mar-1994 #sequence_revision 23-Apr-1999 #text_change 23-Jul-1999

C/Accession: S40381
R/Klein, R.; Jaenichen, R.; Zachau, H.G.

Eur. J. Immunol. 23, 3248-3271, 1993
A/Title: Expressed human immunoglobulin chi genes and their hypermutation.

A/Reference number: S40312; MUID:94080891; PMID:828341
A/Accession: S40381

A/Status: translation not shown
A/Molecule type: mRNA

A/Residues: 1-54 <KLS>
A/Cross-reference: EMBL:X72491; NID:G441450; PIDN:GAS51159.1; PID:G441451

C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin

Query Match Best Local Similarity 100.0%; Score 32; DB 2; Length 54;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GASSRRAT 7
DB 9 GASSRRAT 15

RESULT 3

A25521
Ig kappa chain V region (321) - human (fragment)
C/Species: Homo sapiens (man)
C/Date: 21-May-1988 #sequence_revision 21-May-1990 #text_change 09-May-1997
C/Accession: A25521
R/Chen, P.P.; Albrandt, K.; Orida, N.K.; Radoux, V.; Chen, E.Y.; Schrantz, R.; Liu, F.T.
Proc. Natl. Acad. Sci. U.S.A. 83, 8318-8322, 1986
A/Title: Genetic basis for the cross-reactive idiotypes on the light chains of human IgM
A/Reference number: A94135; MUID:87041448; PMID:3095834
A/Accession: A25521
A/Molecule type: DNA
A/Residues: 1-54 <CHE>
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin

Query Match 100.0%; Score 32; DB 2; Length 54;
Best Local Similarity 100.0%; Pred. No. 1.1;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GASSRAT 7
Db 9 GASSRAT 15

RESULT 4

I30601
Ig kappa chain V-III region (Boc) - human (fragment)
C/Species: Homo sapiens (man)
C/Date: 29-Jun-1989 #sequence_revision 29-Jun-1989 #text_change 09-May-1997
C/Accession: I30601
R/Goni, P.R.; Chen, P.P.; McGinnis, D.; Arjonilla, M.L.; Fernandez, J.; Carson, D.; Sold
J. Immunol. 142, 3158-3163, 1989
A/Title: Structural and idiotypic characterization of the L chains of human IgM autoantibody
A/Reference number: A30601; MUID:89215279; PMID:2496160
A/Accession: I30601
A/Status: preliminary
A/Molecule type: protein
A/Residues: 1-62 <GON>
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin

Query Match 100.0%; Score 32; DB 2; Length 62;
Best Local Similarity 100.0%; Pred. No. 1.3;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GASSRAT 7
Db 51 GASSRAT 57

RESULT 5

I30607
Ig kappa chain V-III region (Wei) - human (fragments)
C/Species: Homo sapiens (man)
C/Date: 29-Jun-1989 #sequence_revision 29-Jun-1989 #text_change 09-May-1997
C/Accession: I30607
R/Goni, P.R.; Chen, P.P.; McGinnis, D.; Arjonilla, M.L.; Fernandez, J.; Carson, D.; Sold
J. Immunol. 142, 3158-3163, 1989
A/Title: Structural and idiotypic characterization of the L chains of human IgM autoantibody
A/Reference number: A30601; MUID:89215279; PMID:2496160
A/Accession: I30607
A/Status: preliminary
A/Molecule type: protein
A/Residues: 1-83 <GON>
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin

Query Match 100.0%; Score 32; DB 2; Length 83;
Best Local Similarity 100.0%; Pred. No. 1.7;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GASSRAT 7
Db 51 GASSRAT 57

RESULT 6

S16843
Ig kappa chain V region - human (fragment)
C/Species: Homo sapiens (man)
C/Date: 19-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000
C/Accession: S16843
R/Blaison, G.; Kuntz, J.L.; Pasquali, J.L.
Eur. J. Immunol. 21, 1221-1227, 1991
A/Title: Molecular analysis of V(kappa)III variable regions of polyclonal rheumatoid arthritis sera
A/Reference number: S16823; MUID:91243737; PMID:1903706
A/Accession: S16843
A/Status: preliminary; translation not shown
A/Molecule type: mRNA
A/Residues: 1-87 <BLA>
A/Cross-references: EMBL:X54841
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin
F/7-82/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 32; DB 2; Length 87;
Best Local Similarity 100.0%; Pred. No. 1.8;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GASSRAT 7
Db 42 GASSRAT 48

RESULT 7

S16823
Ig kappa chain V region - human (fragment)
C/Species: Homo sapiens (man)
C/Date: 19-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000
C/Accession: S16823
R/Blaison, G.; Kuntz, J.L.; Pasquali, J.L.
Eur. J. Immunol. 21, 1221-1227, 1991
A/Title: Molecular analysis of V(kappa)III variable regions of polyclonal rheumatoid arthritis sera
A/Reference number: S16823; MUID:91243737; PMID:1903706
A/Accession: S16823
A/Status: preliminary; translation not shown
A/Molecule type: mRNA
A/Residues: 1-87 <BLA>
A/Cross-references: EMBL:X54821
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin
F/7-82/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 32; DB 2; Length 87;
Best Local Similarity 100.0%; Pred. No. 1.8;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GASSRAT 7
Db 42 GASSRAT 48

RESULT 8

S34096
Ig kappa chain V region - human
C/Species: Homo sapiens (man)
C/Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 21-Jan-2000
C/Accession: S34096
R/Wagner, S.D.; Luzatto, L.
Eur. J. Immunol. 23, 391-397, 1993
A/Title: V-kappa gene segments rearranged in chronic lymphocytic leukemia are distributed in a clonal fashion
A/Reference number: S34076; MUID:93170387; PMID:8436174
A/Accession: S34096
A/Status: preliminary

A:Molecule type: DNA
A:Residues: 1-89 <MAG>
C:Accession: S37520
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F/9-84/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 32; DB 2; Length 89;
Best Local Similarity 100.0%; Pred. No. 1.9;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GASSRAT 7
|||||
Db 44 GASSRAT 50

RESULT 9
S37520
Ig kappa chain V region (V-kappa 3) - human (fragment)

C:Species: Homo sapiens (man)
C>Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999
C/Accession: S37520
R/Klein, U.; Kupepers, R.; Rajewsky, K.
submitted to the EMBL Data Library, September 1993
A:Description: Human IGM(+) Igd(+) cells, the major B cell subset in the peripheral blood
A:Reference number: S37501
A:Accession: S37520
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-91 <KLE>
C:Cross-references: EMBL:Z26612; NID:G405682; PIDN:CAA81365.1; PID:G405683
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin

Query Match 100.0%; Score 32; DB 2; Length 91;
Best Local Similarity 100.0%; Pred. No. 1.9;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GASSRAT 7
|||||
Db 34 GASSRAT 40

RESULT 10
S67940

Ig kappa chain V region, subgroup III (clone MH52) - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 19-Mar-1997 #sequence_revision 09-May-1997 #text_change 20-Mar-1998
C/Accession: S67940
R/Hexham, J.M.; Furmaniak, J.; Pegg, C.; Burton, D.R.; Smith, B.R.
Autoimmunity 12, 135-141, 1992
A>Title: Cloning of a human autoimmune response: preparation and sequencing of a human A:
A:Reference number: S67940; MUID:92314301; PMID:1617110
A:Accession: S67940
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-91 <HEX>
C:Cross-references: EMBL:X73852
C:Superfamily: immunoglobulin V region; immunoglobulin homology

Query Match 100.0%; Score 32; DB 2; Length 91;
Best Local Similarity 100.0%; Pred. No. 1.9;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GASSRAT 7
|||||
Db 32 GASSRAT 38

RESULT 11
S37524
Ig kappa chain V region (V-kappa 3) - human (fragment)
C:Species: Homo sapiens (man)

C>Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999
C:Accession: S37524
R/Klein, U.; Kupepers, R.; Rajewsky, K.
submitted to the EMBL Data Library, September 1993
A:Description: Human IGM(+) Igd(+) cells, the major B cell subset in the peripheral blood
A:Reference number: S37501
A:Accession: S37524
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-92 <KLE>
C:Cross-references: EMBL:Z26620; NID:G405690; PIDN:CAA81373.1; PID:G405691
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin

Query Match 100.0%; Score 32; DB 2; Length 92;
Best Local Similarity 100.0%; Pred. No. 1.9;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GASSRAT 7
|||||
Db 34 GASSRAT 40

RESULT 12
S37513

Ig kappa chain V region (V-kappa 3) - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999
C/Accession: S37513
R/Klein, U.; Kupepers, R.; Rajewsky, K.
submitted to the EMBL Data Library, September 1993
A:Description: Human IGM(+) Igd(+) cells, the major B cell subset in the peripheral blood
A:Reference number: S37501
A:Accession: S37513
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-92 <KLE>
C:Cross-references: EMBL:Z26598; NID:G405668; PIDN:CAA81352.1; PID:G405669
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin

Query Match 100.0%; Score 32; DB 2; Length 92;
Best Local Similarity 100.0%; Pred. No. 1.9;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GASSRAT 7
|||||
Db 34 GASSRAT 40

RESULT 13
S37519

Ig kappa chain V region (V-kappa 3) - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999
C/Accession: S37519
R/Klein, U.; Kupepers, R.; Rajewsky, K.
submitted to the EMBL Data Library, September 1993
A:Description: Human IGM(+) Igd(+) cells, the major B cell subset in the peripheral blood
A:Reference number: S37501
A:Accession: S37519
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-92 <KLE>
C:Cross-references: EMBL:Z26613; NID:G405680; PIDN:CAA81366.1; PID:G405681
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin

Query Match 100.0%; Score 32; DB 2; Length 92;
Best Local Similarity 100.0%; Pred. No. 1.9;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GASSRAT 7

Db 34 GASSRAT 40

RESULT 14

S37517

Ig kappa chain V region (V-kappa 3) - human (fragment)

C/Species: Homo sapiens (man)

C/Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999

C/Accession: S37517

R/Klein, U.; Kuipers, R.; Rajewsky, K.

submitted to the EMBL Data Library, September 1993

A/Description: Human IGM(+) IGD(+) cells, the major B cell subset in the peripheral blood

A/Reference number: S37501

A/Accession: S37517

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-92 <KLE>

A/Cross-references: EMBL:Z26515; NID:9405676; PIDN:CAA81368.1; PID:9405677

C/Superfamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: heterotetramer; immunoglobulin

Query Match

Best Local Similarity 100.0%; Score 32; DB 2; Length 92;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GASSRAT 7

Db 34 GASSRAT 40

RESULT 15

S37514

Ig kappa chain V region (V-kappa 3) - human (fragment)

C/Species: Homo sapiens (man)

C/Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999

C/Accession: S37514

R/Klein, U.; Kuipers, R.; Rajewsky, K.

submitted to the EMBL Data Library, September 1993

A/Description: Human IGM(+) IGD(+) cells, the major B cell subset in the peripheral blood

A/Reference number: S37501

A/Accession: S37514

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-92 <KLE>

A/Cross-references: EMBL:Z26597; NID:9405670; PIDN:CAA81351.1; PID:9405671

C/Superfamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: heterotetramer; immunoglobulin

Query Match

Best Local Similarity 100.0%; Score 32; DB 2; Length 92;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GASSRAT 7

Db 34 GASSRAT 40

Search completed: June 3, 2003, 08:22:40
 Job time: 1.26621 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 3, 2003, 08:02:44 ; Search time 0.645051 Seconds
(without alignments)
450.095 Million cell updates/sec

Title: US-09-644-668a-30

Sequence: 1 GASSRAT 7

Scoring table: BIOSUM62
Gapop 10.0, Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	32	100.0	109	KV3B_HUMAN	P01620 homo sapien
2	32	100.0	109	KV3E_HUMAN	P01623 homo sapien
3	32	100.0	109	KV3G_HUMAN	P04206 homo sapien
4	32	100.0	129	KV3L_HUMAN	P18135 homo sapien
5	32	100.0	129	KV3M_HUMAN	P18136 homo sapien
6	32	90.6	100	KV3C_HUMAN	P01621 homo sapien
7	29	90.6	109	KV3F_HUMAN	P01624 homo sapien
8	29	90.6	116	KV3J_HUMAN	P04434 homo sapien
9	29	90.6	129	KV3H_HUMAN	P04207 homo sapien
10	29	90.6	316	CYPK_STRCO	O02055 streptomyc
11	29	90.6	316	GPDA_RICPR	O09240 rickettsia
12	29	90.6	543	SRVA_DROSU	O07965 drosophila
13	28	87.5	108	KV3A_HUMAN	P01619 homo sapien
14	27	84.4	83	PRRP_RAT	P81278 rattus norv
15	27	84.4	567	HXTF_YEAST	P54854 saccharomyc
16	27	84.4	567	HXTF_YEAST	P47185 saccharomyc
17	27	84.4	690	TRF1_SALSA	P80426 salmo salar
18	27	84.4	691	TRF2_SALSA	P80429 salmo salar
19	27	84.4	908	SYA_MYCLE	O09240 mycobacteri
20	27	84.4	3386	POLG_DENA	P09866 d genome po
21	26	81.2	109	KV3D_HUMAN	P01622 homo sapien
22	26	81.2	225	ROU2_HUMAN	P07029 homo sapien
23	26	81.2	228	HXB6_BRARE	P15861 brachydantio
24	26	81.2	301	PHLP_RAT	O63737 rattus norv
25	26	81.2	338	BZTA_RHOCA	O52663 rhodobacter
26	26	81.2	344	HRCA_STRMU	O06940 streptococc
27	26	81.2	393	NIFS_BRAJA	P37030 bradyrhicob
28	26	81.2	463	Y102_MYCTU	O53951 mycobacteri
29	26	81.2	507	ALAT_YEAST	P52892 saccharomyc
30	26	81.2	524	YC90_MYCTU	O10616 mycobacteri
31	26	81.2	524	THS3_HALVO	O99842 halobacteri
32	26	81.2	543	YDE3_SCHPO	O10437 schizosacch
33	26	81.2	607	RIB1_HUMAN	P04843 homo sapien

34	26	81.2	928	1	MAY4_SCHCO	P37935 schizopylli
35	26	81.2	1150	1	APMT_PIG	P12021 sus scrofa
36	26	81.2	1174	1	CIKE_DROME	O02280 drosophila
37	25	78.1	155	1	IGF2_BOVIN	P07456 bos taurus
38	25	78.1	175	1	RL22_MYCLE	O02986 mycobacteri
39	25	78.1	221	1	YAC9_STRCO	O04310 streptomyc
40	25	78.1	267	1	PSB7_SCHPO	O09841 schizosacch
41	25	78.1	273	1	PSBA_HUMAN	P40306 homo sapien
42	25	78.1	273	1	PSBA_MOUSE	O35935 mus musculu
43	25	78.1	277	1	PSB7_HUMAN	O99436 homo sapien
44	25	78.1	277	1	PSB7_MOUSE	P70195 mus musculu
45	25	78.1	277	1	PSB7_RAT	O9jhwo rattus norv

ALIGNMENTS

```

RESULT 1
KV3B_HUMAN          STANDARD,      PRT,   109 AA.
AC P01620;
DT 21-JUL-1986 (Rel. 01, Created)
DR 21-JUL-1986 (Rel. 01, Last sequence update)
DE 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG kappa chain V-III region SIE.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=82046598; PubMed=6794615;
RA Andrews D.W., Capra J.D.;
RT "Amino acid sequence of the variable regions of light chains from two
RT idiotypically cross-reactive human IGM anti-gamma-globulins of the Wa
RT group."
RL Biochemistry 20:5816-5822(1981).
CC -I- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGM WITH ANTI-GAMMA
CC GLOBULIN ACTIVITY.
CC PIR; A01892; K3HUS1.
DR HSSP; P80362; IWTI.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IgV; 1.
KW Immunoglobulin V region.
FT DISULFID 23 89
FT NON TER 109 109
FT SEQUENCE 109 AA; 11775 MW; 7689C3ECD646FFB4 CRC64;

Query Match.          100.0%; Score 32; DB 1; Length 109;
Best Local Similarity 100.0%; Pred. No. 0.68;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GASSRAT 7
   |||||
Db 51 GASSRAT 57

RESULT 2
KV3E_HUMAN          STANDARD,      PRT,   109 AA.
AC P01623;
DT 21-JUL-1986 (Rel. 01, Created)
DR 21-JUL-1986 (Rel. 01, Last sequence update)
DE 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG kappa chain V-III region WOL.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.

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RX MEDLINE=82046598; PubMed=6794615;
 RA Andrews D.W., Capra J.D.;
 RT "Amino acid sequence of the variable regions of light chains from two
 RT idiotypically cross-reactive human IgM anti-gamma-globulins of the Wa
 RT group.";
 RL Biochemistry 20:5816-5822(1981).
 CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGM WITH ANTI-GAMMA
 CC GLOBULIN ACTIVITY.
 DR PIR; A01896; K3HUM1.
 DR HSSP; P80362; IWTU.
 DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR003596; Ig_V.
 DR Pfam; PF00047; Ig; 1.
 DR SMART; SM00406; IgV; 1.
 KW Immunoglobulin V region.
 FT DISULFID 23 89
 FT NON TER 109 109 BY SIMILARITY.
 SQ SEQUENCE 109 AA; 11746 MW; 566C115E6B9C8EE CRC64;

Query Match 100.0%; Score 32; DB 1; Length 109;
 Best Local Similarity 100.0%; Pred. No. 0.68;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GASSRAT 7
 DB 51 GASSRAT 57

RESULT 3
 ID KV3G HUMAN STANDARD; PRT; 109 AA.
 AC P04206;
 DT 20-MAR-1987 (Rel. 04, Created)
 DT 20-MAR-1987 (Rel. 04, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Ig kappa chain V-III region GOL (Rheumatoid factor).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=86230578; PubMed=3086710;
 RA Newkirk M., Chen P.P., Carson D.A., Posnett D., Capra J.D.;
 RT "Amino acid sequence of a light chain variable region of a human
 RT rheumatoid factor of the Wa idiotype group, in part predicted by its
 RT reactivity with antipeptide antibodies.";
 RL Mol. Immunol. 23:239-244(1986).
 DR PIR; A01893; K3HUGO.
 DR HSSP; P80362; IWTU.
 DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR003596; Ig_V.
 DR Pfam; PF00047; Ig; 1.
 DR SMART; SM00406; IgV; 1.
 KW Immunoglobulin V region.
 FT DISULFID 23 89
 FT NON TER 109 109 BY SIMILARITY.
 SQ SEQUENCE 109 AA; 11830 MW; 9349A5B1D9358B6 CRC64;

Query Match 100.0%; Score 32; DB 1; Length 109;
 Best Local Similarity 100.0%; Pred. No. 0.68;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GASSRAT 7
 DB 51 GASSRAT 57

RESULT 4
 ID KV3L HUMAN STANDARD; PRT; 129 AA.
 AC P18135;
 DT 01-NOV-1990 (Rel. 16, Created)

DT 01-NOV-1990 (Rel. 16, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Ig kappa chain V-III region HAH precursor.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=88171307; PubMed=3127527;
 RA Kipps T.J., Tomhave E., Chen P.P., Carson D.A.;
 RT "Autoantibody-associated kappa light chain variable region gene
 RT expressed in chronic lymphocytic leukemia with little or no somatic
 RT mutation. Implications for etiology and immunotherapy.";
 RL J. Exp. Med. 167:840-852(1988).
 CC -1- DISEASE: THE PROTEIN IS ONE OF THE SURFACE IMMUNOGLOBULIN M
 CC AUTOANTIBODIES EXPRESSED IN PATIENTS WITH CHRONIC LYMPHOCYTIC
 CC LEUKEMIA.
 DR PIR; P10022; K3HUMA.
 DR HSSP; P80362; IWTU.
 DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR003596; Ig_V.
 DR Pfam; PF00047; Ig; 1.
 DR SMART; SM00406; IgV; 1.
 KW Immunoglobulin V region; Signal.
 FT SIGNAL 1 20
 FT CHAIN 21 129 IG KAPPA CHAIN V-III REGION HAH.
 FT DOMAIN 21 43 FRAMEWORK-1.
 FT DOMAIN 44 55 COMPLEMENTARITY-DETERMINING-1.
 FT DOMAIN 56 70 FRAMEWORK-2.
 FT DOMAIN 71 77 COMPLEMENTARITY-DETERMINING-2.
 FT DOMAIN 78 109 FRAMEWORK-3.
 FT DOMAIN 110 118 COMPLEMENTARITY-DETERMINING-3.
 FT DOMAIN 119 129 JKL SEGMENT.
 FT DISULFID 43 109 BY SIMILARITY.
 FT NON TER 129 129
 SQ SEQUENCE 129 AA; 14073 MW; D3C55292772774D0 CRC64;

Query Match 100.0%; Score 32; DB 1; Length 129;
 Best Local Similarity 100.0%; Pred. No. 0.81;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GASSRAT 7
 DB 71 GASSRAT 77

RESULT 5
 ID KV3M HUMAN STANDARD; PRT; 129 AA.
 AC P18136;
 DT 01-NOV-1990 (Rel. 16, Created)
 DT 01-NOV-1990 (Rel. 16, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Ig kappa chain V-III region HIC precursor.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=88171307; PubMed=3127527;
 RA Kipps T.J., Tomhave E., Chen P.P., Carson D.A.;
 RT "Autoantibody-associated kappa light chain variable region gene
 RT expressed in chronic lymphocytic leukemia with little or no somatic
 RT mutation. Implications for etiology and immunotherapy.";
 RL J. Exp. Med. 167:840-852(1988).
 CC -1- DISEASE: THE PROTEIN IS ONE OF THE SURFACE IMMUNOGLOBULIN M
 CC AUTOANTIBODIES EXPRESSED IN PATIENTS WITH CHRONIC LYMPHOCYTIC
 CC LEUKEMIA.
 DR PIR; P10021; K3HUMI.
 DR HSSP; P80362; IWTU.
 DR InterPro; IPR003006; Ig_MHC.


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DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IgV; 1.
KM Immunoglobulin V region; Signal.
FT SIGNAL 1 20
FT CHAIN 21 129 IG KAPPA CHAIN V-III REGION HIC.
FT DOMAIN 21 43 FRAMEWORK-1.
FT DOMAIN 44 55 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 56 70 FRAMEWORK-2.
FT DOMAIN 71 77 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 78 109 FRAMEWORK-3.
FT DOMAIN 110 118 COMPLEMENTARITY-DETERMINING-3.
FT DISULFID 119 129 JKI SEGMENT.
FT NON TER 129 129 BY SIMILARITY.
SQ SEQUENCE 129 AA; 14070 MW; 7395528EA2BB74D6 CRC64;

Query Match 100.0%; Score 32; DB 1; Length 129;
Best Local Similarity 100.0%; Pred. No. 0.81;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GASSRAT 7
DB 71 GASSRAT 77

RESULT 6
KV3J_HUMAN
ID KV3J_HUMAN STANDARD; PRT; 100 AA.
AC P01621;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DE 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-III region NG9 precursor (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=84093600; PubMed=6419127;
RA Bentley D.L.;
RT "Most kappa immunoglobulin mRNA in human lymphocytes is homologous to
a small family of germ-line V genes.";
RL Nature 307:77-80(1984).
DE 1- MISCELLANEOUS: THIS GENE WAS ISOLATED FROM THE NG9/9.1 HYBRIDOMA.
DR PIR; A01894; K3HUNG.
DR HSSP; P80362; 1WTL.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PR00047; Ig; 1.
DR SMART; SM00406; IgV; 1.
KM Immunoglobulin V region; Signal; Hybridoma.
FT NON TER 1 1
FT SIGNAL <1 4
FT CHAIN 5 100 IG KAPPA CHAIN V-III REGION NG9.
FT DISULFID 27 93 BY SIMILARITY.
FT NON TER 100 100
SQ SEQUENCE 100 AA; 10729 MW; 5D9AF363CC52632F CRC64;

Query Match 90.6%; Score 29; DB 1; Length 100;
Best Local Similarity 85.7%; Pred. No. 3.3;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GASSRAT 7
DB 55 GASSRAT 61

RESULT 7
KV3F_HUMAN
ID KV3F_HUMAN STANDARD; PRT; 109 AA.
AC P01624;

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DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Ig kappa chain V-III region POM.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=76276460; PubMed=60899;
RA Klapper D.G., Capra J.D.;
RT "The amino acid sequence of the variable regions of the light chains
from two idiotypically cross reactive IGM anti-gamma globulins.";
RL Ann. Immunol. (Paris) 127C:261-271(1976).
DE 1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGM WITH ANTI-GAMMA
GLOBULIN ACTIVITY.
DR PIR; A01897; K3HUPM.
DR HSSP; P80362; 1WTL.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IgV; 1.
KM Immunoglobulin V region.
FT DISULFID 23 89 BY SIMILARITY.
FT NON TER 109 109
SQ SEQUENCE 109 AA; 11922 MW; 62821DDC6A8ABA86 CRC64;

Query Match 90.6%; Score 29; DB 1; Length 109;
Best Local Similarity 85.7%; Pred. No. 3.6;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GASSRAT 7
DB 51 GASSRAT 57

RESULT 8
KV3J_HUMAN
ID KV3J_HUMAN STANDARD; PRT; 116 AA.
AC P04434;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DE 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-III region VH precursor (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=85087932; PubMed=6440122;
RA Pech M., Zachau H.G.;
RT "Immunoglobulin genes of different subgroups are interdigitated
within the VK locus.";
RL Nucleic Acids Res. 12:9229-9236(1984).
DE 1- MISCELLANEOUS: THIS SWISS-PROT entry is copyright. It is produced through a collaboration
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or send an email to license@isb-sib.ch).
DR EMBL; X02725; -; NOT_ANNOTATED_CDS.
DR PIR; A01801; K3HUPH.
DR HSSP; P80362; 1WTL.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IgV; 1.
KM Immunoglobulin V region; Signal.

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FT SIGNAL 1 20 IG KAPPA CHAIN V-III REGION VH.
FT CHAIN 21 >116
FT DOMAIN 21 43 FRAMEWORK-1.
FT DOMAIN 44 55 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 56 70 FRAMEWORK-2.
FT DOMAIN 71 77 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 78 109 FRAMEWORK-3.
FT DOMAIN 110 116 COMPLEMENTARITY-DETERMINING-3.
FT DISULFID 43 109 BY SIMILARITY.
FT NON TER 116 116
SQ SEQUENCE 116 AA; 12757 MW; 51CD55BA53B21929 CRC64;

Query Match
Best Local Similarity 90.6%; Score 29; DB 1; Length 116;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 GASSRAT 7
Db 71 GASTRAT 77

RESULT 9
KV3H HUMAN STANDARD; PRT; 129 AA.
ID KV3H HUMAN
AC P04207;
DT 20-MAR-1987 (Rel. 04, Created)
DT 01-NOV-1980 (Rel. 16, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG kappa chain V-III region C1L precursor (Rheumatoid factor).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN (1)
RP SEQUENCE FROM N.A.
RX MEDLINE=8617570; PubMed=3083417;
RA Jirik P.R., Sorge J., Fong S., Heltmann J.G., Cud J.G., Chen P.P.,
RA Goldfien R., Carson D.A.;
RT "Cloning and sequence determination of a human rheumatoid factor
RT light-chain gene.";
RL Proc. Natl. Acad. Sci. U.S.A. 83:2195-2199(1986).
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; M12740; AA58592.1; -
DR PIR; A01898; KAHUCL.
DR HSSP; P80362; IWTU.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF00047; Ig_1.
DR SMART; SM00406; IgV_1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 20
FT CHAIN 21 129 IG KAPPA CHAIN V-III REGION C1L.
FT DOMAIN 21 43 FRAMEWORK-1.
FT DOMAIN 44 54 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 55 69 FRAMEWORK-2.
FT DOMAIN 70 76 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 77 108 FRAMEWORK-3.
FT DOMAIN 109 118 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 119 129 JKL SEGMENT.
FT DISULFID 43 108 BY SIMILARITY.
FT NON TER 129 129
SQ SEQUENCE 129 AA; 14275 MW; 5C1B411BE60CC14 CRC64;

Query Match
Best Local Similarity 90.6%; Score 29; DB 1; Length 129;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 GASSRAT 7
Db 70 GASTRAT 76

RESULT 10
CYPR_STRCO STANDARD; PRT; 316 AA.
ID CYPR_STRCO
AC 002055;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Actinorhodin polyketide synthase bifunctional cyclase/dehydratase
DE (acti ORF4) (ACTVII).
GN SC05090 OR SCBAC2861.16.
OS Streptomyces coelicolor.
OC Bacteria; Actinobacteria; Actinobacteria (class); Actinobacteridae;
OC Actinomycetales; Streptomycetaceae; Streptomycetaceae; Streptomycetes.
OX NCBI_TaxID=1902;
RN (1)
RP SEQUENCE FROM N.A.
RX STRAIN=A3(2) / M145;
RX MEDLINE=92406871; PubMed=1527048;
RA Fernandez-Moreno M.A., Martinez E., Boto L., Hopwood D.A.,
RA Malpartida F.;
RT "Nucleotide sequence and deduced functions of a set of cotranscribed
RT genes of Streptomyces coelicolor A3(2) including the polyketide
RT synthase for the antibiotic actinorhodin.";
RL J. Biol. Chem. 267:19278-19290(1992).
RN (2)
RP SEQUENCE FROM N.A.
RX STRAIN=A3(2) / M145;
RX MEDLINE=21996410; PubMed=12000953;
RA Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L.,
RA Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieseer H.,
RA Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,
RA Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,
RA Huang C.-H., Kieseer T., Larke L., Murphy L., Oliver K., O'Neill S.,
RA Rabbitt-Mitch E., Rajandream M.A., Rutherford K., Rutter S.,
RA Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,
RA Warren T., Wietzorrek A., Woodward J., Barrell B.G., Parkhill J.,
RA Hopwood D.A.;
RT "Complete genome sequence of the model actinomycete Streptomyces
RT coelicolor A3(2) ";
RL Nature 417:141-147(2002).
CC -----
CC -1- FUNCTION: IS NEEDED FOR CORRECT CYCLIZATION OF THE OLIGOKETIDE
CC LEADING TO ISOCHROMANEQUINONE FORMATION.
CC -1- PATHWAY: Polyketide antibiotic actinorhodin biosynthesis.
CC -----
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CC -----
DR EMBL; X63449; CAA5046.1; -
DR EMBL; AL593842; CAC44203.1; -
DR PIR; S25843; S25843.
DR InterPro; IPR005031; Polyketet_CYC.
DR Pfam; PF03364; Polyketide_cyc_2.
KW Antibiotic biosynthesis; Complete proteome.
SQ SEQUENCE 316 AA; 34665 MW; E9C946F9A0FD23D3 CRC64;

Query Match
Best Local Similarity 90.6%; Score 29; DB 1; Length 316;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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DB 298 GANSRAT 304

RESULT 11

GPDA_RICPR STANDARD; PRT; 316 AA.

AC Q9ZDNO.1 (Rel. 40, Created)

DT 16-OCT-2001 (Rel. 40, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last sequence update)

DE 16-OCT-2001 (Rel. 40, Last annotation update)

DE Glycerol-3-phosphate dehydrogenase [NAD(P)+] (EC 1.1.1.94) (NAD(P)-H-dependent glycerol-3-phosphate dehydrogenase).

GN GSEA OR RP442.

OS Rickettsia prowazekii.

OC Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;

CC Rickettsiaceae; Rickettsiae; Rickettsia.

OX NCBI_TaxID=782;

RN [1]

RP SEQUENCE FROM N.A.

RA STRAIN=Madrid E;

RX MEDLINE=99039499; PubMed=9823893;

RA Andersson S.G.E., Zomorodipour A., Andersson J.O.,

RA Sierberitz-Ponten T., Alsmark U.C.M., Podewski R.M., Naslund A.K.,

RA Eriksson A.-S., Winkler H.H., Kuriland C.G.,

RT "The genome sequence of Rickettsia prowazekii and the origin of mitochondria."

RL Nature 396:133-140(1998).

CC -1- CATALYTIC ACTIVITY: Sn-glycerol 3-phosphate + NAD(P) (+) =

CC -1- glycerone phosphate + NAD(P)H.

CC -1- PATHWAY: De novo phospholipid biosynthesis; glycerol-3 phosphate formation.

CC -1- SUBCELLULAR LOCATION: Cytoplasmic (Probable).

CC -1- SIMILARITY: BELONGS TO THE NAD-DEPENDENT GLYCEROL-3-PHOSPHATE DEHYDROGENASE FAMILY.

CC -----

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CC -----

DR EMBL: AJ235271; CAI4899.1; -

DR InterPro: IPR001652; NAD_GLY3P_dh.

DR Pfam: PF01210; NAD_GLY3P_dh; 1.

DR PRINTS: PR00077; GPDHDEGNASE.

DR Prodom: PD001649; NAD_GLY3P_dh; 1.

DR PROSITE: PS00957; NAD_G3PDH; FALSE NEG.

KW Phospholipid biosynthesis; Oxidoreductase; NAD; Complete proteome.

SO SEQUENCE 316 AA; 34487 MW; EBA9BE4E19874D42 CRC64;

Query Match 90.6%; Score 29; DB 1; Length 316;

Best Local Similarity 85.7%; Pred. No. 11;

Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 GANSRAT 7

DB 208 GANSRAT 214

RESULT 12

SRVA_DROGU STANDARD; PRT; 543 AA.

AC Q07965; (Rel. 32, Created)

DT 01-NOV-1995 (Rel. 32, Last sequence update)

DT 01-NOV-1995 (Rel. 32, Last sequence update)

DE Serendipity locus alpha protein.

GN SRV-A OR SRV-ALPHA.

OS Drosophila subobscura (Fruit fly).

OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;

CC Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;

OC Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

OX NCBI_TaxID=7241;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=94116447; PubMed=8287797;

RA Imasoua S., Schweisguth F., de Billy G., Vincent A.,

RT "Relationship between expression of serendipity alpha and cellularization of the Drosophila embryo as revealed by interspecific transformation."

RL Development 119:471-483(1993).

CC -1- FUNCTION: REQUIRED FOR THE CELLULARIZATION OF THE EMBRYO. INVOLVED IN THE LOCALIZATION OF THE ACTIN FILAMENTS JUST PRIOR TO AND DURING PLASMA MEMBRANE INVAGINATION. SRV-ALPHA TOGETHER WITH NULLO AND BNR MAY PROVIDE AUXILIARY FUNCTIONS, BY ACTING BOTH TO STABILIZE A LARGE AND DYNAMIC MICROFILAMENT STRUCTURE AND REGULATE ITS FUNCTIONS (BY SIMILARITY).

CC -1- SUBCELLULAR LOCATION: INNER MEMBRANE-ASSOCIATED AND CYTOPLASMIC. COLOCALIZES WITH THE STRUCTURAL TRANSITIONS IN THE MICROFILAMENT NETWORK DURING CELLULARIZATION (BY SIMILARITY).

CC -1- DEVELOPMENTAL STAGE: BLASTODERM.

CC -----

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CC -----

DR EMBL: L19535; AAA17044.1; -

DR FlyBase: FBGN0012949; Dsub\Srv-alpha.

KW Developmental protein.

SO SEQUENCE 543 AA; 61450 MW; 07006B594692C838 CRC64;

Query Match 90.6%; Score 29; DB 1; Length 543;

Best Local Similarity 85.7%; Pred. No. 19;

Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 GANSRAT 7

DB 88 GANSRAT 94

RESULT 13

KV3A_HUMAN STANDARD; PRT; 108 AA.

AC P01619;

DT 21-JUL-1986 (Rel. 01, Created)

DT 21-JUL-1986 (Rel. 01, Last sequence update)

DT 15-JUL-1999 (Rel. 38, Last annotation update)

DE Ig kappa chain V-II region B6.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

CC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE.

RA Milstein C.

RT "The basic sequences of immunoglobulin kappa chains: sequence studies of Bence Jones proteins Rad, Fr4 and B6."

RL FEBS Lett. 2:301-304(1969).

CC -1- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.

DR PIR: A01891; K3HUB6.

DR HSSP: P80362; IWTL.

DR InterPro: IPR003006; IG_MHC.

DR InterPro: IPR003596; IG_V.

DR Pfam: PF00047; Ig; 1.

DR SMART: SM00406; IGV; 1.

KW Immunoglobulin V region; Bence-Jones protein.

FT DISULFID 23 89

FT NON TER 108 108

SO SEQUENCE 108 AA; 11635 MW; 8BC14FF07A119E3D CRC64;

Query Match 87.5%; Score 28; DB 1; Length 108;
 Best Local Similarity 85.7%; Pred. No. 6.3;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GASSRA 7
 DB 51 GVSSRA 57

RESULT 14

PRP_RAT STANDARD; PRT; 83 AA.
 ID PRP_RAT
 AC P81278;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Proactin-releasing peptide precursor (PRP) (Proactin-releasing hormone) [Contains: Proactin-releasing peptide PRP31; Proactin-releasing peptide PRP20].
 GN Rattus norvegicus (Rat).
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OC NCBI_TaxID=10116;
 RX MEDLINE=98268761; PubMed=9607765;
 RA Hinuma S., Habata Y., Fujii R., Kawamata Y., Hosoya M., Fukusumi S., Kltada C., Masuo Y., Asano T., Matsumoto H., Sekiguchi M., Kurokawa T., Nishimura O., Onda H., Fujino M.;
 RT "A proactin-releasing peptide in the brain.";
 RL Nature 393:272-276(1998).
 RN [2]
 RP TISSUE SPECIFICITY
 RC MEDLINE=9942652; PubMed=10498338;
 RA Fujii R., Fukusumi S., Hosoya M., Kawamata Y., Habata Y., Hinuma S., Sekiguchi M., Kltada C., Kurokawa T., Nishimura O., Onda H., Fujino M.;
 RT "Tissue distribution of proactin-releasing peptide (PRP) and its receptor.";
 RL Regul. Pept. 83:1-10(1999).
 CC -1- FUNCTION: Stimulates proactin (PR) release and regulates the expression of proactin through its receptor GRP10. May stimulate lactotrophs directly to secrete PR.
 CC -1- TISSUE SPECIFICITY: Widely expressed, with highest levels in medulla oblongata and hypothalamus.
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 CC EMBL, AB015418; BAA29026.1;
 DR Hormone; Amidation; Signal; Cleavage on pair of basic residues.
 KM SIGNAL
 FT 1 21
 FT PEPTIDE 22 52 PROACTIN-RELEASING PEPTIDE PRP31.
 FT PEPTIDE 33 52 PROACTIN-RELEASING PEPTIDE PRP20.
 FT MOD RES 52 52 AMIDATION (G-53 PROVIDE AMIDE GROUP).
 SQ SEQUENCE 83 AA; 9215 MW; DDC75A264EBR4F29 CRC64;

Query Match 84.4%; Score 27; DB 1; Length 83;
 Best Local Similarity 100.0%; Pred. No. 8.4;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GASSRA 6
 DB 19 GASSRA 24

RESULT 15
 HXTE YEAST STANDARD; PRT; 567 AA.
 ID HXTE YEAST
 AC P54854;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Hexose transporter HXT15.
 GN HXT15 OR YDL245C.
 OS Saccharomyces cerevisiae (Baker's yeast).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomycetales; Saccharomycetaceae; Saccharomyces.
 OC NCBI_TaxID=4932;
 RX MEDLINE=97051587; PubMed=8896264;
 RA Barques M., Salom D., Gomez A., Particio N., Perez-Alonso M., Perez-Ortin J.E.;
 RT "Sequencing analysis of a 4.1 kb subclonemic region from yeast chromosome IV identifies HXT15, a new member of the hexose transporter family.";
 RL Yeast 12:1005-1011(1996).
 CC -1- FUNCTION: PROBABLE GLUCOSE TRANSPORTER.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- SIMILARITY: BELONGS TO THE SUGAR TRANSPORTER FAMILY.

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 CC EMBL, X92891; CAA63484.1;
 DR EMBL, Z74293; CAA98825.1;
 DR SGD: S0002404; HXT15
 DR InterPro: IPR003663; CHO transporter.
 DR InterPro: IPR003662; sub-transporter.
 DR Pfam: PF00083; sugar tr. 1.
 DR PRINTS: PR00171; SUGSTRNSPORT.
 DR TIGRFAMs: TIGR00879; SP. 1.
 DR PROSITE: PS00216; SUGAR_TRANSPORT_1; 1.
 DR PROSITE: PS00217; SUGAR_TRANSPORT_2; 1.
 KW Repeat; Transmembrane; Sugar transporter; Transport.
 FT DOMAIN 1 55
 FT TRANSMEM 56 76
 FT DOMAIN 77 112
 FT TRANSMEM 113 133
 FT DOMAIN 134 139
 FT TRANSMEM 140 160
 FT DOMAIN 161 170
 FT TRANSMEM 171 191
 FT DOMAIN 192 197
 FT TRANSMEM 198 218
 FT DOMAIN 219 232
 FT TRANSMEM 233 253
 FT DOMAIN 254 336
 FT TRANSMEM 337 353
 FT DOMAIN 354 359
 FT TRANSMEM 360 377
 FT DOMAIN 378 384
 FT TRANSMEM 385 405
 FT DOMAIN 406 427
 FT TRANSMEM 428 448
 FT DOMAIN 449 465
 FT TRANSMEM 466 486
 FT DOMAIN 487 487
 FT TRANSMEM 488 508
 FT DOMAIN 509 567
 SQ SEQUENCE 567 AA; 62931 MW; 5CD762482D130 CRC64;

Query Match 84.4%; Score 27; DB 1; Length 567;
Best Local Similarity 85.7%; Pred. No. 62;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 GASSRAT 7
|||
Db 543 GASSRET 549

Search completed: June 3, 2003, 08:15:48
Job time : 2.64505 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 3, 2003, 08:07:54 ; Search time 3.48805 Seconds
(without alignments)
413.506 Million cell updates/sec

Title: US-09-644-668A-30
Perfect score: 32
Sequence: 1 GASSRAT 7

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 671580 seqs, 206047115 residues
Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

SPTREMBL 21:*

- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mhc:*
- 8: sp_organelle:*
- 9: sp_phage:*
- 10: sp_plant:*
- 11: sp_rodent:*
- 12: sp_virus:*
- 13: sp_vertebrate:*
- 14: sp_unclassified:*
- 15: sp_virus:*
- 16: sp_bacteriopl:*
- 17: sp_archaeopl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	32	100.0	109	4 Q9UL78	Q9UL78 homo sapien
2	29	90.6	95	15 Q68986	Q68986 human endog
3	29	90.6	107	16 Q9L0H4	Q9L0H4 streptomyce
4	29	90.6	109	4 Q9UL85	Q9UL85 homo sapien
5	29	90.6	211	16 Q92227	Q92227 rhizobium m
6	29	90.6	335	10 Q9SE65	Q9SE65 arabidopsis
7	29	90.6	335	10 Q9LNE3	Q9LNE3 arabidopsis
8	29	90.6	346	2 Q9F152	Q9F152 bifidobacte
9	28	87.5	102	17 Q9YBUS	Q9YBUS aetopyrium p
10	28	87.5	109	4 Q9UL86	Q9UL86 homo sapien
11	28	87.5	119	17 Q9YDK0	Q9YDK0 aetopyrium p
12	28	87.5	141	2 Q53755	Q53755 streptomyce
13	28	87.5	161	16 Q9LJY8	Q9LJY8 pseudomonas
14	28	87.5	204	10 Q9AK93	Q9AK93 arabidopsis
15	28	87.5	266	16 Q9MYN6	Q9MYN6 thermotoga
16	28	87.5	277	5 Q62102	Q62102 caenorhabdi

17	28	87.5	322	5 Q8T915	Q8T915 drosophila
18	28	87.5	503	12 Q99FW7	Q99FW7 human papill
19	28	87.5	506	16 Q9S2V5	Q9S2V5 streptomyce
20	28	87.5	511	16 Q8YEX8	Q8YEX8 brucella me
21	28	87.5	546	16 Q83836	Q83836 treponema p
22	28	87.5	554	6 Q95L89	Q95L89 bos taurus
23	28	87.5	568	10 Q8RX66	Q8RX66 arabidopsis
24	28	87.5	580	6 Q8WML4	Q8WML4 bos taurus
25	28	87.5	606	10 Q9CAU7	Q9CAU7 arabidopsis
26	28	87.5	667	5 Q9GYB5	Q9GYB5 leishmania
27	28	87.5	725	12 Q8ORW1	Q8ORW1 chimpanzee
28	28	87.5	779	8 Q9MR93	Q9MR93 podospira a
29	28	87.5	779	8 Q02719	Q02719 podospira a
30	28	87.5	1018	5 Q9BJM6	Q9BJM6 toxoplasma
31	28	87.5	1106	5 Q9GR19	Q9GR19 leishmania
32	28	87.5	1171	5 Q9VTW8	Q9VTW8 drosophila
33	28	87.5	1469	5 Q9U190	Q9U190 leishmania
34	28	87.5	2564	5 Q9U755	Q9U755 toxoplasma
35	27	84.4	27	12 Q8QSL5	Q8QSL5 hepatitis c
36	27	84.4	27	12 Q8QSL4	Q8QSL4 hepatitis c
37	27	84.4	27	12 Q8QSL3	Q8QSL3 hepatitis c
38	27	84.4	27	12 Q8QSL0	Q8QSL0 hepatitis c
39	27	84.4	95	17 Q8Z286	Q8Z286 pyrobaculum
40	27	84.4	121	17 Q8T129	Q8T129 methanobarc
41	27	84.4	189	2 Q9XC10	Q9XC10 streptococc
42	27	84.4	194	2 Q9X6U3	Q9X6U3 streptococc
43	27	84.4	195	2 Q9LSW8	Q9LSW8 streptococc
44	27	84.4	196	2 Q9RNU4	Q9RNU4 streptococc
45	27	84.4	213	2 Q9S3P6	Q9S3P6 streptococc

ALIGNMENTS

RESULT 1

Q9UL78 PRELIMINARY; PRT; 109 AA.
 ID Q9UL78
 AC Q9UL78
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE Myosin-reactive immunoglobulin light chain variable region
 DS (Fragment).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 CX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98277139; PubMed=9614934;
 RA Wu X., Liu B., Van der Merwe P.L., Kallis N.N., Berney S.M.,
 RA Young D.C.,
 RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
 RT fetus.";
 RL Clin. Immunol. Immunopathol. 87:184-192(1998).
 DR EMBL; AF035036; AAD56272.1; -.
 DR HSSP; P80362; IWTL.
 DR InterPro; IPR003006; IG_MHC.
 DR InterPro; IPR003596; IG_V.
 DR Pfam; PF00047; IG_1.
 DR SMART; SM00406; IGV_1.
 FT NON_TER 1
 FT NON_TER 109
 SQ SEQUENCE 109 AA; 11646 MW; 5F675C52EC7BE197 CRC64;

Query Match 100.0%; Score 32; DB 4; Length 109;
 Best Local Similarity 100.0%; Pred. No. 5;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GASSRAT 7
 |||||
 DB 51 GASSRAT 57

RESULT 2
ID 068986 PRELIMINARY; PRT; 95 AA.
AC 068986; (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE Pol polypeptide (Fragment).
GN POL.
OS Human endogenous retrovirus.
OC Viruses; Retroviral viruses; Retroviridae.
OX NCBI_TaxID=11827;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=XA37;
EX MEDLINE=96332499; PubMed=8760409;
RA Wiegman B., Kjellman C., Aminoff S., Sahlfjord L.G., Sjogren H.O.;
RT "The structure and phylogeny of a new family of human endogenous
retroviruses."
RL J. Gen. Virol. 77:1631-1641 (1996).
DR EMBL; U29658; AAB19069.1; -
DR InterPro; IPR002156; RNaseH.
DR Pfam; PF00075; RNaseH; 1.
KM Polypeptide.
FT NON TER
SQ SEQUENCE 95 AA; 10370 MW; 98A2CD076DE73E2 CRC64;

Query Match 90.6%; Score 29; DB 15; Length 95;
Best Local Similarity 85.7%; Pred. No. 23;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Oy 1 GASSRAT 7
Db 8 GASSRAT 14

RESULT 3
ID 0910H4 PRELIMINARY; PRT; 107 AA.
AC 0910H4;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE Hypothetical protein SCO4783.
GN SCO4783 OR SCD63.15.
OS Streptomyces coelicolor.
OC Bacteria; Filicutes; Actinobacteria; Actinobacteridae;
OC Actinomycetales; Streptomycetaceae; Streptomyces.
OX NCBI_TaxID=1902;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=AA(2) / M145;
RA Bentley S.D., Chater K.F., Cerdano-Tarraga A.-M., Challis G.L.,
RA Thomson N.R., Harris K.D., Quail M.A., Kleiser H.,
RA Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,
RA Cronin A., Fraser A., Goble A., Hidalgo J., Hornby T., Howarth S.,
RA Huang C.-H., Kleiser T., Larke L., Murphy L., Oliver K., O'Neill S.,
RA Rabinowitz E., Rajandream M.A., Rutherford K., Rutter S.,
RA Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,
RA Warren T., Wietzorek A., Woodward J., Barrett B.G., Parkhill J.,
RA Hopwood D.A.;
RT "Complete genome sequence of the model actinomycete Streptomyces
coelicolor A3(2)."
RL Nature 417:141-147 (2002).
DR EMBL; AL161755; CAB82022.1; -
KM Hypothetical protein.
SQ SEQUENCE 107 AA; 10322 MW; F68C78C5C767B092 CRC64;

Query Match 90.6%; Score 29; DB 16; Length 107;
Best Local Similarity 85.7%; Pred. No. 26;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Oy 1 GASSRAT 7
Db 81 GASSRAT 87

RESULT 4
ID 090L85 PRELIMINARY; PRT; 109 AA.
AC 090L85;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE Myosin-reactive immunoglobulin kappa chain variable region
(Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kallis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
fetus."
RL Clin. Immunol. Immunopathol. 87:184-192 (1998).
DR EMBL; AF035029; AAD56265.1; -
DR HSSP; P80362; 1WTL.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IgV; 1.
FT NON TER
SQ SEQUENCE 109 AA; 11761 MW; FB1E43E7C7AFACCC CRC64;

Query Match 90.6%; Score 29; DB 4; Length 109;
Best Local Similarity 85.7%; Pred. No. 26;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Oy 1 GASSRAT 7
Db 50 GASSRAT 56

RESULT 5
ID 092227 PRELIMINARY; PRT; 211 AA.
AC 092227;
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
DE Hypothetical protein RA0684.
GN RA0684 OR SMA1254.
OS Rhizobium meliloti (Sinorhizobium meliloti).
OG Plantid psyma (megaplasmid 1).
OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
OC Rhizobiaceae; Sinorhizobium.
OX NCBI_TaxID=382;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=1021;
RX MEDLINE=21396509; PubMed=11481432;
RA Barnett M.J., Fisher R.F., Jones T., Komp C., Apola A.P.,
RA Barloy-Hubler F., Bowser L., Capela D., Galibert F., Gouzy J.,
RA Gurjal M., Hong A., Huizar L., Hyman R.W., Kahn D., Kahn M.L.,
RA Kalman S., Keating D.H., Palm C., Peck M.C., Surzycki R., Wells D.H.,
RA Yeh K.-C., Davis R.W., Federspiel N.A., Long S.R.;
RT "Nucleotide sequence and predicted functions of the entire
Sinorhizobium meliloti psyma megaplasmid."
RL Proc. Natl. Acad. Sci. U.S.A. 98:9883-9888 (2001).
DR EMBL; AE007256; AAK65341.1; -
KM Plasmid; Hypothetical protein; Complete proteome.

SQ SEQUENCE 211 AA; 22789 MW; 7E7F9A51D787DB4A CRC64;
 Query Match 90.6%; Score 29; DB 16; Length 211;
 Best Local Similarity 85.7%; Pred. No. 53;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GASSRAT 7
 DB 21 GSSSRAT 27
 RESULT 6
 Q9SEGS PRELIMINARY; PRT; 335 AA.
 AC Q9SEGS;
 DT 01-MAY-2000 (TREMBlrel. 13, Created)
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
 DT 01-MAY-2000 (TREMBlrel. 13, Last annotation update)
 DE 107 protein.
 GN 107.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC Eurosidia II; Brassicales; Brassicaceae; Arabidopsids.
 CX NCBI_TaxId=3702;
 RN (1)
 RP SEQUENCE FROM N.A.
 RC STRAIN=CV. COLUMBIA;
 RA Kwon H.-B.;
 RT "Molecular Cloning and Characterization of a Gibberellin-responsive
 RT Gene from Arabidopsis thaliana."
 RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
 RL EMBL; AF134217; AAF22161.1;
 SQ SEQUENCE 335 AA; 36545 MW; 7B101929E464748B CRC64;
 Query Match 90.6%; Score 29; DB 10; Length 335;
 Best Local Similarity 85.7%; Pred. No. 86;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GASSRAT 7
 DB 99 GSSSRAT 105
 RESULT 7
 Q9LN63 PRELIMINARY; PRT; 335 AA.
 AC Q9LN63;
 DT 01-OCT-2000 (TREMBlrel. 15, Created)
 DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
 DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
 DE F18014.7 (Atg19350/F18014.4)
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC Eurosidia II; Brassicales; Brassicaceae; Arabidopsids.
 CX NCBI_TaxId=3702;
 RN (1)
 RP SEQUENCE FROM N.A.
 RA Shinn P., Brooks S., Buehler E., Chao Q., Johnson-Hopson C., Khan S.,
 RA Kim C., Altafi H., Bel Q., Chin C., Chioi J., Choi E., Conn L.,
 RA Conway A., Gonzales A., Hansen N., Howling B., Koo T., Lam B., Lee J.,
 RA Lenz C., Li J., Liu A., Liu K., Liu S., Mukharbek N., Nguyen M.,
 RA Palm C., Pham P., Sakano H., Schwartz J., Southwick A., Thayer A.,
 RA Toriumi M., Vaynsberg M., Yu G., Federpriel N.A., Theologis A.,
 RA Ecker J.R.;
 RT "Genomic sequence for Arabidopsis thaliana BAC F18014 from chromosome
 RT 1."
 RL Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.
 RN (2)
 RP SEQUENCE FROM N.A.
 RC STRAIN=K1;
 RA Cheuk R., Chen H., Kim C.J., Koesema E., Meyers M.C., Banh J.,
 RA Bower L., Carninci P., Chang E., Dale J.M., Goldsmith A.D.,

RA Hayashizaki Y., Ishida J., Jones T., Kamiya A., Karlin-Neumann G.,
 RA Kawai J., Lam B., Lee J.M., Lin J., Miranda M., Narusaka M.,
 RA Nguyen M., Onodera C.S., Palm C.J., Quach H.L., Sakurai T., Satou M.,
 RA Seki M., Southwick A., Tang C.C., Toriumi M., Wu H.C., Yamada K.,
 RA Yamamura Y., Yu G., Yu S., Shinozaki K., Davis R.W., Theologis A.,
 RA Ecker J.R.;
 RT "Arabidopsis cDNA clones."
 RT Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
 RL EMBL; AC025808; AAF79422.1;
 DR EMBL; AY065041; AAL57677.1;
 SQ SEQUENCE 335 AA; 36485 MW; 7B0AA929FED4748B CRC64;
 Query Match 90.6%; Score 29; DB 10; Length 335;
 Best Local Similarity 85.7%; Pred. No. 86;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GASSRAT 7
 DB 99 GSSSRAT 105
 RESULT 8
 Q9F152 PRELIMINARY; PRT; 346 AA.
 AC Q9F152;
 DT 01-MAR-2001 (TREMBlrel. 16, Created)
 DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
 DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
 DE Mobilization protein MobB.
 GN MOB.
 OS Bifidobacterium longum.
 OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
 OC Bacteroidetes; Bifidobacteriales; Bifidobacteriaceae; Bifidobacterium.
 CX NCBI_TaxId=1679;
 RN (1)
 RP SEQUENCE FROM N.A.
 RC STRAIN=KJ;
 RA Ji G.B., Park M.S., Shin D.W.;
 RT "Sequence analysis of pkj36 from Bifidobacterium longum."
 RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
 RL EMBL; AF139129; AAG43281.1;
 DR InterPro; IPR005053; MobA_MobB.
 DR Pfam; PF03389; MobA_MobB; 1.
 KW PfamId.
 SQ SEQUENCE 346 AA; 39171 MW; 8F49CF64A4E0D4AD CRC64;
 Query Match 90.6%; Score 29; DB 2; Length 346;
 Best Local Similarity 85.7%; Pred. No. 89;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GASSRAT 7
 DB 314 GATSRAT 320
 RESULT 9
 Q9YB05 PRELIMINARY; PRT; 102 AA.
 AC Q9YB05;
 DT 01-NOV-1999 (TREMBlrel. 12, Created)
 DT 01-NOV-1999 (TREMBlrel. 12, Last sequence update)
 DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
 DE Hypothetical protein APE1504.
 GN APE1504.
 OS Aeropyrum pernix.
 OC Archaea; Crenarchaeota; Thermoprotei; Desulfurococcaceae;
 OC Desulfurococcaceae; Aeropyrum.
 CX NCBI_TaxId=56636;
 RN (1)
 RP SEQUENCE FROM N.A.
 RC STRAIN=K1;
 RX MEDLINE=99310339; PubMed=10382966;

RA Kwarabayasi Y., Hino Y., Horikawa H., Yamazaki S., Halkawa Y.,
 RA Jin-no K., Takahashi M., Sekine M., Baba S.-I., Aikai A., Kosugi H.,
 RA Hosoyma A., Fukui S., Nagai Y., Nishijima K., Nakazawa H.,
 RA Takamiya M., Masuda S., Funahashi T., Tanaka T., Kudoh Y.,
 RA Yamazaki J., Kuehida N., Oguchi A., Aoki K.-I., Kubota K.,
 RA Nakamura Y., Nomura N., Sako Y., Kikuchi H.,
 RT "Complete genome sequence of an aerobic hyper-thermophilic
 RT crenarchaeon, Aeropyrum pernix K1.";
 RL DNA Res. 6:83-101(1999).
 DR EMBL: AP000061; BAA80503.1;
 KW Hypothetical protein; Complete proteome.
 SQ SEQUENCE 102 AA; 1113 MW; 307353A9E6C6968 CRC64;

Query Match 87.5%; Score 28; DB 17; Length 102;
 Best Local Similarity 85.7%; Pred. No. 43;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GASSRAT 7
 DB 31 GASSRAT 37

RESULT 10

ID Q9UL86 PRELIMINARY; PRT; 109 AA.

AC Q9UL86;
 DT 01-MAY-2000 (TREMBlrel. 13, Created)
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
 DE Myosin-reactive immunoglobulin kappa chain variable region
 DE (Fragment).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98277139; PubMed=9614934;
 RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Bernay S.M.,
 RA Young D.C.;
 RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
 RT fetus."
 RL Clin. Immunol. Immunopathol. 87:184-192(1998).
 DR EMBL: AF035028; AAD56264.1;
 DR HSSP; P80362; IWT.
 DR InterPro; IPR003006; IG_MHC.
 DR InterPro; IPR003596; IG_V.
 DR Pfam; PF00477; IG_1.
 DR SMART; SM00406; IGV; 1.
 FT NON_TER 1
 FT 109
 SQ SEQUENCE 109 AA; 11928 MW; 243325F72C7DAC83 CRC64;

Query Match 87.5%; Score 28; DB 4; Length 109;
 Best Local Similarity 85.7%; Pred. No. 46;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GASSRAT 7
 DB 51 GASSRAT 57

RESULT 11

ID Q9YDKO PRELIMINARY; PRT; 119 AA.

AC Q9YDKO;
 DT 01-NOV-1999 (TREMBlrel. 12, Created)
 DT 01-NOV-1999 (TREMBlrel. 12, Last sequence update)
 DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
 DE Hypothetical protein AFB0913.
 GN AFB0913.
 OS Aeropyrum pernix.
 OC Archaea; Crenarchaeota; Thermoprotei; Desulfurococcaceae;

OC Desulfurococcaceae; Aeropyrum.
 OX NCBI_TaxID=56636;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=K1;
 RX MEDLINE=99310339; PubMed=10382966;
 RA Kwarabayasi Y., Hino Y., Horikawa H., Yamazaki S., Halkawa Y.,
 RA Jin-no K., Takahashi M., Sekine M., Baba S.-I., Aikai A., Kosugi H.,
 RA Hosoyma A., Fukui S., Nagai Y., Nishijima K., Nakazawa H.,
 RA Takamiya M., Masuda S., Funahashi T., Tanaka T., Kudoh Y.,
 RA Yamazaki J., Kuehida N., Oguchi A., Aoki K.-I., Kubota K.,
 RA Nakamura Y., Nomura N., Sako Y., Kikuchi H.,
 RT "Complete genome sequence of an aerobic hyper-thermophilic
 RT crenarchaeon, Aeropyrum pernix K1.";
 RL DNA Res. 6:83-101(1999).
 DR EMBL: AP000060; BAA79897.1;
 KW Hypothetical protein; Complete proteome.
 SQ SEQUENCE 119 AA; 12285 MW; 05ED45A38A43879F CRC64;

Query Match 87.5%; Score 28; DB 17; Length 119;
 Best Local Similarity 85.7%; Pred. No. 50;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GASSRAT 7
 DB 84 GASSRAT 90

RESULT 12

ID Q53755 PRELIMINARY; PRT; 141 AA.
 AC Q53755;
 DT 01-NOV-1996 (TREMBlrel. 01, Created)
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
 DT 01-NOV-1998 (TREMBlrel. 08, Last annotation update)
 DE Minor sigma-like factor (RpoZ) (Fragment).
 OS Streptomyces aureofaciens.
 OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
 OC Actinomycetales; Streptomycetales; Streptomycetaceae; Streptomyces.
 OX NCBI_TaxID=1894;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CCM 3239;
 RX MEDLINE=94259284; PubMed=8200523;
 RA Kormanec J., Potuckova L., Rezuchova B.;
 RT "The Streptomyces aureofaciens homologue of the whiG gene encoding a
 RT putative sigma factor essential for sporulation."
 RL Gene 143:101-103(1994).
 DR EMBL: M90414; AAC36890.1;
 FT NON_TER 1
 FT 141
 SQ SEQUENCE 141 AA; 14996 MW; 8432DEF526460506 CRC64;

Query Match 87.5%; Score 28; DB 2; Length 141;
 Best Local Similarity 85.7%; Pred. No. 60;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GASSRAT 7
 DB 130 GASSRAT 136

RESULT 13

ID Q912Y8 PRELIMINARY; PRT; 161 AA.

AC Q912Y8;
 DT 01-MAR-2001 (TREMBlrel. 16, Created)
 DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
 DT 01-OCT-2001 (TREMBlrel. 18, Last annotation update)
 DE Hypothetical protein PA1749.
 GN PA1749.
 OS Pseudomonas aeruginosa.
 OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
 OC Pseudomonas.

```

OX NCBI_TaxID=287;
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 15692 / PAOI;
RX MEDLINE=20437337; PubMed=10984043;
RA Stover C.K., Pham X.-Q.T., Eryin A.L., Mizoguchi S.D., Warrenner P.,
RA Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.,
RA Garber R.L., Goltzy L., Tolentino E., Westbrook-Wadman S., Yuan Y.,
RA Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M.,
RA Smith K.K., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,
RA Reizer J., Satter M.H., Hancock R.E.W., Lory S., Olson M.V.;
RT "Complete genome sequence of Pseudomonas aeruginosa PAOI, an
RT opportunistic pathogen.";
RL Nature 406:959-964 (2000).
RW EMBL; AE004601; AAG05138.1;
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 161 AA; 17672 MW; 564AD9223097F23 CRC64;

Query Match 87.5%; Score 28; DB 16; Length 161;
Best Local Similarity 85.7%; Pred. No. 69;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GASSRAT 7
DB 45 GASSRAT 51

RESULT 14
O94K93 PRELIMINARY; PRT; 204 AA.
AC O94K93;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DE 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Putative kinase
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC euroids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN (1)
RP SEQUENCE FROM N.A.
RA Yamada K., Liu S.X., Sakano H., Pham P.K., Banh J., Chung M.K.,
RA Goldsmith A.D., Lee J.M., Quach H.L., Tang C., Toriumi M., Yu G.,
RA Bower L., Carninci P., Chen H., Cheuk R., Hayashizaki Y., Ishida J.,
RA Jones T., Kamiya A., Karlin-Neumann G., Kawai J., Kim C., Koesema E.,
RA Lam B., Lin J., Meyers M.C., Miranda M., Narusaka M., Nguyen M.,
RA Palm C.J., Sakurai T., Satou M., Seki M., Shinn P., Southwick A.,
RA Shinozaki K., Davis R.W., Ecker J.R., Theologis A.;
RT "Full length cDNA of gene T9J14.24/AT3G04810 (GI:12322861).";
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF370162; AAK43977.1; -.
KW Kinase.
SQ SEQUENCE 204 AA; 22823 MW; 328AB8CE7415D73D CRC64;

Query Match 87.5%; Score 28; DB 10; Length 204;
Best Local Similarity 85.7%; Pred. No. 89;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GASSRAT 7
DB 124 GASSRAT 130

RESULT 15
O9WYN6 PRELIMINARY; PRT; 266 AA.
AC O9WYN6;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-OCT-2001 (TrEMBLrel. 18, Last annotation update)
DE Keto/oxoacid ferredoxin oxidoreductase, beta subunit, putative.
GN TM0405.

```

```

OS Thermotoga maritima.
OC Bacteria; Thermotogae; Thermotogales; Thermotogaceae; Thermotoga.
OX NCBI_TaxID=2336;
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN=MSB / DSM 3109;
RX MEDLINE=99287316; PubMed=10360571;
RA Nelson K.E., Clayton R.A., Gill S.R., Gwinn M.L., Dodson R.J.,
RA Haft D.H., Hickey E.K., Peterson J.D., Nelson W.C., Ketchum K.A.,
RA McDonald L., Utterback T.R., Malek J.A., Linher K.D., Garrett M.M.,
RA Stewart A.M., Cotton M.D., Pratt M.S., Phillips C.A., Richardson D.,
RA Heidelberg J., Sutton G.G., Fleischmann R.D., Eisen J.A., White O.,
RA Salzberg S.L., Smith H.O., Venter J.C., Fraser C.M.;
RT "Evidence for lateral gene transfer between Archaea and Bacteria from
RT genome sequence of Thermotoga maritima.";
RL Nature 399:323-329 (1999).
RW EMBL; AE001720; AAD35490.1; -.
DR TIGR; TM0405; -.
DR InterPro; IPR000399; TPP_enzyme.
DR Pfam; PF02775; TPP_enzymes_C; 1;
KW Complete proteome.
SQ SEQUENCE 266 AA; 29679 MW; FDCF88F57E39909 CRC64;

Query Match 87.5%; Score 28; DB 16; Length 266;
Best Local Similarity 85.7%; Pred. No. 1.2e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GASSRAT 7
DB 53 GASSRAT 59

Search completed: June 3, 2003, 08:20:53
Job time : 6.48805 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 3, 2003, 08:02:14 ; Search time 3.15358 Seconds
(without alignments)
295.776 Million cell updates/sec

Title: US-09-644-668A-30

Sequence: 1 GA55RAT 7

Scoring table: BLASTN62
Gapop 10.0, Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: A_Geneseq_101002:*

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22:	/SID52/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.*
23:	/SID52/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	32	100.0	7	21	AAB52198
2	32	100.0	7	22	AAU08351
3	32	100.0	7	22	AAB67499
4	32	100.0	7	23	AAU81258
5	32	100.0	7	23	AAU70332
6	32	100.0	14	6	AA51247
7	32	100.0	14	12	AA15355
8	32	100.0	57	23	ABG30474
9	32	100.0	57	23	ABG30475
10	32	100.0	101	23	ABB07181

11	32	100.0	105	23	ABG30468	Human anti-CD40 mo
12	32	100.0	106	18	AAW31722	Alpha light chain
13	32	100.0	107	14	AAK38593	Human lambda light
14	32	100.0	107	19	AAW58493	Human kappa light
15	32	100.0	107	22	AA62271	Human HIV-1 monocl
16	32	100.0	107	22	AB807229	Anti-IL-4 receptor
17	32	100.0	108	21	AA52200	Human anti-HBs ant
18	32	100.0	108	22	AA693666	Human anti-Rh(D) a
19	32	100.0	108	22	AA662755	Humanized CMV5 ant
20	32	100.0	108	22	AA62775	Human HIV-1 monocl
21	32	100.0	108	22	AA62770	Human anti-CD40 mo
22	32	100.0	108	23	ABG30470	Human anti-CD40 mo
23	32	100.0	108	23	ABG30492	Human anti-CD40 mo
24	32	100.0	108	23	ABG30495	Human anti-CD40 mo
25	32	100.0	108	23	AA021549	Antibody screening
26	32	100.0	109	15	AA50218	HSV glycoprotein p
27	32	100.0	109	20	AAW84096	Human V kappa subg
28	32	100.0	109	22	AA62766	Human HIV-1 monocl
29	32	100.0	109	22	AA62773	Human HIV-1 monocl
30	32	100.0	109	23	AB807231	Anti-IL-4 receptor
31	32	100.0	109	23	AB807233	Anti-IL-4 and IL-1
32	32	100.0	110	18	AAW27545	Human Ab light cha
33	32	100.0	110	22	AA62767	Human HIV-1 monocl
34	32	100.0	110	22	AA62784	Human HIV-1 monocl
35	32	100.0	110	22	AA62782	MS-GPC-6 light cha
36	32	100.0	110	23	AAU83804	HLA-DR-specific pr
37	32	100.0	110	23	AB57554	HLA-DR-specific pr
38	32	100.0	110	23	AB57556	HLA-DR-specific pr
39	32	100.0	110	23	AB57558	HLA-DR-specific pr
40	32	100.0	110	23	AB57562	Human trkC antibod
41	32	100.0	112	23	AAU81282	Human trkC antibod
42	32	100.0	112	23	AAU81283	Human V-kappa frag
43	32	100.0	116	15	AA62930	Human V-kappa yk5
44	32	100.0	116	15	AA62930	Human V-kappa yk5
45	32	100.0	116	17	AAW03948	DNA fragment yk65.

ALIGNMENTS

RESULT 1
AAB52198 standard; Peptide; 7 AA.
XX
AC AAB52198;
XX
DT 22-FEB-2001 (first entry)
XX
DE Human anti-HBs antibody heavy chain CDR-2 peptide SEQ ID 16.
XX
KW Anti-hepatitis B monoclonal antibody; human; hepatitis B; prevention;
XX
KW antiinflammatory; hepatotropic.
XX
OS Homo sapiens.
XX
PN JP2000253878-A.
XX
PD 19-SEP-2000.
XX
PF 09-MAR-1999; 99JP-0061930.
XX
PR 09-MAR-1999; 99JP-0061930.
XX
PA (NISN) NISCHINO IND INC.
XX
PA (MEIP) MEIDI MILK PROD CO LTD.
XX
DR WPI, 2000-675345/66.
XX
PT Novel anti-hepatitis B monoclonal antibody used for the prevention of
XX
PT hepatitis B.
XX
PS Claim 11; Page 13; 27pp; Japanese.
XX

CC This invention relates to a human anti-hepatitis B monoclonal antibody.
CC Included in the invention are polynucleotide sequences AAC96948 -
CC AAC96955 which encode fragments of the heavy and light chains of the
CC antibody. Proteins and peptides represented by sequences AAB52185 -
CC AAB52210 are fragments of the anti-hepatitis B light and heavy chains.
CC Also included in the invention are PCR primers AAC96956 - AAC96977 which
CC are used in the construction of the antibody. The antibody exhibits
CC anti-inflammatory, and hepatotropic activity, and can be used in a drug
CC effective at preventing hepatitis B infection.
CC
CC
SQ Sequence 7 AA;
Query Match 100.0%; Score 32; DB 21; Length 7;
Best Local Similarity 100.0%; Pred. No. 7.8e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Dn 1 GASSRAT 7
1 GASSRAT 7
RESULT 2
AAU08351
ID AAU08351 standard; peptide; 7 AA.
AC AAU08351;
XX 17-DEC-2001 (first entry)
DT
XX Antibody light chain variable region CDR2 #3.
DE
XX Antibody; light chain; CDR2; complementarity determining region; OPGbp;
KW osteoprotegerin; osteoprotegerin binding protein; osteoclast formation;
KM bone resorption; loss of bone mass; bone tumour; osteoporosis;
KM bone cancer; rheumatoid arthritis; hypercalcaemia of malignancy;
XX steroid-induced osteoporosis.
XX
OS Synthetic.
XX WO200162932-A1.
PN 30-AUG-2001.
PD
XX 23-FEB-2001; 2001WO-US05973.
PF
XX 23-FEB-2000; 2000US-0511139.
PR 22-FEB-2001; 2001US-0791153.
XX (AMGE-) AMGEN INC.
PA
XX Deshpande RV, Hitz A, Boyle WJ, Sullivan JK;
PI WPI; 2001-557706/62.
DR
XX Antibodies that bind antagonistically to osteoprotegerin binding
PT protein, useful for treating osteoporosis, metastasis of cancer to
PT bone, rheumatoid arthritis, hypercalcaemia of malignancy and
PT steroid-induced osteoporosis -
XX
PS Claim 14; Page 129; 239pp; English.
XX
XX The invention relates to an antibody or antigen binding domain (or
CC fragment, variant or derivative), which binds to an osteoprotegerin
CC binding protein (OPGbp) and which is an antagonistic antibody.
CC The antibody or antigen binding domain may be administered to inhibit
CC osteoclast formation or activation, inhibit bone resorption in a mammal,
CC prevent or treat loss of bone mass in a mammal and to prevent or treat
CC tumour cell growth in bone. The loss of bone mass results from
CC osteoporosis, metastasis of cancer to bone, rheumatoid arthritis,
CC hypercalcaemia of malignancy and steroid-induced osteoporosis. The
CC present sequence is an antibody light chain variable region
CC complementarity determining region, CDR2, which can be incorporated into
CC an antibody/antigen binding domain of the invention.

XX
SQ Sequence 7 AA;
Query Match 100.0%; Score 32; DB 22; Length 7;
Best Local Similarity 100.0%; Pred. No. 7.8e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Dn 1 GASSRAT 7
1 GASSRAT 7
RESULT 3
AAB67499
ID AAB67499 standard; peptide; 7 AA.
AC AAB67499;
XX 29-MAY-2001 (first entry)
DT
XX Human light chain complementarity determining region 2 (CDR2).
DE
XX Complementarity determining region; CDR; immune response; antibody;
KW cytotoxic T lymphocyte associated antigen-4; CTLA-4; B7 ligand; cancer;
KM autoimmune disease; infectious disease; inflammation; allergy;
KM rheumatoid arthritis; myasthenia gravis; lupus erythematosus;
KM multiple sclerosis; insulin-dependent diabetes mellitus; inflammation;
KW transplant rejection; graft versus host disease.
XX
OS Homo sapiens.
XX WO200114424-A2.
PN 01-MAR-2001.
PD
XX 24-AUG-2000; 2000WO-US23356.
PF
XX 24-AUG-1999; 99US-0150452.
PR (MEDA-) MEDAREX INC.
XX
XX Korman AJ, Halk EL, Lomberg N;
PI WPI; 2001-202933/20.
DR
XX Novel human sequence antibody that binds to human cytotoxic T
PT lymphocyte associated antigen-4, useful for inducing, augmenting or
PT prolonging immune response to antigen or for suppressing immune
PT response in patient -
XX
PS Claim 31; Page 100; 127pp; English.
XX
XX AAB67490-99 and AAB67501-06 represents complementarity determining
CC regions (CDRs) of human antibodies. The antibodies specifically bind to
CC human cytotoxic T lymphocyte associated antigen-4 (CTLA-4). Such
CC antibodies are used in methods for inducing, augmenting or prolonging
CC an immune response to an antigen in a patient, where the antibodies
CC block binding of human CTLA-4 to human B7 ligands. The antibodies are
CC also useful for treating autoimmune disease in a subject caused or
CC exacerbated by increased activity of T cells and for treating prostate
CC cancer, melanoma or epithelial cancer. A polyvalent or polyclonal
CC antibody preparation comprising two antibodies of the invention are
CC useful for suppressing an immune response in a patient. They are used for
CC treating cancer, infectious diseases and promoting beneficial autoimmune
CC reactions for the treatment of diseases with inflammatory or allergic
CC components. The polyvalent or polyclonal preparations are useful for
CC treating autoimmune diseases such as rheumatoid arthritis, myasthenia
CC gravis and lupus erythematosus, multiple sclerosis, insulin-dependent
CC diabetes mellitus, transplant rejection, and inflammation. Graft versus
CC host disease.
XX
SQ Sequence 7 AA;

Query Match 100.0%; Score 32; DB 22; Length 7;
 Best Local Similarity 100.0%; Pred. No. 7.8e+05;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GASSRAT 7
 |||||
 Db 1 GASSRAT 7

RESULT 4

AAU81258 standard; Peptide; 7 AA.

AC AAU81258;

DT 09-APR-2002 (first entry)

DE Human tRkC antibody light chain CDR2 of variable region #3.

KW Human, mouse; anti-tRkC agonist monoclonal antibody; tRkC; antibody;
 tRkA; tRkB; cisplatin-induced neuropathy; pyridoxine-induced neuropathy;
 peripheral neuropathy; diabetic neuropathy; neurodegenerative disease;
 large-fibre sensory neuropathy; amyotrophic lateral sclerosis; tumour;
 nerve cell injury; blood cell disorder; leukaemia; eosinophilia; wound;
 basopenia; lymphopenia; monocytopenia; neutropenia; cancer; ulcer;
 Alzheimer's disease; Parkinson's disease; Huntington's disease; diabetes;
 sickle cell disease; cardiac ischaemia; cerebrovascular disorder;
 cellular degeneration; gene therapy.

OS Homo sapiens.

PN MO200198361-A2.

PD 27-DEC-2001.

PF 22-JUN-2001; 2001MO-US20153.

PR 22-JUN-2000; 2000US-213141P.

PR 05-OCT-2000; 2000US-238319P.

PA (GETH) GENENTECH INC.

PI Devaux B, Hongo JS, Presta LG, Shelton DL;

DR WPI; 2002-130790/17.

PT Novel anti-tRkC agonist monoclonal antibody useful for treating
 neurodegenerative disease, shows no significant cross-reactivity with
 tRkA/tRkB, and recognizes epitope in domain 5 of tRkC -
 PS Claim 13; Fig 11; 121pp; English.

XX The invention relates to an anti-tRkC agonist monoclonal antibody which
 CC shows no significant cross-reactivity with tRkA or tRkB, and recognizes
 CC an epitope in domain 5 of tRkC. The antibodies of the invention are
 CC effective in the treatment of cisplatin- or pyridoxine-induced
 CC neuropathy, peripheral neuropathy, diabetic neuropathy and large-fibre
 CC sensory neuropathy, neurodegenerative disease including amyotrophic
 CC lateral sclerosis, nerve cell injuries, disorders of insufficient blood
 CC cells such as leukaemia including eosinophilia, basopenia,
 CC lymphopenia, monocytopenia, neutropenia, Alzheimer's disease,
 CC Parkinson's disease, Huntington's disease and tumours. The sequences are
 CC also useful for inducing angiogenesis for treating wounds, ulcers and
 CC diabetic complications of sickle cell disease, for treating cardiac
 CC ischaemia and cerebrovascular disorders and in the diagnosis of diseases
 CC involving cellular degeneration. Sequences AAU81229-AAU81284 represent
 CC human and mouse anti-tRkC agonist monoclonal antibodies and antibody
 CC fragments of the invention.

SO Sequence 7 AA;

Query Match 100.0%; Score 32; DB 23; Length 7;
 Best Local Similarity 100.0%; Pred. No. 7.8e+05;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GASSRAT 7
 |||||
 Db 1 GASSRAT 7

RESULT 5

AAU70332 standard; Peptide; 7 AA.

AC AAU70332;

DT 14-FEB-2002 (first entry)

DE Human Kappa III light chain CDR2.

KW Immunoglobulin; antibody; light chain; heavy chain; CDR; FR;
 KW complementarily determining region; framework region; IgBP;
 KW transgenic plant; immunoglobulin binding protein array;
 KW IgM; IgG; IgA; IgD; IgE; IgY; IgW; kappa; lambda; CHBP.

OS Homo sapiens.

PN MO200183806-A1.

PD 08-NOV-2001.

PF 02-MAY-2001; 2001MO-US14349.

PR 02-MAY-2000; 2000US-0563222.

PA (EPIC-) EPICYTE PHARM INC.

PI Hiatt AC, Hein MB;

DR WPI; 2002-055482/07.

PT Preparing immunoglobulin binding protein array in plant cells by
 PT transforming the cells with different polynucleotides encoding binding
 PT protein polypeptides specific to ligand, selecting plant cells for
 PT preparing array -
 XX PS Disclosure; Page 14; 129pp; English.

XX The invention relates to transforming a population of cells (e.g. plant
 CC cells), comprising using a library of two different polynucleotides
 CC encoding different immunoglobulin binding protein (IgBP) polypeptides
 CC that specifically bind to a ligand or form one or more disulphide bonds
 CC with polypeptides in transfected cells, to generate an IgBP that
 CC binds to a ligand, and transformed plant cells are selected, and
 CC preparing an IgBP array in plant cells. At least one peptide sequence has
 CC at least 75% sequence identity to a framework region (FR) of a native
 CC IgM, IgG, IgA, IgD, IgE, IgY, kappa or lambda immunoglobulin molecule.
 CC The method is useful for preparing an immunoglobulin binding protein
 CC array, preferably heavy chain binding protein (CHBP) array in eukaryotic
 CC cells, especially plant cells (e.g. Agrobacterium tumefaciens or maize)
 CC or other eukaryotic cells (e.g. insect cells or mammalian cells). The
 CC CHBP is useful for discovery of e.g. screening assays of IgBps having
 CC desired characteristics. The present sequence is a mammalian
 CC immunoglobulin derived peptide that may be incorporated into an IgBP of
 CC the invention.

SO Sequence 7 AA;

Query Match 100.0%; Score 32; DB 23; Length 7;
 Best Local Similarity 100.0%; Pred. No. 7.8e+05;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GASSRAT 7
 |||||
 Db 1 GASSRAT 7

RESULT 6
AAP51247
ID AAP51247 standard; peptide; 14 AA.
XX
XX
AC AAP51247;
XX
DT 03-OCT-2002 (updated)
DT 03-AUG-1992 (first entry)
XX
DE Sequence that corresp. to the sequence of an idiotypic antigenic determinant of an immunoglobulin.
XX
XX Idiotypic antigenic determinant; immunoglobulin; antibody;
KW autoimmune disease; therapy; beta-lymphocyte; diagnosis;
KW human rheumatoid factor; Igm.
XX
OS Synthetic.
XX
PN WO8502909-A.
PD 04-JUL-1985.
XX
PE 28-DEC-1984; 84WO-US02116.
XX
PR 28-DEC-1983; 83US-0566172.
XX
PA (SCRI-) SCRIPPS CLINIC RES.
XX
PI Carson DA, Houghten R, Chen PP, Vaughan JH, Lerner RA,
PI Fong S;
XX
DR WPI; 1985-171405/28.
XX
PT New synthetic polypeptide(s) - for inducing anti-idiotypic
PT antibody prodn. for treatment of autoimmune diseases and for
PT immunoassays
XX
PS Claim 4; Page 69; 86pp; English.
XX
CC The synthetic polypeptides of the invention (AAP51243-PS1237) mimic
CC idiotypic antigenic determinants on immunoglobulin molecules and
CC elicit prodn. of antibodies which are useful for treatment of
CC autoimmune disease and diseases of beta-lymphocytes and which are
CC also useful in diagnostic tests. The immunoglobulin may be a human
CC rheumatoid factor of the Igm class.
CC (updated on 03-OCT-2002 to add missing OS field.)
CC
XX
SQ Sequence 14 AA;
Query Match 100.0%; Score 32; DB 6; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.7;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GASSRAT 7
Db 2 GASSRAT 8

RESULT 7
AAR15365
ID AAR15365 standard; peptide; 14 AA.
XX
XX
AC AAR15365;
XX
DT 05-MAR-1992 (first entry)
DE Ig idiotypic determinant PS12.
XX
KW Rheumatoid factor; RF; SIE; antigen; light chain; CDR; Igm.
OS Synthetic.
XX
XX

FF Key Location/Qualifiers
FT Region 1
FT Region /note= "residue belonging to adjacent framework region"
FT Region 8..13
FT Region /note= "residues belonging to adjacent framework region"
FT Region 14
FT Region /note= "residue added for coupling purposes"
XX
XX US5068177-A.
XX
PD 26-NOV-1991.
XX
PE 05-AUG-1985; 85US-0762698.
XX
PR 05-AUG-1985; 85US-0762698.
PR 28-DEC-1983; 83US-0566172.
XX
PA (SCRI-) SCRIPPS CLINIC RES.
XX
PI Carson DA, Fong S, Chen PP;
PI Fong S;
XX
DR WPI; 1991-368612/50.
XX
XX
XX Synthetic polypeptide(s) for inducing anti-idiotypic antibodies -
PT useful for treating autoimmune-, endocrine- and
PT rheumatic-diseases and myasthenia gravis
XX
PS Claim 1; Page 42; 44pp; English.
XX
XX The sequence is as reported by Capra et al. (Proc. Natl. Acad.
CC Sci. USA, 71:4032 (1974); and Proc. Natl. Acad. Sci. USA, 78:
CC 3699 (1981)). N.B.: the sequence of Claim 6 comprises UI instead
CC of YL. PS12 means as follows:
CC 'P' designates that the code named material is a synthetic peptide;
CC the second letter designates the corresp. parent protein (SIE 49-61);
CC the third letter designates the light (L) chain;
CC the numeral designates the CDR, the idiotypic antigenic determinant
CC of the Igm-rheumatoid factor.
CC See also AAR15365-74 and AAR15375.
CC
XX
SQ Sequence 14 AA;
Query Match 100.0%; Score 32; DB 12; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.7;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GASSRAT 7
Db 2 GASSRAT 8

RESULT 8
ABG30474
ID ABG30474 standard; Protein; 57 AA.
XX
XX
AC ABG30474;
XX
DT 07-OCT-2002 (first entry)
DE Human anti-CD40 monoclonal antibody 12D9 light chain #1.
XX
XX Human; light chain; CD40; autoimmune disease; multiple sclerosis;
KW systemic lupus erythematosus; psoriasis; inflammatory bowel disease;
KW Crohn's disease; rheumatoid arthritis; organ rejection; lymphoma;
KW non-Hodgkin's lymphoma; monoclonal antibody; B cell; glycoprotein;
KW proliferation.
XX
OS Homo sapiens.
XX
XX
XX WO200228904-A2.

PA	(CHTR) CHIRON CORP.
XX	
PI	Chu K, Wang C, Yoshinara C, Donnelly JJ;
XX	
DR	WPI, 2002-402142/43.
XX	
XX	A human anti-CD40 monoclonal antibody or fragment useful for inhibiting
PT	proliferation, growth or differentiation of a normal human B cells and
PT	treating autoimmune disease such as rheumatoid arthritis or systemic
PT	lupus erythematosus -
PS	Claim 1; Fig 5; 75pp; English.
XX	
CC	The invention relates to a human monoclonal antibody or fragment capable
CC	of specifically binding to a human CD40 antigen (a glycoprotein expressed
CC	on the surface of human B cells), where the antibody or fragment is free
CC	or significant agonistic activity when it binds to the CD40 antigen, and
CC	the growth or differentiation is inhibited. The fragments comprise
CC	the complementarily determining region (CDR) of the light and heavy
CC	chains of the monoclonal antibodies secreted by a hybridoma consisting of
CC	158B, 20C ₄ , 12D9, 9F7 and 1J84. Also included are the nucleic acids
CC	encoding the antibody (or fragments). The antibodies or fragments
CC	are used for inhibiting proliferation, growth or differentiation of a
CC	normal human B cells and to inhibit antibody production by B cells.
CC	They may also be useful for treating autoimmune diseases, such as
CC	systemic lupus erythematosus, psoriasis, multiple sclerosis, inflammatory
CC	bowel disease (Crohn's disease), rheumatoid arthritis, and lymphoma
CC	(especially Non-Hodgkin's Lymphoma). The present sequence represents
CC	the antibody 20C ₄ light chain.
XX	
XX	Sequence 57 AA:
Query Match	100.0%; Score 32; DB:23; Length 57;
Best Local Similarity	100.0%; Pred. No. 7.2;
Matches	7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy	1 GAASSRAT 7
Db	51 GAASSRAT 57
RESULT 10	
ABBO7181	ID ABB07181 standard; Protein; 101 AA.
XX	
AC	ABB07181;
XX	
DT	13-MAR-2002 (first entry)
DE	CB2IE12 kappa chain variable region.
XX	
XX	Neuromodulatory; central nervous system; CNS; SHIGM22; LYM 22; AKJR4;
KW	ebvHIGM MGII19D10; ebv HIGM CB2IB68; CB2IE12; CB2IE7; MS119E5; valnucide;
KX	antiParkinsonian; neuroprotective; nootropic; vulnary.
XX	
OS	Homo sapiens.
XX	
FN	WO200185797-A1.
XX	
PD	15-NOV-2001.
XX	
PF	30-MAY-2000; 2000MO-US14902.
XX	
PR	10-MAY-2000; 2000US-0568351.
XX	
PA	(MAYO-) MAYO FOUND MEDICAL EDUCATION RES.
XX	
PI	Rodriguez M, Miller DJ, Pease LR;
XX	
DR	WPI; 2002-066596/09.
DR	N-PADB; ABA94228.
XX	
PT	Novel neuromodulatory agent (a human Igm monoclonal antibody);

PT promoting neurite outgrowth, regeneration, remyelination and
 PT neuroprotection in central nervous system, useful to treat
 PT post-infectious encephalomyelitis -
 PS Claim 24; Fig 40; 21pp; English.
 XX
 CC The invention provides a neuromodulatory agent (I) capable of promoting
 CC neurite outgrowth, regeneration, remyelination and neuroprotection in
 CC central nervous system (CNS). (I) is capable of inducing remyelination,
 CC promoting cellular proliferation of glial cells, and promoting Ca²⁺
 CC signaling with oligodendrocytes. A humanised antibody to (I) can be
 CC selected from antibody SHGM22 (LYM 22), ebvHGM Mait19D10, ebv HGM
 CC CB2b09, AKR4, CB21E12, CB21E7 or MS119E5. (I) is useful for stimulating
 CC remyelination of CNS axons, stimulating proliferation of glial cells in
 CC CNS axons, or treating demyelinating disease of CNS in a mammal in need
 CC of such therapy. (I) is capable of binding to structures and cells within
 CC CNS. (I) is preferably useful for treating a demyelinating disease of CNS
 CC of a mouse infected with Strain DA of Theiler's murine encephalomyelitis
 CC (TMEV) or for treating a human being having multiple sclerosis, or a post-
 CC human or domestic animal with a viral demyelinating disease, or a post-
 CC neural disease of CNS. (I) is also useful for an in vitro method of
 CC stimulating the proliferation of glial cells from mixed cell culture.
 CC (I) is also useful for stimulating remyelination of CNS axons. The
 CC antibodies are useful for preventing infection by a bacterium, virus or
 CC like pathogen that causes demyelination or other neurodegenerative
 CC condition in a subject. Methods where (I) is administered to a patient
 CC are useful for treating multiple sclerosis, Parkinson's disease,
 CC Alzheimer's disease, amyotrophic lateral sclerosis (ALS), a viral
 CC demyelinating disease, CNS diseases, and other conditions in the CNS
 CC where nerves are damaged as by trauma. The present sequence represents
 CC the CB21E12 kappa chain variable region.
 XX
 SQ Sequence 101 AA;
 Query Match 100.0%; Score 32; DB 23; Length 101;
 Best Local Similarity 100.0%; Pred. No. 13;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GASSRAT 7
 |||||
 DB 51 GASSRAT 57
 RESULT 11
 ABG30468
 ID ABG30468 standard; Protein; 105 AA.
 XX
 AC ABG30468;
 XX
 DT 07-OCT-2002 (first entry)
 XX
 DE Human anti-CD40 monoclonal antibody 12D9 VK.1 region.
 XX
 KW Human; VK.1; kappa chain variable region; CD40;
 KW autoimmune disease; systemic lupus erythematosus; psoriasis;
 KW multiple sclerosis; inflammatory bowel disease; Crohn's disease;
 KW rheumatoid arthritis; organ rejection; lymphoma; non-Hodgkin's lymphoma;
 KW monoclonal antibody; B cell; glycoprotein; proliferation.
 XX
 OS Homo sapiens.
 XX
 PN WO200228904-A2.
 XX
 PD 11-APR-2002.
 XX
 PF 02-OCT-2001; 2001WO-US30857.
 XX
 PR 02-OCT-2000; 2000US-237556P.
 XX
 XX (CHIR) CHIRON CORP.
 XX
 XX Chu K, Wang C, Yoshihara C, Donnelly JJ,
 XX

DR WPI; 2002-402142/43.
 XX
 XX
 PT A human anti-CD40 monoclonal antibody or fragment useful for inhibiting
 PT proliferation, growth or differentiation of a normal human B cell and
 PT treating autoimmune disease such as rheumatoid arthritis or systemic
 PT lupus erythematosus -
 PS Claim 8; Fig 14; 75pp; English.
 XX
 CC The invention relates to a human monoclonal antibody or fragment capable
 CC of specifically binding to a human CD40 antigen (a glycoprotein expressed
 CC on the surface of human B cells), where the antibody or fragment is free
 CC of significant agonistic activity when it binds to the CD40 antigen, and
 CC the growth or differentiation is inhibited. The fragments comprise
 CC the complementarity determining region (CDR) of the light and heavy
 CC chains of the monoclonal antibodies secreted by a hybridoma consisting of
 CC 15B9, 20C4, 12D9, 9F7 and 13B4. Also included are the nucleic acids
 CC encoding the antibody (or fragments). The antibodies or fragments
 CC are used for inhibiting proliferation, growth or differentiation of a
 CC normal human B cells and to inhibit antibody production by B cells.
 CC They may also be useful for treating autoimmune diseases, such as
 CC systemic lupus erythematosus, psoriasis, multiple sclerosis, inflammatory
 CC bowel disease (Crohn's disease), rheumatoid arthritis, and lymphoma
 CC (especially Non-Hodgkin's lymphoma). The present sequence represents
 CC the antibody 12D9 kappa chain variable region VK.1.
 XX
 SQ Sequence 105 AA;
 Query Match 100.0%; Score 32; DB 23; Length 105;
 Best Local Similarity 100.0%; Pred. No. 13;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GASSRAT 7
 |||||
 DB 51 GASSRAT 57
 RESULT 12
 AAW31722
 ID AAW31722 standard; Peptide; 106 AA.
 XX
 AC AAW31722;
 XX
 DT 29-APR-1998 (first entry)
 XX
 DE Alpha light chain amino acid sequence of the Fab molecule clone 1.5.
 XX
 KW Alpha light chain; Fab molecule; binding; hepatitis C virus; HCV;
 KW B2 antigen; combinatorial antibody library; vaccine; antibody;
 KW recombinant human monoclonal antibody; immunological binding affinity;
 KW passive immunity.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Region 23..34
 FT /note= "CDR 1"
 FT Region 49..56
 FT /note= "CDR 2"
 FT Region 88..97
 FT /note= "CDR 3"
 XX
 PN WO9740176-A1.
 XX
 PD 30-OCT-1997.
 XX
 PF 18-APR-1997; 97WO-EP01977.
 XX
 PR 17-APR-1997; 97US-0844215.
 XX
 PR 19-APR-1996; 96US-0635109.
 XX
 XX (ALTA/) ALLANDER T E.
 XX (PERS/) PERSSON M A.

XX Allander TE, Persson MA;
 PI MPI, 1997-535657/49.
 DR N-PSDB; AAR88833.
 XX New human monoclonal antibodies to hepatitis C virus E2 antigen -
 PT obtained using a combinatorial antibody library prepared using RNA
 PT from a HCV infected subject, useful for vaccine preparation
 XX
 PS Claim 5, Fig 2A; 103pp; English.
 CC The present sequence represents the alpha light chain peptide sequence
 CC of the Fab molecule, clone 1:5. This immunoglobulin molecule is
 CC capable of specifically binding with the hepatitis C virus (HCV)
 CC E2 antigen. The present sequence was obtained from a combinatorial
 CC antibody library. The alpha light chain peptide can be used to construct
 CC a recombinant human monoclonal antibody (Mab). The monoclonal antibodies
 CC exhibit immunological binding affinity for HCV E2 antigen and are
 CC cross-reactive with different HCV strains. They can be used to produce
 CC vaccine compositions which can be used to provide antibodies to HCV in
 CC a subject or to provide passive immunity or to treat HCV infected
 CC subjects. They can also be used to detect HCV and to monitor anti-HCV
 CC therapeutic treatment.
 SQ Sequence 106 AA;
 Query Match 100.0%; Score 32; DB 18; Length 106;
 Best Local Similarity 100.0%; Pred. No. 14;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GASSRAT 7
 DB 49 GASSRAT 55
 RESULT 13
 AAR38593
 ID AAR38593 standard; peptide; 107 AA.
 AC AAR38593;
 XX 28-OCT-1993 (first entry)
 DT
 XX Human lambda light chain subgroup 3 (HL3).
 DE
 XX Antibody; variable domain; light; L; heavy; H; consensus;
 KM affinity; antigen; immunogenicity; humanisation; framework.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 96
 FT /note= "residue conserved in less than 50% of the
 FT known sequences of HL3"
 XX
 PN WO9311794-A.
 XX
 PD 24-JUN-1993.
 XX
 PR 14-DEC-1992; 92MO-US10906.
 XX
 PR 13-DEC-1991; 91US-0808464.
 XX
 PA (XOMA) XOMA CORP.
 XX
 PI Fishwild DM, Kohn FR, Little RG, Studnicka GM;
 DR MPI, 1993-213827/26.
 XX
 XX Antibodies prepn. used for treatment of auto-immune diseases - by
 PT replacement of critical residues to reduce immunogenicity but
 PT retain binding affinity, etc.

XX Claim 2; Page 93-94; 160pp; English.
 PS
 CC The consensus amino acid sequences for the subgroups of light
 CC chains (hK1 - AAR38590, hK3 - NGK, hK2 - GST, hL1 - AAR38591, hL2 -
 CC AAR38592, hL3 - AAR38594, hL6 - AAR38595, hL4 -
 CC AAR38596, and hL5 - AAR38597) and heavy chains (hH3 - AAR38598, hH1 -
 CC AAR38599, and hH2 - AAR38600) of human variable domains may be used to
 CC prepare, for example, a modified mouse antibody variable domain that
 CC retains the affinity of the natural domain for antigen while exhibiting
 CC reduced immunogenicity in humans.
 CC Unlike other methods of humanisation, which advocate the
 CC replacement of entire antibody framework regions with those of human
 CC antibodies, this method involves only the introduction of human
 CC residues into those positions not critical for antigen binding.
 CC This ensures that the binding properties of the modified antibody
 CC are not diminished.
 SQ Sequence 107 AA;
 Query Match 100.0%; Score 32; DB 14; Length 107;
 Best Local Similarity 100.0%; Pred. No. 14;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GASSRAT 7
 DB 50 GASSRAT 56
 RESULT 14
 AAM58493
 ID AAM58493 standard; protein; 107 AA.
 AC AAM58493;
 XX 18-AUG-1998 (first entry)
 DT
 XX Human kappa light chain subgroup 3 consensus sequence hK3.
 DE
 XX Humanised; human; mouse; CD5; anti-CD5 antibody; immunoglobulin;
 KM depletion; cytotoxic; immunconjugate; fusion protein; porphyrin;
 XX autoimmune disease; rheumatoid arthritis; type I diabetes.
 XX
 OS Synthetic.
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 96
 FT /note= "not specified"
 XX
 PN US5770196-A.
 XX
 PD 23-JUN-1998.
 XX
 PR 07-JUN-1995; 95US-0472788.
 XX
 PR 23-JUN-1993; 93US-0082842.
 XX
 PR 13-DEC-1991; 91US-0808464.
 XX
 PR 14-DEC-1992; 92MO-US10906.
 XX
 PR 07-JUN-1995; 95US-0472788.
 XX
 PA (XOMA) XOMA CORP.
 XX
 PI Studnicka GM;
 DR MPI, 1998-376744/32.
 XX
 XX Depletion of CD5-positive cells in vivo - using anti-CD5 antibodies
 PT with humanised variable regions
 PT
 PS Disclosure; Column 51-54; 77pp; English.
 XX
 CC A method has been developed of depleting CD5+ cells in an animal. The

CC method comprises administering a cytotoxic protein containing a modified
CC immunoglobulin (Ig) variable domain, where the protein is an anti-CD5 Ig
CC molecule or an immunconjugate or fusion protein containing an anti-CD5
CC Ig molecule, and where the modified Ig variable domain comprises at
CC least one of (a) a modified light chain variable region (see AAW58478 or
CC AAW58480), and (b) a modified heavy chain variable region (see AAW58479
CC or AAW58481), where AAW58478 and AAW58479 are humanised forms of the H65
CC light and heavy chain variable domains with low risk amino acid
CC substitutions [i.e. low risk of reducing antigen-binding specificity.]
CC and AAW58480 and AAW58481 are humanised forms of the H65 light and heavy
CC chain variable domains with moderate risk amino acid substitutions and
CC are present in humanised H65 antibody hex (AYCC HB 11206). The method is
CC useful for treating autoimmune diseases, especially systemic lupus
CC erythematosus, rheumatoid arthritis, psoriasis or type I diabetes. The
CC present sequence represents a consensus amino acid sequence for light
CC chain subgroups of human antibody variable domains, from the present
CC invention.

XX Sequence 107 AA;

Query Match 100.0%; Score 32; DB 19; Length 107;

Best Local Similarity 100.0%; Pred. No. 14;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GASSRAT 7
|||
Db 50 GASSRAT 56

RESULT 15

AAB62771 AAB62771 standard; Protein; 107 AA.

XX AAB62771;

DT 03-APR-2001 (first entry)

XX Human HIV-1 monoclonal antibody SEQ ID NO: 70.

XX Human immunodeficiency virus-1; HIV-1; human monoclonal antibody;

XX envelope glycoprotein; gp120; diagnosis.

XX Homo sapiens.

XX WO200106678-A1.

XX 04-JAN-2001.

XX 23-JUN-2000; 2000WO-US17327.

XX 30-JUN-1999; 99US-0141701.

XX (USSH) US DEPT HEALTH & HUMAN SERVICES.

XX Watkins BA, Reitz MS;

XX WPI; 2001-112438/12.

XX N-PSDB; AAF29072.

XX Novel human monoclonal antibody immunoreactive with human

XX immunodeficiency virus-1 glycoprotein gp120, useful for detecting HIV-1

XX in biological sample and providing passive immunotherapy to HIV-1

XX infected mammal

XX Claim 1; Page 66-67; 81pp; English.

Query Match 100.0%; Score 32; DB 22; Length 107;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GASSRAT 7
|||
Db 50 GASSRAT 56

Search completed: June 3, 2003, 08:14:49
Job time : 3.15358 secs

XX The present invention provides the protein and coding sequences for the
XX variable regions of human monoclonal antibodies which are immunoreactive
XX with human immunodeficiency virus-1 (HIV-1) envelope glycoprotein gp120.
XX These can be used in diagnosis and therapy of HIV-1 infection.

XX Sequence 107 AA;

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OM protein - protein search, using sw model

Run on: June 3, 2003, 08:21:07 ; Search time 1.66041 Seconds

(without alignments)
426.742 Million cell updates/sec

Title: US-09-644-668A-30

Perfect score: 32

Sequence: 1 GASSRAT 7

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 383519 seqs, 101223694 residues

Total number of hits satisfying chosen parameters: 383519

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:*

- 1: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
- 2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
- 4: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
- 5: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
- 6: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
- 7: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep.*
- 8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
- 9: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
- 10: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep.*
- 11: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
- 12: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep.*
- 13: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
- 14: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	32	100.0	7	US-09-563-222-12	Sequence 12, Appl
2	32	100.0	7	US-09-828-708-45	Sequence 45, Appl
3	32	100.0	7	US-09-828-708-47	Sequence 47, Appl
4	32	100.0	7	US-09-828-708-48	Sequence 48, Appl
5	32	100.0	7	US-09-828-708-49	Sequence 49, Appl
6	32	100.0	7	US-10-125-687-23	Sequence 23, Appl
7	32	100.0	7	US-10-025-687-23	Sequence 23, Appl
8	32	100.0	7	US-10-194-975-82	Sequence 82, Appl
9	32	100.0	7	US-10-153-382-22	Sequence 22, Appl
10	32	100.0	7	US-09-828-708-6	Sequence 6, Appl
11	32	100.0	7	US-09-828-708-3	Sequence 3, Appl
12	32	100.0	7	US-09-828-708-5	Sequence 5, Appl
13	32	100.0	7	US-09-828-708-7	Sequence 7, Appl
14	32	100.0	7	US-08-844-215-8	Sequence 8, Appl
15	32	100.0	7	US-09-848-798-178	Sequence 178, Appl
16	32	100.0	7	US-10-125-687-10	Sequence 10, Appl
17	32	100.0	7	US-10-073-644C-8	Sequence 8, Appl
18	32	100.0	7	US-10-025-687-10	Sequence 10, Appl
19	32	100.0	7	US-10-001-934-40	Sequence 40, Appl

20	32	100.0	139	9	US-10-153-382-25	Sequence 25, Appl
21	32	100.0	141	9	US-10-153-382-23	Sequence 23, Appl
22	32	100.0	141	9	US-10-153-382-24	Sequence 24, Appl
23	32	100.0	146	9	US-10-153-382-28	Sequence 28, Appl
24	32	100.0	224	9	US-09-453-234-44	Sequence 44, Appl
25	32	100.0	224	9	US-09-453-234-52	Sequence 52, Appl
26	32	100.0	224	9	US-09-453-234-76	Sequence 76, Appl
27	32	100.0	224	9	US-09-453-234-78	Sequence 78, Appl
28	32	100.0	226	9	US-09-453-234-48	Sequence 48, Appl
29	32	100.0	226	9	US-09-453-234-42	Sequence 42, Appl
30	32	100.0	226	9	US-09-453-234-50	Sequence 50, Appl
31	32	100.0	226	9	US-09-453-234-72	Sequence 72, Appl
32	32	100.0	226	9	US-09-453-234-74	Sequence 74, Appl
33	32	100.0	226	9	US-09-453-234-86	Sequence 86, Appl
34	32	100.0	233	9	US-10-153-382-11	Sequence 11, Appl
35	32	100.0	233	9	US-10-153-382-7	Sequence 7, Appl
36	32	100.0	236	10	US-09-859-053-34	Sequence 34, Appl
37	32	100.0	236	10	US-09-859-053-38	Sequence 38, Appl
38	32	100.0	245	9	US-09-880-748-1896	Sequence 1896, Ap
39	32	100.0	246	9	US-09-880-748-1264	Sequence 1264, Ap
40	32	100.0	249	9	US-09-880-748-1035	Sequence 1035, Ap
41	32	100.0	251	9	US-09-880-748-1219	Sequence 1219, Ap
42	32	100.0	253	9	US-09-880-748-1499	Sequence 1499, Ap
43	29	90.6	7	9	US-09-977-797A-30	Sequence 30, Appl
44	29	90.6	88	10	US-09-905-243-32	Sequence 32, Appl
45	29	90.6	95	9	US-10-194-975-84	Sequence 84, Appl

ALIGNMENTS

RESULT 1
US-09-563-222-12
; Sequence 12, Application US/09563222
; Publication No. US20030079253A1
GENERAL INFORMATION:
APPLICANT: Hiatt, Andrew
APPLICANT: Hehn, Mich B.
TITLE OF INVENTION: IMMUNOGLOBULIN BINDING PROTEIN ARRAYS IN
FILE REFERENCE: 310098.406
CURRENT FILING DATE: 2000-05-02
CURRENT FILING DATE: 2000-05-02
NUMBER OF SEQ ID NOS: 197
SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-563-222-12

Query Match 100.0%; Score 32; DB 9; Length 7;
Best Local Similarity 100.0%; Pred. No. 3.4e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0;
Gaps 0;

Qy 1 GASSRAT 7
|||
Db 1 GASSRAT 7

RESULT 2
US-09-828-708-45
; Sequence 45, Application US/09828708
; Patent No. US20020146753A1
GENERAL INFORMATION:
APPLICANT: Ditzel, H.
APPLICANT: Burton, D.
APPLICANT: Schaller, M.
TITLE OF INVENTION: Autoantibodies to glucose-6-phosphate isomerase and their parti
FILE REFERENCE: 1361.005US1
CURRENT FILING DATE: 2001-09-24

NUMBER OF SEQ ID NOS: 123
 SOFTWARE: FastSeq for Windows Version 4.0
 SEQ ID NO 45
 LENGTH: 7
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-09-828-708-45

Query Match
 Best Local Similarity 100.0%; Score 32; DB 10; Length 7;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GASSRAT 7
 Db 1 GASSRAT 7

RESULT 3
 US-09-828-708-47
 Sequence 47, Application US/09828708
 Patent No. US20020146753A1
 GENERAL INFORMATION:
 APPLICANT: Ditzel, H.
 APPLICANT: Burton, D.
 APPLICANT: Schaller, M.
 TITLE OF INVENTION: Autoantibodies to glucose-6-phosphate isomerase and their partic
 FILE REFERENCE: 1361.005US1
 CURRENT APPLICATION NUMBER: US/09/828,708
 CURRENT FILING DATE: 2001-09-24
 NUMBER OF SEQ ID NOS: 123
 SOFTWARE: FastSeq for Windows Version 4.0
 SEQ ID NO 47
 LENGTH: 7
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-09-828-708-47

Query Match
 Best Local Similarity 100.0%; Score 32; DB 10; Length 7;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GASSRAT 7
 Db 1 GASSRAT 7

RESULT 4
 US-09-828-708-48
 Sequence 48, Application US/09828708
 Patent No. US20020146753A1
 GENERAL INFORMATION:
 APPLICANT: Ditzel, H.
 APPLICANT: Burton, D.
 APPLICANT: Schaller, M.
 TITLE OF INVENTION: Autoantibodies to glucose-6-phosphate isomerase and their partic
 FILE REFERENCE: 1361.005US1
 CURRENT APPLICATION NUMBER: US/09/828,708
 CURRENT FILING DATE: 2001-09-24
 NUMBER OF SEQ ID NOS: 123
 SOFTWARE: FastSeq for Windows Version 4.0
 SEQ ID NO 48
 LENGTH: 7
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-09-828-708-48

Query Match
 Best Local Similarity 100.0%; Score 32; DB 10; Length 7;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GASSRAT 7

Db 1 GASSRAT 7

RESULT 5
 US-09-828-708-49
 Sequence 49, Application US/09828708
 Patent No. US20020146753A1
 GENERAL INFORMATION:
 APPLICANT: Ditzel, H.
 APPLICANT: Burton, D.
 APPLICANT: Schaller, M.
 TITLE OF INVENTION: Autoantibodies to glucose-6-phosphate isomerase and their pa
 FILE REFERENCE: 1361.005US1
 CURRENT APPLICATION NUMBER: US/09/828,708
 CURRENT FILING DATE: 2001-09-24
 NUMBER OF SEQ ID NOS: 123
 SOFTWARE: FastSeq for Windows Version 4.0
 SEQ ID NO 49
 LENGTH: 7
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-09-828-708-49

Query Match
 Best Local Similarity 100.0%; Score 32; DB 10; Length 7;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GASSRAT 7
 Db 1 GASSRAT 7

RESULT 6
 US-10-125-687-23
 Sequence 23, Application US/10125687
 Publication No. US20030054407A1
 GENERAL INFORMATION:
 APPLICANT: Luo, Peter
 TITLE OF INVENTION: STRUCTURE-BASED CONSTRUCTION OF HUMAN ANTIBODY LIBRARY
 FILE REFERENCE: 26050-705
 CURRENT APPLICATION NUMBER: US/10/125,687
 CURRENT FILING DATE: 2002-04-17
 NUMBER OF SEQ ID NOS: 28
 SOFTWARE: PatentIn version 3.1
 SEQ ID NO 23
 LENGTH: 74
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-10-125-687-23

Query Match
 Best Local Similarity 100.0%; Score 32; DB 9; Length 74;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GASSRAT 7
 Db 44 GASSRAT 50

RESULT 7
 US-10-025-687-23
 Sequence 23, Application US/10025687
 Patent No. US20020142255A1
 GENERAL INFORMATION:
 APPLICANT: Luo, Peter
 TITLE OF INVENTION: STRUCTURE-BASED CONSTRUCTION OF HUMAN ANTIBODY LIBRARY
 FILE REFERENCE: 26050-705
 CURRENT APPLICATION NUMBER: US/10/025,687
 CURRENT FILING DATE: 2002-04-17
 NUMBER OF SEQ ID NOS: 28
 SOFTWARE: PatentIn version 3.1

SEQ ID NO: 73
LENGTH: 74
TYPE: PRT
ORGANISM: Homo sapiens
US-10-025-687-23

Query Match
Best Local Similarity 100.0%; Score 32; DB 12; Length 74;
Pred. No. 4.2; Mismatches 0; Indels 0; Gaps 0;
Matches 7; Conservative 0;

QY 1 GASSRAT 7
|||||
Db 44 GASSRAT 50

RESULT 8
US-10-194-975-82
Sequence 82, Application US/10194975
Publication No. US20030039649A1
GENERAL INFORMATION:

APPLICANT: Foote, Jefferson
TITLE OF INVENTION: Super Humanized Antibodies
FILE REFERENCE: 501231.01
CURRENT APPLICATION NUMBER: US/10/194,975
CURRENT FILING DATE: 2002-10-10
PRIOR APPLICATION NUMBER: US 60/305,111
PRIOR FILING DATE: 2001-07-12
NUMBER OF SEQ ID NOS: 122
SOFTWARE: PatentIn version 3.1
SEQ ID NO 82
LENGTH: 96
TYPE: PRT
ORGANISM: Homo sapiens
US-10-194-975-82

Query Match
Best Local Similarity 100.0%; Score 32; DB 9; Length 96;
Pred. No. 5.4; Mismatches 0; Indels 0; Gaps 0;
Matches 7; Conservative 0;

QY 1 GASSRAT 7
|||||
Db 51 GASSRAT 57

RESULT 9
US-10-153-382-22

Sequence 22, Application US/10153382
Publication No. US20030066930A1
GENERAL INFORMATION:

APPLICANT: PRIZER PRODUCTS INC.
TITLE OF INVENTION: USES OF ANTI-CTLA-4 ANTIBODIES
FILE REFERENCE: PC23019A
CURRENT APPLICATION NUMBER: US/10/153,382
CURRENT FILING DATE: 2002-05-22
PRIOR APPLICATION NUMBER: 60/293042
PRIOR FILING DATE: 2001-05-23
NUMBER OF SEQ ID NOS: 39
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 22
LENGTH: 96
TYPE: PRT
ORGANISM: Homo sapiens
US-10-153-382-22

Query Match
Best Local Similarity 100.0%; Score 32; DB 9; Length 96;
Pred. No. 5.4; Mismatches 0; Indels 0; Gaps 0;
Matches 7; Conservative 0;

QY 1 GASSRAT 7
|||||
Db 51 GASSRAT 57

RESULT 10
US-09-828-708-6
Sequence 6, Application US/09828708
Patent No. US20020146753A1
GENERAL INFORMATION:

APPLICANT: Ditzel, H.
APPLICANT: Burton, D.
APPLICANT: Schaller, M.
TITLE OF INVENTION: Autoantibodies to glucose-6-phosphate isomerase and their partic
FILE REFERENCE: 1361.005U1
CURRENT APPLICATION NUMBER: US/09/828,708
CURRENT FILING DATE: 2001-09-24
NUMBER OF SEQ ID NOS: 123
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 6
LENGTH: 104
TYPE: PRT
ORGANISM: Homo sapiens
US-09-828-708-6

Query Match
Best Local Similarity 100.0%; Score 32; DB 10; Length 104;
Pred. No. 5.9; Mismatches 0; Indels 0; Gaps 0;
Matches 7; Conservative 0;

QY 1 GASSRAT 7
|||||
Db 44 GASSRAT 50

RESULT 11
US-09-828-708-3
Sequence 3, Application US/09828708
Patent No. US20020146753A1
GENERAL INFORMATION:

APPLICANT: Ditzel, H.
APPLICANT: Burton, D.
APPLICANT: Schaller, M.
TITLE OF INVENTION: Autoantibodies to glucose-6-phosphate isomerase and their partic
FILE REFERENCE: 1361.005U1
CURRENT APPLICATION NUMBER: US/09/828,708
CURRENT FILING DATE: 2001-09-24
NUMBER OF SEQ ID NOS: 123
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 3
LENGTH: 105
TYPE: PRT
ORGANISM: Homo sapiens
US-09-828-708-3

Query Match
Best Local Similarity 100.0%; Score 32; DB 10; Length 105;
Pred. No. 5.9; Mismatches 0; Indels 0; Gaps 0;
Matches 7; Conservative 0;

QY 1 GASSRAT 7
|||||
Db 44 GASSRAT 50

RESULT 12
US-09-828-708-5
Sequence 5, Application US/09828708
Patent No. US20020146753A1
GENERAL INFORMATION:

APPLICANT: Ditzel, H.
APPLICANT: Burton, D.
APPLICANT: Schaller, M.
TITLE OF INVENTION: Autoantibodies to glucose-6-phosphate isomerase and their partic
FILE REFERENCE: 1361.005U1
CURRENT APPLICATION NUMBER: US/09/828,708
CURRENT FILING DATE: 2001-09-24

NUMBER OF SEQ ID NOS: 123
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 5
LENGTH: 105
TYPE: PRT
ORGANISM: Homo sapiens
US-09-828-708-5

Query Match
Best Local Similarity 100.0%; Score 32; DB 10; Length 105;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GASSRAT 7
|||||
DB 44 GASSRAT 50

RESULT 13
US-09-828-708-7

Sequence 7, Application US/09828708
Patent No. US20020146753A1
GENERAL INFORMATION:

APPLICANT: Dietzel, H.
APPLICANT: Burton, D.
APPLICANT: Schaller, M.
TITLE OF INVENTION: Autoantibodies to glucose-6-phosphate isomerase and their particl
TITLE OF INVENTION: autoimmune disease
FILE REFERENCE: 1361.005US1
CURRENT APPLICATION NUMBER: US/09/828,708
CURRENT FILING DATE: 2001-09-24
NUMBER OF SEQ ID NOS: 123
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 7
LENGTH: 105
TYPE: PRT
ORGANISM: Homo sapiens
US-09-828-708-7

Query Match
Best Local Similarity 100.0%; Score 32; DB 10; Length 105;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GASSRAT 7
|||||
DB 44 GASSRAT 50

RESULT 14
US-08-844-215-8

Sequence 8, Application US/08844215
Patent No. US20020016445A1
GENERAL INFORMATION:

APPLICANT: PERSSON, MATS AXEL
APPLICANT: ALLANDER, TOBIAS ERIK
TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES SPECIFIC FOR
TITLE OF INVENTION: HEPATITIS C VIRUS (HCV) E2 ANTIGEN
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
ADDRESSEE: ROBINS & ASSOCIATES
STREET: 90 MIDDLEFIELD ROAD, SUITE 200
CITY: MENLO PARK
STATE: CA
COUNTRY: USA
ZIP: 94025

COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/844,215
FILING DATE: 17-APR-1997
CLASSIFICATION: 435

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/635,109
FILING DATE: 19-APR-1996
ATTORNEY/AGENT INFORMATION:
NAME: MCCracken, THOMAS P.
REGISTRATION NUMBER: 38,548
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 325-7812
TELEFAX: (650) 325-7823
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 107 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-844-215-8

Query Match
Best Local Similarity 100.0%; Score 32; DB 8; Length 107;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GASSRAT 7
|||||
DB 50 GASSRAT 56

RESULT 15
US-09-848-798-178

Sequence 178, Application US/09848798
Publication No. US20030040605A1
GENERAL INFORMATION:

APPLICANT: Siegel, Donald L.
TITLE OF INVENTION: RH(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
FILE REFERENCE: 09596-4202
CURRENT APPLICATION NUMBER: US/09/848,798
CURRENT FILING DATE: 2001-05-04
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/240,274
PRIOR FILING DATE: EARLIER FILING DATE: 1999-01-29
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/028,550
PRIOR FILING DATE: EARLIER FILING DATE: 1996-10-11
NUMBER OF SEQ ID NOS: 224
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 178
LENGTH: 108
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:

OTHER INFORMATION: anti-Rh(D) antibody clone SH52
US-09-848-798-178

Query Match
Best Local Similarity 100.0%; Score 32; DB 9; Length 108;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GASSRAT 7
|||||
DB 50 GASSRAT 56

Search completed: June 3, 2003, 08:52:54
Job time: 1.66041 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 3, 2003, 08:10:19 / Search time 1.06314 Seconds
(without alignments)
193.728 Million cell updates/sec

Title: US-09-644-668a-30

Sequence: 1 GASSRAT 7

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database:

Issued Patents AA:*

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- 2: /cgn2_6/ptodata/1/1aa/5B.COMB.pep:*
- 3: /cgn2_6/ptodata/1/1aa/6A.COMB.pep:*
- 4: /cgn2_6/ptodata/1/1aa/6B.COMB.pep:*
- 5: /cgn2_6/ptodata/1/1aa/PTUS.COMB.pep:*
- 6: /cgn2_6/ptodata/1/1aa/backfilest.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	* Query Match Length	DB ID	Description
1	32	100.0	56 1 US-08-162-102C-39	Sequence 39, App1
2	32	100.0	107 1 US-08-107-669D-14	Sequence 14, App1
3	32	100.0	107 1 US-08-472-788A-14	Sequence 14, App1
4	32	100.0	107 2 US-08-477-51B-14	Sequence 14, App1
5	32	100.0	107 2 US-08-652-558-49	Sequence 49, App1
6	32	100.0	107 2 US-08-082-842A-14	Sequence 14, App1
7	32	100.0	108 1 US-07-634-278-86	Sequence 86, App1
8	32	100.0	108 1 US-08-477-728-86	Sequence 86, App1
9	32	100.0	108 1 US-08-474-040-86	Sequence 86, App1
10	32	100.0	108 1 US-08-467-200-86	Sequence 86, App1
11	32	100.0	108 1 US-08-488-113B-150	Sequence 150, App1
12	32	100.0	108 1 US-08-477-484B-150	Sequence 150, App1
13	32	100.0	108 2 US-08-646-360-150	Sequence 150, App1
14	32	100.0	108 2 US-08-232-081B-42	Sequence 42, App1
15	32	100.0	108 4 US-08-839-765-150	Sequence 150, App1
16	32	100.0	108 4 US-09-136-389-150	Sequence 150, App1
17	32	100.0	108 4 US-08-484-537-86	Sequence 86, App1
18	32	100.0	108 4 US-09-240-274-178	Sequence 178, App1
19	32	100.0	108 4 US-09-610-838-150	Sequence 150, App1
20	32	100.0	109 1 US-08-162-102C-24	Sequence 24, App1
21	32	100.0	109 4 US-09-025-769B-16	Sequence 16, App1
22	32	100.0	109 5 PCT-US95-08786-24	Sequence 24, App1
23	32	100.0	110 4 US-09-025-769B-30	Sequence 30, App1
24	32	100.0	110 4 US-09-025-769B-47	Sequence 47, App1
25	32	100.0	116 1 US-08-053-131-183	Sequence 183, App1
26	32	100.0	116 2 US-08-096-762-183	Sequence 183, App1
27	32	100.0	116 4 US-09-042-353-46	Sequence 46, App1

28	32	100.0	116 4 US-08-758-417A-311	Sequence 311, App1
29	32	100.0	129 2 US-08-480-774A-4	Sequence 4, App1
30	29	90.6	57 1 US-08-162-102C-38	Sequence 38, App1
31	29	90.6	104 1 US-08-276-852-92	Sequence 92, App1
32	29	90.6	104 1 US-08-899-575-92	Sequence 92, App1
33	29	90.6	104 1 US-08-899-575-92	Sequence 92, App1
34	29	90.6	104 5 PCT-US95-08743-92	Sequence 92, App1
35	29	90.6	107 1 US-08-276-852-87	Sequence 87, App1
36	29	90.6	107 1 US-08-899-575-87	Sequence 87, App1
37	29	90.6	107 1 US-08-899-575-87	Sequence 87, App1
38	29	90.6	107 5 PCT-US95-08743-87	Sequence 87, App1
39	29	90.6	108 1 US-08-276-852-88	Sequence 88, App1
40	29	90.6	108 1 US-08-276-852-88	Sequence 88, App1
41	29	90.6	108 1 US-08-899-575-88	Sequence 88, App1
42	29	90.6	108 1 US-08-899-575-88	Sequence 88, App1
43	29	90.6	108 1 US-08-899-575-88	Sequence 88, App1
44	29	90.6	108 1 US-08-899-575-88	Sequence 88, App1
45	29	90.6	108 5 PCT-US95-08743-88	Sequence 88, App1

ALIGNMENTS

RESULT 1
US-08-162-102C-39
Sequence 39, Application US/08162102C
Patent No. 5762905
GENERAL INFORMATION:
APPLICANT: Burton, Dennis R.
APPLICANT: Barbas, IIT, Carlos F.
APPLICANT: Chanock, Robert M.
APPLICANT: Murphy, Brian R.
APPLICANT: Crowe, Jr., James E.
TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
TITLE OF INVENTION: TO RESPIRATORY SYNCTIAL VIRUS
NUMBER OF SEQUENCES: 49
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 4225 Executive Square, Suite 1400
CITY: La Jolla
STATE: California
COUNTRY: USA
ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/162,102C
FILING DATE: 10-DEC-1993
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Halle, Ph.D., Lisa A.
REGISTRATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: 07300/007001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 678-5070
TELEFAX: (619) 678-5099
INFORMATION FOR SEQ ID NO: 39:
SEQUENCE CHARACTERISTICS:
LENGTH: 56 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-162-102C-39
Query Match 100.0%; Score 32; DB 1; Length 56;
Best Local Similarity 100.0%; Pred. No. 1.4;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
CY 1 GASSRAT 7

DB 50 GASSRAT 56

RESULT 2

US-08-107-669D-14
Sequence 14, Application US/08107669D

Patent No. 5766886

GENERAL INFORMATION:

APPLICANT: Studnicka, Gary M.

TITLE OF INVENTION: Modified Antibody Variable Domains (as amended)

NUMBER OF SEQUENCES: 67

CORRESPONDENCE ADDRESSES:

ADDRESSEE: Sterne, Kessler, Goldstein and Fox P.L.L.C.

STREET: 1100 New York Ave., N.W., Suite 600

CITY: Washington

STATE: D.C.

COUNTRY: United States of America

ZIP: 20005-3934

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/107,669D

FILING DATE: 13-AUG-1993

CLASSIFICATION: 424

PRIOR APPLICATION NUMBER: PCT/US92/10906

FILING DATE: 14-DEC-1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/808,464

FILING DATE: 13-DEC-1991

ATTORNEY/AGENT INFORMATION:

NAME: Michele A. Cimbala

REGISTRATION NUMBER: 33,851

REFERENCE/DOCKET NUMBER: 0610.1000001/MAC

TELECOMMUNICATION INFORMATION:

TELEPHONE: 202/371-2540

TELEFAX: 202/371-2600

INFORMATION FOR SEQ ID NO: 14:

SEQUENCE CHARACTERISTICS:

LENGTH: 107 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-107-669D-14

Query Match 100.0%; Score 32; DB 1; Length 107;

Best Local Similarity 100.0%; Pred. No. 2.8;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GASSRAT 7
DB 50 GASSRAT 56

RESULT 3

US-08-472-788A-14

Sequence 14, Application US/08472788A

Patent No. 5770196

GENERAL INFORMATION:

APPLICANT: Studnicka, Gary M.

TITLE OF INVENTION: Modified Antibody Variable Domains

NUMBER OF SEQUENCES: 69

CORRESPONDENCE ADDRESSES:

ADDRESSEE: Sterne, Kessler, Goldstein and Fox P.L.L.C.

STREET: 1100 New York Ave., N.W., Suite 600

CITY: Washington

STATE: D.C.

COUNTRY: USA

ZIP: 20005-3934

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/472,788A

FILING DATE: 07-JUN-1995

CLASSIFICATION: 424

PRIOR APPLICATION NUMBER: 08/082,842

FILING DATE: 23-JUN-1993

PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/US92/10906

FILING DATE: 14-DEC-1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/808,464

FILING DATE: 13-DEC-1991

ATTORNEY/AGENT INFORMATION:

NAME: Cimbala, Michele A.

REGISTRATION NUMBER: 33,851

REFERENCE/DOCKET NUMBER: 0610.1000003

TELECOMMUNICATION INFORMATION:

TELEPHONE: 202/371-2540

TELEFAX: 202/371-2600

INFORMATION FOR SEQ ID NO: 14:

SEQUENCE CHARACTERISTICS:

LENGTH: 107 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-472-788A-14

Query Match 100.0%; Score 32; DB 1; Length 107;

Best Local Similarity 100.0%; Pred. No. 2.8;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GASSRAT 7
DB 50 GASSRAT 56

RESULT 4

US-08-477-531B-14

Sequence 14, Application US/08477531B

Patent No. 5821123

GENERAL INFORMATION:

APPLICANT: Studnicka, Gary M.

TITLE OF INVENTION: Modified Antibody Variable Domains (as amended)

NUMBER OF SEQUENCES: 67

CORRESPONDENCE ADDRESSES:

ADDRESSEE: Sterne, Kessler, Goldstein and Fox P.L.L.C.

STREET: 1100 New York Ave., N.W., Suite 600

CITY: Washington

STATE: D.C.

COUNTRY: United States of America

ZIP: 20005-3934

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/477,531B

FILING DATE: 07-JUN-1995

CLASSIFICATION: 436

PRIOR APPLICATION NUMBER: 08/107,669

FILING DATE: 13-AUG-1993

PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/US92/10906

FILING DATE: 14-DEC-1992

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/808,464
FILING DATE: 13-DEC-1991
ATTORNEY/AGENT INFORMATION:
NAME: Michele A. Cimbalà
REGISTRATION NUMBER: 33,851
REFERENCE/DOCKET NUMBER: 0610.1000004/MAC
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202/371-2600
TELEFAX: 202/371-2540
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 107 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-477-531B-14

Query Match 100.0%; Score 32; DB 2; Length 107;
Best Local Similarity 100.0%; Pred. No. 2.8;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GASSRAT 7
|||||
Db 50 GASSRAT 56

RESULT 5
US-08-652-558-49
Sequence 49, Application US/08652558
Patent No. 5861155
GENERAL INFORMATION:
APPLICANT: LIN, AUGUSTINE YEE-THARN
TITLE OF INVENTION: HUMANIZED ANTIBODIES AND USES
TITLE OF INVENTION: THEREOF
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
ADDRESSER: BANNER & WITCOFF
STREET: 75 STATE STREET, 23RD FLOOR
CITY: BOSTON
STATE: MASSACHUSETTS
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch diskette, 1.4 Mb storage
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect 6.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/652,558
FILING DATE: JUNE 6, 1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/IB94/00387
FILING DATE: NOVEMBER 21, 1994
ATTORNEY/AGENT INFORMATION:
NAME: YANKWICH, LEON R.
REGISTRATION NUMBER: 30,237
REFERENCE/DOCKET NUMBER: 95,497-L
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-345-9100
TELEFAX: 617-345-9111
INFORMATION FOR SEQ ID NO: 49:
SEQUENCE CHARACTERISTICS:
LENGTH: 107 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-652-558-49

Query Match 100.0%; Score 32; DB 2; Length 107;
Best Local Similarity 100.0%; Pred. No. 2.8;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GASSRAT 7
|||||
Db 50 GASSRAT 56

RESULT 6
US-08-082-842A-14
Sequence 14, Application US/08082842A
Patent No. 5869619
GENERAL INFORMATION:
APPLICANT: Studnicka, Gary M.
TITLE OF INVENTION: Modified Antibody Variable Domains
NUMBER OF SEQUENCES: 89
CORRESPONDENCE ADDRESS:
ADDRESSER: Sterne, Kesaler, Goldstein and Fox P.L.L.C.
STREET: 1100 New York Ave., N.W., Suite 600
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/082,842A
FILING DATE: 23-JUN-1993
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/10906
FILING DATE: 14-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/808,464
FILING DATE: 13-DEC-1991
ATTORNEY/AGENT INFORMATION:
NAME: Cimbalà, Michele A.
REGISTRATION NUMBER: 33,851
REFERENCE/DOCKET NUMBER: 0610.1000002
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202/371-2600
TELEFAX: 202/371-2540
TELEX:
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 107 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-082-842A-14

Query Match 100.0%; Score 32; DB 2; Length 107;
Best Local Similarity 100.0%; Pred. No. 2.8;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GASSRAT 7
|||||
Db 50 GASSRAT 56

RESULT 7
US-07-634-278-86
Sequence 86, Application US/07634278
Patent No. 5530101
GENERAL INFORMATION:
APPLICANT: QUEEN, Cary L.
APPLICANT: CO, Man Sung
APPLICANT: SCHNEIDER, William P.
APPLICANT: LANDOLFI, Nicholas F.
APPLICANT: CORLINGH, Kathleen L.
APPLICANT: SELICK, Harold E.
TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS

NUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Kourie and Crew
STREET: 379 Lytton Avenue
CITY: Palo Alto
STATE: California
COUNTRY: US
ZIP: 94301
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US 07/634,278
FILING DATE: 19-DEC-1990
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/590,274
FILING DATE: 28-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/310,252
FILING DATE: 13-FEB-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/290,975
FILING DATE: 28-DEC-1988
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 11823-002600
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 86:
SEQUENCE CHARACTERISTICS:
LENGTH: 108 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-07-634-278-86

Query Match 100.0%; Score 32; DB 1; Length 108;
Best Local Similarity 100.0%; Pred. No. 2.8;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GASSRAT 7
Db 51 GASSRAT 57

RESULT 8
US-08-477-728-86
Sequence 86, Application US/08477728
Patent No. 5585089
GENERAL INFORMATION:
APPLICANT: QUEEN, Cary L.
APPLICANT: SCHNEIDER, William P.
APPLICANT: SELICK, Harold E.
TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
NUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: Palo Alto
STATE: California
COUNTRY: US
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/477,728
FILING DATE: 07-JUN-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/634,278
FILING DATE: 19-DEC-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/590,274
FILING DATE: 28-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/310,252
FILING DATE: 13-FEB-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/290,975
FILING DATE: 28-DEC-1988
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 11823-002600
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 86:
SEQUENCE CHARACTERISTICS:
LENGTH: 108 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-477-728-86

Query Match 100.0%; Score 32; DB 1; Length 108;
Best Local Similarity 100.0%; Pred. No. 2.8;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GASSRAT 7
Db 51 GASSRAT 57

RESULT 9
US-08-474-040-86
Sequence 86, Application US/08474040
Patent No. 5693761
GENERAL INFORMATION:
APPLICANT: QUEEN, Cary L.
APPLICANT: CO, Man Sung
APPLICANT: SCHNEIDER, William P.
APPLICANT: LANDOLFI, Nicholas F.
APPLICANT: COELINGH, Kathleen L.
APPLICANT: SELICK, Harold E.
TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
NUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Kourie and Crew
STREET: 379 Lytton Avenue
CITY: Palo Alto
STATE: California
COUNTRY: US
ZIP: 94301
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/474,040
FILING DATE: 07-JUN-1995
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/634,278
FILING DATE: 19-DEC-1990

APPLICATION NUMBER: US 07/590,274
FILING DATE: 28-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/310,252
FILING DATE: 13-FEB-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/290,975
FILING DATE: 28-DEC-1988
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 11823-002600
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 86:
SEQUENCE CHARACTERISTICS:
LENGTH: 108 amino acids
TYPE: amino acid
STRANDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-474-040-86

Query Match 100.0%; Score 32; DB 1; Length 108;
Best Local Similarity 100.0%; Pred. No. 2.8;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GASSRAT 7
|||||
51 GASSRAT 57

RESULT 10
US-08-487-200-86
Sequence 86, Application US/08487200
Patent No. 5693762

GENERAL INFORMATION:

APPLICANT: QUEEN, Gary L.
APPLICANT: CO, Man Sung
APPLICANT: SCHNEIDER, William P.
APPLICANT: LANDOLFI, Nicholas P.
APPLICANT: COELINGH, Kathleen L.

APPLICANT: SELICK, Harold E.

TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
NUMBER OF SEQUENCES: 113

CORRESPONDENCE ADDRESSES:

ADDRESS: Townsend and Townsend and Crew
STREET: 379 Lytton Avenue
CITY: Palo Alto

STATE: California

COUNTRY: US

ZIP: 94301

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/487,200

FILING DATE: 7-JUN-1995

CLASSIFICATION: 424

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/534,278

FILING DATE: 19-DEC-1990

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/590,274

FILING DATE: 28-SEP-1990

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/310,252

FILING DATE: 13-FEB-1989

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/290,975

FILING DATE: 28-DEC-1988
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 11823-002610
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 86:
SEQUENCE CHARACTERISTICS:
LENGTH: 108 amino acids
TYPE: amino acid
STRANDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-487-200-86

Query Match 100.0%; Score 32; DB 1; Length 108;
Best Local Similarity 100.0%; Pred. No. 2.8;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GASSRAT 7
|||||
51 GASSRAT 57

RESULT 11
US-08-488-113B-150

Sequence 150, Application US/08488113B
Patent No. 5744580

GENERAL INFORMATION:

APPLICANT: Better, Marc D.

APPLICANT: Carroll, Stephen F.

APPLICANT: Studinka, Gary M.

TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating

NUMBER OF SEQUENCES: 169

CORRESPONDENCE ADDRESSES:

ADDRESS: McAndrews, Held & Malloy, Ltd.

STREET: 500 West Madison Street, 34th floor

CITY: Chicago

STATE: Illinois

COUNTRY: USA

ZIP: 60661

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/488,113B

FILING DATE: 07-JUN-1995

CLASSIFICATION: 530

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/425,336

FILING DATE: 18-APR-1995

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/064,691

FILING DATE: 12-MAY-1993

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/988,430

FILING DATE: 09-DEC-1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/901,707

FILING DATE: 19-JUN-1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/787,567

FILING DATE: 04-NOV-1991

ATTORNEY/AGENT INFORMATION:

NAME: McNicholas, Janet M.

REGISTRATION NUMBER: 32,918

REFERENCE/DOCKET NUMBER: 11022US07/200-70.P3.C2A

TELECOMMUNICATION INFORMATION:

TELEPHONE: 312/707-8889
TELEFAX: 312/707-9155
TELEX: 650 388-1248
INFORMATION FOR SEQ ID NO: 150:
SEQUENCE CHARACTERISTICS:
LENGTH: 108 amino acids
TYPE: amino acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-468-113B-150

Query Match 100.0%; Score 32; DB 1; Length 108;
Best Local Similarity 100.0%; Pred. No. 2.8;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GASSRAT 7
DB 51 GASSRAT 57

RESULT 12
US-08-477-484B-150
Sequence 150, Application US/08477484B
Patent No. 5756699
GENERAL INFORMATION:
APPLICANT: Better, Marc D.
APPLICANT: Carroll, Stephen F.
APPLICANT: Studnika, Gary M.
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
NUMBER OF SEQUENCES: 169
CORRESPONDENCE ADDRESSES:
ADDRESSEE: McAndrews, Held & Malloy, Ltd.
STREET: 500 West Madison Street, 34th floor
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60661
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/477,484B
FILING DATE: 07-JUN-1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/425,336
FILING DATE: 18-APR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/064,691
FILING DATE: 12-MAY-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/988,430
FILING DATE: 09-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/901,707
FILING DATE: 19-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/787,567
FILING DATE: 04-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: McNicholas, Janet M.
REGISTRATION NUMBER: 32,918
REFERENCE/DOCKET NUMBER: 11022US07/200-70.P3.C2A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/707-8889
TELEFAX: 312/707-9155
TELEX: 650 388-1248
INFORMATION FOR SEQ ID NO: 150:
SEQUENCE CHARACTERISTICS:

LENGTH: 108 amino acids
TYPE: amino acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-477-484B-150

Query Match 100.0%; Score 32; DB 1; Length 108;
Best Local Similarity 100.0%; Pred. No. 2.8;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GASSRAT 7
DB 51 GASSRAT 57

RESULT 13
US-08-646-360-150
Sequence 150, Application US/08646360
Patent No. 5837491
GENERAL INFORMATION:
APPLICANT: Better, Marc D.
APPLICANT: Carroll, Stephen F.
APPLICANT: Studnika, Gary M.
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
NUMBER OF SEQUENCES: 173
CORRESPONDENCE ADDRESSES:
ADDRESSEE: McAndrews, Held & Malloy, Ltd.
STREET: 500 West Madison Street, 34th floor
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60661
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/646,360
FILING DATE: 13-MAY-1996
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/05348
FILING DATE: 12-MAY-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/064,691
FILING DATE: 12-MAY-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/988,430
FILING DATE: 09-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/901,707
FILING DATE: 19-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/787,567
FILING DATE: 04-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: McNicholas, Janet M.
REGISTRATION NUMBER: 32,918
REFERENCE/DOCKET NUMBER: 200-70.P4
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/707-8889
TELEFAX: 312/707-9155
TELEX: 650 388-1248
INFORMATION FOR SEQ ID NO: 150:
SEQUENCE CHARACTERISTICS:
LENGTH: 108 amino acids
TYPE: amino acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: protein

US-08-646-360-150

Query Match 100.0%; Score 32; DB 2; Length 108;
Best Local Similarity 100.0%; Pred. No. 2.8;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GASSRAT 7
|||||
Db 51 GASSRAT 57

RESULT 14

US-08-232-081B-42
; Sequence 42; Application US/08232081B
; Patent No. 5886152
; GENERAL INFORMATION:
; APPLICANT: NAKATANI, TOMOYUKI
; APPLICANT: GOMI, HIDEYUKI
; APPLICANT: WIDENES, JOHN
; APPLICANT: NOGUCHI, HIROSHI
; TITLE OF INVENTION: HUMANIZED B-B10
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BIRCH, STEWART, KOLASCH AND BIRCH
; STREET: PO BOX 747
; CITY: FALLS CHURCH
; STATE: VA
; COUNTRY: USA
; ZIP: 22040-0747
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/232,081B
; FILING DATE:
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: SVENSSON, LEONARD R
; REGISTRATION NUMBER: 30,330
; REFERENCE/DOCKET NUMBER: 20-3484
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 205-8000
; TELEFAX: (703) 205-8050
; INFORMATION FOR SEQ. ID NO: 42:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 108 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-232-081B-42

Query Match 100.0%; Score 32; DB 2; Length 108;
Best Local Similarity 100.0%; Pred. No. 2.8;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GASSRAT 7
|||||
Db 51 GASSRAT 57

RESULT 15

US-08-839-765-150
; Sequence 150; Application US/08839765
; Patent No. 6146631
; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
; APPLICANT: Carroll, Stephen F.
; APPLICANT: Studnicka, Gary M.
; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
; TITLE OF INVENTION: Proteins

NUMBER OF SEQUENCES: 169

; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McAndrews, Held & Malloy, Ltd.
; STREET: 500 West Madison Street, 34th floor
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60661
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/839,765
; FILING DATE: 15-APR-1997
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/425,336
; FILING DATE: 18-APR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/064,691
; FILING DATE: 12-MAY-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/988,430
; FILING DATE: 09-DEC-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/901,707
; FILING DATE: 19-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/787,567
; FILING DATE: 04-NOV-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: McNicholas, Janet M.
; REGISTRATION NUMBER: 32,918
; REFERENCE/DOCKET NUMBER: 11022US09/200-70.P3.C3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/707-8889
; TELEFAX: 312/707-9155
; INFORMATION FOR SEQ. ID NO: 150:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 108 amino acids
; TYPE: amino acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-839-765-150

Query Match 100.0%; Score 32; DB 4; Length 108;
Best Local Similarity 100.0%; Pred. No. 2.8;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GASSRAT 7
|||||
Db 51 GASSRAT 57

Search completed: June 3, 2003, 08:24:19
Job time : 1.06314 secs

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OM protein - protein search, using sw model

Run on: June 3, 2003, 08:09:29 ; Search time 3.07509 Seconds
(without alignments)
531.460 Million cell updates/sec

Title: US-09-644-668a-33
Perfect score: 92
Sequence: 1 FIRYDGSNKHYADSVKG 17

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues
Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 73:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	81	88.0	98	2 S29543	Ig heavy chain V r
2	81	88.0	117	2 S36259	Ig heavy chain V r
3	81	88.0	134	2 S31688	Ig heavy chain V r
4	81	88.0	135	2 S31598	Ig heavy chain V r
5	81	88.0	140	2 S70442	Ig heavy chain pre
6	80	87.0	94	2 PI0120	Ig heavy chain V-I
7	80	87.0	97	2 S44115	Ig heavy chain V-I
8	80	87.0	98	2 PI0116	Ig heavy chain V-I
9	80	87.0	98	2 S29546	Ig heavy chain V-I
10	80	87.0	109	2 PI1644	Ig heavy chain V r
11	80	87.0	109	2 PI1646	Ig heavy chain V r
12	80	87.0	111	2 PI1643	Ig heavy chain V r
13	80	87.0	111	2 S31645	Ig heavy chain V r
14	80	87.0	113	2 S38490	Ig heavy chain V r
15	80	87.0	114	2 S46390	Ig heavy chain V r
16	80	87.0	114	2 S46392	Ig heavy chain V r
17	80	87.0	117	2 S36270	Ig heavy chain V r
18	80	87.0	118	2 S31677	Ig heavy chain V r
19	80	87.0	118	2 S31116	Ig heavy chain V r
20	80	87.0	119	2 R36005	Ig heavy chain V r
21	80	87.0	120	2 S31112	Ig heavy chain V r
22	80	87.0	121	2 S19666	Ig heavy chain V r
23	80	87.0	121	2 G36005	Ig heavy chain V r
24	80	87.0	122	2 R36005	Ig heavy chain V r
25	80	87.0	122	2 S31119	Ig heavy chain V r
26	80	87.0	123	2 S38493	Ig heavy chain - h
27	80	87.0	130	2 PI0098	Ig heavy chain pre
28	80	87.0	132	2 S31603	Ig heavy chain V r
29	80	87.0	134	2 S31679	Ig heavy chain V r

30	80	87.0	139	2 S31674	Ig heavy chain V r
31	76	82.6	76	2 S31592	Ig heavy chain V r
32	76	82.6	133	2 S31510	Ig heavy chain V r
33	75	81.5	137	2 S31701	Ig heavy chain V r
34	73	79.3	108	2 S31642	Ig heavy chain V r
35	73	79.3	114	2 S46391	Ig heavy chain V r
36	73	79.3	119	2 S31111	Ig heavy chain V r
37	73	79.3	122	2 S31117	Ig heavy chain - h
38	73	79.3	128	2 S46797	Ig heavy chain V r
39	73	79.3	133	2 A49028	Ig heavy chain V r
40	72	78.3	118	2 PI1652	Ig heavy chain V-I
41	70	76.1	121	2 PI1651	Ig heavy chain V r
42	69	75.0	118	2 PI1660	Ig heavy chain V r
43	69	75.0	119	1 GIH0N1	Ig heavy chain V r
44	69	75.0	122	1 M3H0AM	Ig heavy chain V-I
45	69	75.0	138	2 B56701	Ig heavy chain V r

ALIGNMENTS

RESULT 1
S29543
Ig heavy chain V region (COS 3) - human (fragment)
C/Species: Homo sapiens (man)
C/Date: 07-Jan-1994 #sequence_revision 17-Nov-1995 #text_change 23-Jul-1999
C/Accession: S29543
R/Tomlinson, M.; Walter, G.; Cook, G.P.; Winter, G.
submitted to the EMBL Data Library, October 1992
A/Reference number: S29543
A/Accession: S29543
A/Molecule type: DNA
A/Residues: 1-98 <TOM>
A/Cross-references: EMBL:Z17389; NID:G32835; PIDN:CAA78994.1; PID:G32836
A/Superfamily: Immunoglobulin V region; Immunoglobulin homology
C/Keywords: heterotrimer; Immunoglobulin
P/15-98/Domain: Immunoglobulin homology <IMM>

Query Match 88.0%; Score 81; DB 2; Length 98;
Best Local Similarity 88.2%; Pred. No. 76-06;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 FIRYDGSNKHYADSVKG 17
DB 50 FIRYDGSNKHYADSVKG 66

RESULT 2

S36259
Ig heavy chain V region (clone alpha-TNF-A1) - human (fragment)
C/Species: Homo sapiens (man)
C/Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 23-Jul-1999
R/Coffin, A.D.; Malmqvist, M.; Marks, J.D.; Bye, J.M.; Embleton, M.J.; McCafferty, A.
EMBO J. 12, 725-734, 1993
A/Title: Human anti-self antibodies with high specificity from phage display libraries
A/Reference number: S36256; MUID:93178448; PMID:7679990
A/Accession: S36259
A/Status: preliminary; nucleic acid sequence not shown
A/Molecule type: mRNA
A/Residues: 1-117 <GR1>
A/Cross-references: EMBL:Z18850; NID:G33123; PIDN:CAA79302.1; PID:G939902
C/Superfamily: Immunoglobulin V region; Immunoglobulin homology
C/Keywords: heterotrimer; Immunoglobulin
P/15-98/Domain: Immunoglobulin homology <IMM>

Query Match 88.0%; Score 81; DB 2; Length 117;
Best Local Similarity 88.2%; Pred. No. 8.46-06;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 FIRYDGSNKHYADSVKG 17
DB 50 FIRYDGSNKHYADSVKG 66

RESULT 3

831688
Ig heavy chain V region - human
C/Species: Homo sapiens (man)
C/Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C/Accession: S31688
R/CuSinger, A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnelle, C.
Submitted to the EMBL Data Library, June 1992
A/Description: Mechanisms that generate human immunoglobulin diversity operate from the
A/Reference number: S31585
A/Accession: S31688
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-134 <CUI>
A/Cross-references: EMBL:Z14174; NID:G31013; PIDN:CAA78543.1; PID:G31014
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotrimer; immunoglobulin
P/31-114/Domain: immunoglobulin homology <IMM>

Query Match

Best Local Similarity 88.0%; Score 81; DB 2; Length 134;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 F1SYDGSNKHVADSVKG 17
DB 66 F1RYDGSNKHVADSVKG 82

RESULT 4

831598
Ig heavy chain V region - human
C/Species: Homo sapiens (man)
C/Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C/Accession: S31598
R/CuSinger, A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnelle, C.
Submitted to the EMBL Data Library, June 1992
A/Description: Mechanisms that generate human immunoglobulin diversity operate from the
A/Reference number: S31585
A/Accession: S31598
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-135 <CUI>
A/Cross-references: EMBL:Z14170; NID:G31001; PIDN:CAA78539.1; PID:G31002
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotrimer; immunoglobulin
P/31-114/Domain: immunoglobulin homology <IMM>

Query Match

Best Local Similarity 88.0%; Score 81; DB 2; Length 135;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 F1SYDGSNKHVADSVKG 17
DB 66 F1RYDGSNKHVADSVKG 82

RESULT 5

870442
Ig heavy chain precursor V region (mu) - human (fragment)
C/Species: Homo sapiens (man)
C/Date: 24-Jul-1998 #sequence_revision 24-Jul-1998 #text_change 21-Jan-2000
C/Accession: S70442
R/CuSinger, A.M.; Fumoux, P.; Fougereau, M.; Tonnelle, C.
Mol. Immunol. 29, 1363-1373, 1992
A/Title: IGM kappa/lambda EBV human B cell clone: an early step of differentiation of B
A/Reference number: S70442; MWID:93024508; PMID:1383695
A/Accession: S70442
A/Status: not compared with conceptual translation
A/Molecule type: mRNA
A/Residues: 1-140 <CUI>
C/Superfamily: immunoglobulin V region; immunoglobulin homology

F/34-117/Domain: immunoglobulin homology <IMM>

Query Match 88.0%; Score 81; DB 2; Length 140;
Best Local Similarity 88.2%; Pred. No. 1e-05;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 F1SYDGSNKHVADSVKG 17
DB 69 F1RYDGSNKHVADSVKG 85

RESULT 6

PL0120
Ig heavy chain V-III region (TD-Vo) - human (fragment)
C/Species: Homo sapiens (man)
C/Date: 07-Jun-1990 #sequence_revision 07-Jun-1990 #text_change 16-Aug-1996
C/Accession: PL0120
R/Bird, U.; Galli, N.; Link, M.; Stites, D.; Sklar, J.
U. Exp. Med. 168, 229-245, 1988
A/Title: Continuing rearrangement but absence of somatic hypermutation in immunoglobulin
A/Reference number: PL0116; MWID:88286083; PMID:2840480
A/Accession: PL0120
A/Molecule type: mRNA
A/Residues: 1-94 <BIR>
A/Experimental source: B cells from patient TD with acute lymphoblastic leukemia, A
A/Note: the sequence shows the V region (TD-Vo) from a nonproductive DNA rearrangement
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: acute lymphoblastic leukemia; heterotrimer; immunoglobulin
P/31-35/Region: complementarity-determining 1
F/49-65/Region: complementarity-determining 2

Query Match

Best Local Similarity 87.0%; Score 80; DB 2; Length 94;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 ISYDGSNKHVADSVKG 17
DB 51 ISYDGSNKHVADSVKG 66

RESULT 7

S44115
Ig heavy chain V region - human
C/Species: Homo sapiens (man)
C/Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 24-May-2001
C/Accession: S44115
R/Hawkins, R.E.; Zhu, D.; Owecka, M.; Winter, G.; Hamblin, T.J.; Stevenson, F.K.
Submitted to the EMBL Data Library, March 1994
A/Description: Idiotypic vaccination against human B-cell lymphoma: rescue of vari
A/Reference number: S44105
A/Accession: S44115
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-97 <HAM>
A/Cross-references: EMBL:Z31384; NID:G472969; PIDN:CAA83259.1; PID:G940526
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotrimer; immunoglobulin

Query Match

Best Local Similarity 87.0%; Score 80; DB 2; Length 97;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 ISYDGSNKHVADSVKG 17
DB 51 ISYDGSNKHVADSVKG 66

RESULT 8

PL0116
Ig heavy chain V-III region (AW-Vx) - human (fragment)
C/Species: Homo sapiens (man)
C/Date: 07-Jun-1990 #sequence_revision 07-Jun-1990 #text_change 23-Jul-1999
C/Accession: PL0116; S26892

R:Bird, U.; Galili, N.; Link, M.; Scites, D.; Sklar, J.
J. Exp. Med. 168, 229-245, 1988
A:Title: Continging rearrangement but absence of somatic hypermutation in immunoglobulin
A:Reference number: P10116; MUID:88286083; PMID:2840480
A:Accession: P10116
A:Molecule type: mRNA
A:Residues: 1-98 <BIR>
A:Experimental source: B cells from patient AM with acute lymphoblastic leukemia, ALL
A:Note: the sequence shows the V region (AM-Vx) from a nonproductive DNA rearrangement
R:Tomlinson, I.M.; Walter, G.; Marks, J.D.; Llewellyn, M.B.; Winter, G.
J. Mol. Biol. 227, 776-798, 1992
A:Title: The repertoire of human germline V(H) sequences reveals about fifty groups of V
A:Reference number: S26885; MUID:93021117; PMID:1404388
A:Accession: S26892
A:Status: Preliminary
A:Molecule type: DNA
A:Residues: 1-98 <TOM>
A:Cross-references: EMBL:Z12349; NID:G32918; PIDN:CAA78216.1; PID:G32919
C:Superfamily: Immunoglobulin V region; Immunoglobulin homology
C:Keywords: acute lymphoblastic leukemia; heterotetramer; immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMM>
F:31-35/Region: complementarity-determining 1
F:49-65/Region: complementarity-determining 2

Query Match 87.0%; Score 80; DB 2; Length 98;
Best Local Similarity 93.8%; Pred. No. 1e-05;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 2 ISYDGNKHYADSVYKG 17
|||||:|||||
51 ISYDGNKHYADSVYKG 66

RESULT 9
S29546
Ig heavy chain V region (COS-8 / DP-46) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 07-Jan-1994 #sequence_revision 17-Nov-1995 #text_change 23-Jul-1999
R:Tomlinson, I.M.; Walter, G.; Marks, J.D.; Llewellyn, M.B.; Winter, G.
C:Accession: S29546; S26888
A:Note: designated COS-8
R:Tomlinson, I.M.; Walter, G.; Marks, J.D.; Llewellyn, M.B.; Winter, G.
J. Mol. Biol. 227, 776-798, 1992
A:Title: The repertoire of human germline V(H) sequences reveals about fifty groups of V
A:Reference number: S26885; MUID:93021117; PMID:1404388
A:Accession: S26888
A:Status: Preliminary
A:Molecule type: DNA
A:Residues: 1-98 <TO2>
A:Cross-references: EMBL:Z12346; NID:G32912; PIDN:CAA78216.1; PID:G32913
A:Note: designated DP-46
C:Superfamily: Immunoglobulin V region; Immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 87.0%; Score 80; DB 2; Length 98;
Best Local Similarity 93.8%; Pred. No. 1e-05;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 2 ISYDGNKHYADSVYKG 17
|||||:|||||
51 ISYDGNKHYADSVYKG 66

RESULT 10
PH1644
Ig heavy chain V region (clone 5D11) - human (fragment)

C:Species: Homo sapiens (man)
C:Date: 24-Feb-1994 #sequence_revision 24-Feb-1994 #text_change 16-Aug-1996
C:Accession: PH1644
R:Hillson, J.L.; Karr, N.S.; Opplinger, I.R.; Mannik, M.; Sasso, E.H.
J. Exp. Med. 178, 331-336, 1993
A:Title: The structural basis of germline-encoded VH3 immunoglobulin binding to scapry
A:Reference number: PH1642; MUID:93301610; PMID:8315388
A:Accession: PH1644
A:Molecule type: mRNA
A:Residues: 1-109 <HIL>
C:Superfamily: Immunoglobulin V region; Immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:7-90/Domain: immunoglobulin homology <IMM>

Query Match 87.0%; Score 80; DB 2; Length 109;
Best Local Similarity 93.8%; Pred. No. 1.1e-05;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 2 ISYDGNKHYADSVYKG 17
|||||:|||||
43 ISYDGNKHYADSVYKG 58

RESULT 11
PH1646
Ig heavy chain V region (clone 6H12) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 24-Feb-1994 #sequence_revision 24-Feb-1994 #text_change 16-Aug-1996
R:Hillson, J.L.; Karr, N.S.; Opplinger, I.R.; Mannik, M.; Sasso, E.H.
J. Exp. Med. 178, 331-336, 1993
A:Title: The structural basis of germline-encoded VH3 immunoglobulin binding to scapry
A:Reference number: PH1642; MUID:93301610; PMID:8315388
A:Accession: PH1646
A:Molecule type: mRNA
A:Residues: 1-109 <HIL>
C:Superfamily: Immunoglobulin V region; Immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:7-90/Domain: immunoglobulin homology <IMM>

Query Match 87.0%; Score 80; DB 2; Length 109;
Best Local Similarity 93.8%; Pred. No. 1.1e-05;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 2 ISYDGNKHYADSVYKG 17
|||||:|||||
43 ISYDGNKHYADSVYKG 58

RESULT 12
PH1643
Ig heavy chain V region (clone 6H7) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 24-Feb-1994 #sequence_revision 24-Feb-1994 #text_change 16-Aug-1996
C:Accession: PH1643
R:Hillson, J.L.; Karr, N.S.; Opplinger, I.R.; Mannik, M.; Sasso, E.H.
J. Exp. Med. 178, 331-336, 1993
A:Title: The structural basis of germline-encoded VH3 immunoglobulin binding to scapry
A:Reference number: PH1642; MUID:93301610; PMID:8315388
A:Accession: PH1643
A:Molecule type: mRNA
A:Residues: 1-111 <HIL>
C:Superfamily: Immunoglobulin V region; Immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:7-90/Domain: immunoglobulin homology <IMM>

Query Match 87.0%; Score 80; DB 2; Length 111;
Best Local Similarity 93.8%; Pred. No. 1.2e-05;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 2 ISYDGNKHYADSVYKG 17
|||||:|||||
43 ISYDGNKHYADSVYKG 58

RESULT 13

PH1645

Ig heavy chain V region (clone 6C9) - human (fragment)

C/Species: Homo sapiens (man)

C/Date: 24-Feb-1994 #sequence_revision 24-Feb-1994 #text_change 16-Aug-1996

C/Accession: PH1645

R/Hillson, J.L.; Karr, N.S.; Opplinger, I.R.; Mannik, M.; Saaso, E.H.

J. Exp. Med. 178, 331-336, 1993

A/Title: The structural basis of germline-encoded VH3 immunoglobulin binding to staphylococcal protein A

A/Reference number: PH1642; PMID:93301610; PMID:8315388

A/Accession: PH1645

A/Molecule type: mRNA

A/Residues: 1-111 <HIL>

C/Superfamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: heterotetramer; immunoglobulin

F/7-90/Domain: immunoglobulin homology <IMM>

Query Match

Best Local Similarity 87.0%; Score 80; DB 2; Length 111;

Matches 15; Conservativity 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 ISYDGNKRYADSVKG 17

DB 43 ISYDGNKRYADSVKG 58

RESULT 14

S38490

Ig heavy chain - human (fragment)

C/Species: Homo sapiens (man)

C/Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999

C/Accession: S38490

R/Marks, J.D.; Owehah, W.H.; Bye, J.M.; Finern, R.; Gorick, B.D.; Voak, D.; Thorpe, S.

submitted to the EMBL Data Library, June 1993

A/Description: Human antibody fragments specific for human blood group antigens from a F

A/Reference number: S38488

A/Accession: S38490

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-113 <MAR>

C/Superfamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: heterotetramer; immunoglobulin

F/15-98/Domain: immunoglobulin homology <IMM>

Query Match

Best Local Similarity 87.0%; Score 80; DB 2; Length 113;

Matches 15; Conservativity 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 ISYDGNKRYADSVKG 17

DB 51 ISYDGNKRYADSVKG 66

RESULT 15

S46390

Ig heavy chain V region - human

C/Species: Homo sapiens (man)

C/Date: 27-Jan-1995 #sequence_revision 27-Jan-1995 #text_change 20-Jun-2000

C/Accession: S46390

R/Hillson, J.L.; Karr, N.S.; Opplinger, I.R.; Mannik, M.; Saaso, E.H.

J. Exp. Med. 178, 331-336, 1993

A/Title: In vitro assembly of repertoires of antibody chains on the surface of phage by

A/Reference number: S46390; PMID:94254092; PMID:8196048

A/Accession: S46390

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-114 <FIG>

C/Superfamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: heterotetramer; immunoglobulin

F/15-98/Domain: immunoglobulin homology <IMM>

Query Match 87.0%; Score 80; DB 2; Length 114;

Best Local Similarity 93.8%; Pred. No. 1.2e-05;

Matches 15; Conservativity 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 ISYDGNKRYADSVKG 17

DB 51 ISYDGNKRYADSVKG 66

Search completed: June 3, 2003, 08:22:41

Job time: 4.07509 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 3, 2003, 08:02:44 ; Search time 1.56655 Seconds
(Without alignments)

450.095 Million cell updates/sec

Title: US-09-644-668a-33

Sequence: 1 FIDYGSNKHRYADSVKG 17

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	69	75.0	119	1	HV3I_HUMAN
2	69	75.0	122	1	HV3G_HUMAN
3	62	67.4	126	1	HV3X_HUMAN
4	61	66.3	119	1	HV3L_HUMAN
5	59	64.1	122	1	HV3H_HUMAN
6	53	57.6	119	1	HV3M_HUMAN
7	53	57.6	119	1	HV3N_HUMAN
8	52	56.5	114	1	HV3B_HUMAN
9	52	56.5	116	1	HV05_CARAU
10	52	56.5	121	1	HV3J_HUMAN
11	51	55.4	136	1	HV16_MOUSE
12	50	54.3	122	1	HV3A_HUMAN
13	49	53.3	115	1	HV3T_HUMAN
14	48	52.2	115	1	HV3F_HUMAN
15	47	51.1	117	1	HV03_CARAU
16	46	50.0	120	1	HV3U_HUMAN
17	45	48.9	117	1	HV3C_HUMAN
18	44.5	48.4	116	1	HV60_MOUSE
19	44	47.8	98	1	HV57_MOUSE
20	44	47.8	117	1	HV3O_HUMAN
21	44	47.8	117	1	HV54_MOUSE
22	44	47.8	117	1	HV55_MOUSE
23	44	47.8	485	1	6PGD_HUMAN
24	44	47.8	485	1	6PGD_TRBPA
25	43	46.7	610	1	PCKC_CORGL
26	42.5	46.2	846	1	PAC_ECOLI
27	42	45.7	492	1	6PGD_SCHPO
28	42	45.7	4753	1	LKP_CABEL
29	41.5	45.1	844	1	PAC_KLUCI
30	41	44.6	111	1	HV35_MOUSE
31	41	44.6	334	1	Y10A_BPT4
32	41	44.6	481	1	BIND_STRPU
33	41	44.6	1034	1	BGAL_BACKE

34	40.5	44.0	137	1	HV46_MOUSE
35	40	43.5	113	1	HV27_MOUSE
36	40	43.5	113	1	HV28_MOUSE
37	40	43.5	113	1	HV29_MOUSE
38	40	43.5	113	1	HV30_MOUSE
39	40	43.5	113	1	HV31_MOUSE
40	40	43.5	113	1	HV32_MOUSE
41	40	43.5	115	1	HV33_MOUSE
42	40	43.5	115	1	GCAD_BACCL
43	40	43.5	116	1	HV53_MOUSE
44	40	43.5	117	1	HV3E_HUMAN
45	40	43.5	120	1	HV3E_HUMAN

ALIGNMENTS

RESULT 1					
ID	HV3I_HUMAN	STANDARD	PRT	119 AA	
AC	P01770;				
DT	21-JUL-1986 (Rel. 01, Created)				
DR	21-JUL-1986 (Rel. 01, Last sequence update)				
DE	15-JUL-1999 (Rel. 38, Last annotation update)				
OE	Ig heavy chain V-III region N1E.				
OS	Homo sapiens (Human).				
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;				
OX	Mammalia; Euteria; Primates; Catarrhini; Homidae; Homo.				
RN	[1]				
RP	SEQUENCE.				
RX	MEDLINE=77070269; PubMed=826475;				
RA	Ponstingl H., Hilschmann N.;				
RT	"The rule of antibody structure. The primary structure of a monoclonal IgG1 immunoglobulin (myeloma protein N1e). III. The chymotryptic peptides of the H-chain, alignment of the tryptic peptides and discussion of the complete structure."				
RL	Hoppe-Seyler's Z. Physiol. Chem. 357:1571-1604(1976).				
RN	[2]				
RP	DISULFIDE BOND.				
RX	MEDLINE=77070267; PubMed=1002129;				
RA	Dreker L., Schwartz J., Reichel W., Hilschmann N.;				
RT	"Rule of antibody structure. The primary structure of a monoclonal IgG1 immunoglobulin (myeloma protein N1e). I: Purification and characterization of the protein, the L- and H-chains, the cyanogen bromide cleavage products, and the disulfide bridges."				
RL	Hoppe-Seyler's Z. Physiol. Chem. 357:1515-1540(1976).				
CC	-I- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IgG1 MYELOMA PROTEIN.				
DR	PIR; A02053; G1HUNI.				
DR	HSSP; P01772; 2F84.				
DR	InterPro; IPR003006; IG_MHC.				
DR	InterPro; IPR003596; IG_V.				
DR	Pfam; PF00047; Ig_1.				
DR	SMART; SM00406; Igv_1.				
KW	Immunoglobulin V region.				
FT	MOD_RES 1				
FT	DISULFID 22				
FT	NON_TER 119				
SQ	SEQUENCE 119 AA; 13242 MW; C96935A6E55B165B CRC64;				
Query Match					
Best Local Similarity 75.0%; Score 69; DB 1; Length 119;					
Matches 11; Conservative 3; Mismatches 2; Indels 0; Gaps 0;					
RESULT 2					
ID	HV3G_HUMAN	STANDARD	PRT	122 AA	
DB	2 ISYDGSNKHRYADSVKG 17				
QY	51 MSYGBBKHRYADSVKG 66				

AC P01768; 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE IG heavy chain V-II region CAM.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 NCBI_Taxid=9606;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=81013859; PubMed=6774332;
 RA Lehman D.W., Putnam F.W.;
 RT "Amino acid sequence of the variable region of a human mu chain:
 location of a possible JH segment."
 RL Proc. Natl. Acad. Sci. U.S.A. 77:3239-3243(1980).
 CC -1- MISCELLANEOUS: THIS MU CHAIN WAS ISOLATED FROM THE PLASMA OF A
 CC PATIENT WITH MACROGLOBULINEMIA.
 DR PIR; A02051; M3HUM.
 DR HSSP; P01772; 2PB4.
 DR InterPro; IPR003006; IG_MHC.
 DR Pfam; PF00047; IG_1.
 DR SMART; SM00406; IG_1.
 KW Immunoglobulin V region.
 FT MOD RES 1 1
 FT NON_TER 122 122
 SQ SEQUENCE 122 AA; 13668 MW; A42D0F17D525F1C2 CRC64;
 Query Match 75.0%; Score 69; DB 1; Length 122;
 Best Local Similarity 68.8%; Pred. No. 0.00012;
 Matches 11; Conservative 4; Mismatches 1; Indels 0; Gaps 0;
 Oy 2 ISYDGSNKHVADSVKG 17
 Db 51 ISYGBBKRYABSVKG 66

RESULT 3
 HV3J_HUMAN STANDARD; PRT; 126 AA.
 ID P01772;
 AC 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE IG heavy chain V-II region KOL.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 NCBI_Taxid=9606;
 RN [1]
 RP SEQUENCE, AND DISULFIDE BONDS.
 RX MEDLINE=83289131; PubMed=6884994;
 RA Schmidt W.B., Jung H.-D., Palm W., Hilschmann N.;
 RT "Three-dimensional structure determination of antibodies. Primary
 structure of crystallized monoclonal immunoglobulin IgG1 KOL, I.",
 RT Hoppe-Seelyer's Z. Physiol. Chem. 364:713-747(1983).
 RN [2]
 RP X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS).
 RX MEDLINE=81072295; PubMed=7441755;
 RA Marguier M., Deisenhofer J., Huber R., Palm W.;
 RT "Crystallographic refinement and atomic models of the intact
 immunoglobulin molecule KOL and its antigen-binding fragment at 3.0 A
 and 1.0-A resolution."
 RL J. Mol. Biol. 141:369-391(1980).
 DR PIR; A02055; G1HUKL.
 DR PDB; 2PB4; 12-JUL-89.
 DR InterPro; IPR003006; IG_MHC.
 DR Pfam; PF00047; IG_1.
 DR SMART; SM00406; IG_1.
 KW Immunoglobulin V region; 3D-structure.

FT MOD RES 1 1
 FT DISULFID 22 96
 FT DISULFID 105 110
 FT STRAND 3 7
 FT STRAND 11 12
 FT TURN 14 15
 FT STRAND 18 25
 FT HELIX 29 31
 FT STRAND 34 39
 FT TURN 41 42
 FT STRAND 46 51
 FT TURN 53 54
 FT STRAND 58 60
 FT TURN 62 67
 FT STRAND 68 73
 FT TURN 74 77
 FT STRAND 78 83
 FT HELIX 88 90
 FT STRAND 92 99
 FT STRAND 106 106
 FT TURN 107 108
 FT STRAND 109 109
 FT STRAND 113 113
 FT STRAND 120 124
 FT NON_TER 126 126
 SQ SEQUENCE 126 AA; 13718 MW; E4D71B52B16F8776 CRC64;
 Query Match 67.4%; Score 62; DB 1; Length 126;
 Best Local Similarity 84.6%; Pred. No. 0.0019;
 Matches 11; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 Oy 5 DGSNKHVADSVKG 17
 Db 54 DGSDDHVDVSKG 66

RESULT 4
 HV3J_HUMAN STANDARD; PRT; 119 AA.
 ID P01773;
 AC 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE IG heavy chain V-II region BUR.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 NCBI_Taxid=9606;
 RN [1]
 RP SEQUENCE (MYELOMA PROTEIN BUR).
 RX MEDLINE=79151016; PubMed=107164;
 RA Putnam F.W., Liu Y.-S.V., Low T.L.K.;
 RT "Primary structure of a human IgM immunoglobulin. IV. Streptococcal
 RT IgM protease, digestion, Fab and Fc fragments, and the complete
 RT amino acid sequence of the alpha 1 heavy chain."
 RL J. Biol. Chem. 254:2865-2874(1979).
 DR PIR; A02056; A1HUBR.
 DR HSSP; P01772; 2PB4.
 DR InterPro; IPR003006; IG_MHC.
 DR Pfam; PF00047; IG_1.
 DR SMART; SM00406; IG_1.
 KW Immunoglobulin V region; Glycoprotein.
 FT MOD RES 1 1
 FT DISULFID 22 96
 FT CARBOHYD 28 28
 FT NON_TER 119 119
 SQ SEQUENCE 119 AA; 12981 MW; 12A709A75344D024 CRC64;
 Query Match 66.3%; Score 61; DB 1; Length 119;
 Best Local Similarity 68.8%; Pred. No. 0.0026;
 Matches 11; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 2 ISYDGSNKHYADSVYK 17
 DB 51 ISYGBSBZYAASVYK 66

RESULT 5

HV3H HUMAN

ID HV3H HUMAN STANDARD; PRT; 122 AA.

AC P01763;

DT 21-JUL-1986 (Rel. 01, Created)

DT 21-JUL-1986 (Rel. 01, Last sequence update)

DT 15-JUL-1999 (Rel. 38, Last annotation update)

DE Ig heavy chain V-III region GA.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

NCBI_TaxID=9606;

[1]

SEQUENCE.

RX MEDLINE=74175307; PubMed=4208843;

RA Florent G., Lehman D., Putnam F.W.;

RT "The switch point in my heavy chains of human Igm immunoglobulins.";

RL Biochemistry 13:2482-2498(1974).

CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A WALDENSTROM'S

MACROGLOBULIN.

DR HSP; A02052; M3HUGA.

DR HSP; P01772; 2PB4.

DR Interpro: IPR003006; Ig_MHC.

DR Interpro: IPR003596; Ig_v.

DR Pfam: PF00047; Ig; 1.

DR SMART; SM00406; IgV; 1.

KW Immunoglobulin V region.

FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.

FT NON_TER 122 122

SQ SEQUENCE 122 AA; 13166 MW; 745B6959E84100A CRC64;

Query Match 64.1%; Score 59; DB 1; Length 122;

Best Local Similarity 62.5%; Pred. No. 0.0058;

Matches 10; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 2 ISYDGSNKHYADSVYK 17

DB 51 ISYGBSBZYAASVYK 66

RESULT 6

HV3M HUMAN

ID HV3M HUMAN STANDARD; PRT; 119 AA.

AC P01774;

DT 21-JUL-1986 (Rel. 01, Created)

DT 21-JUL-1986 (Rel. 01, Last sequence update)

DT 15-JUL-1999 (Rel. 38, Last annotation update)

DE Ig heavy chain V-III region POM.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

NCBI_TaxID=9606;

[1]

SEQUENCE.

RX MEDLINE=75046755; PubMed=4139708;

RA Capra J.D., Kehoe J.M.;

RT "Structure of antibodies with shared idiotypic: the complete sequence

of the heavy chain variable regions of two immunoglobulin M

anti-gamma globulins."

Proc. Natl. Acad. Sci. U.S.A. 71:4032-4036(1974).

CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM IGM WITH ANTI-GAMMA

GLOBULIN ACTIVITY.

DR HSP; A02057; M3HUPM.

DR HSP; P01772; 2PB4.

DR Interpro: IPR003006; Ig_MHC.

DR Interpro: IPR003596; Ig_v.

DR Pfam: PF00047; Ig; 1.

DR SMART; SM00406; IgV; 1.

KW Immunoglobulin V region.

FT VARIANT 54 54

FT NON_TER 119 119

SQ SEQUENCE 119 AA; 12953 MW; 2E018AF4DCB2610 CRC64;

Query Match 57.6%; Score 53; DB 1; Length 119;

Best Local Similarity 69.2%; Pred. No. 0.057;

Matches 9; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 5 DGSNKHYADSVYK 17

DB 54 NGNDKHYADSVYK 66

RESULT 7

HV3N HUMAN

ID HV3N HUMAN STANDARD; PRT; 119 AA.

AC P01775;

DT 21-JUL-1986 (Rel. 01, Created)

DT 21-JUL-1986 (Rel. 01, Last sequence update)

DT 15-JUL-1999 (Rel. 38, Last annotation update)

DE Ig heavy chain V-III region LAY.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

NCBI_TaxID=9606;

[1]

SEQUENCE.

RX MEDLINE=75046755; PubMed=4139708;

RA Capra J.D., Kehoe J.M.;

RT "Structure of antibodies with shared idiotypic: the complete sequence

of the heavy chain variable regions of two immunoglobulin M

anti-gamma globulins."

Proc. Natl. Acad. Sci. U.S.A. 71:4032-4036(1974).

CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM IGM WITH ANTI-GAMMA

GLOBULIN ACTIVITY.

DR HSP; A02058; M3HULY.

DR HSP; P01772; 2PB4.

DR Interpro: IPR003006; Ig_MHC.

DR Interpro: IPR003596; Ig_v.

DR Pfam: PF00047; Ig; 1.

DR SMART; SM00406; IgV; 1.

KW Immunoglobulin V region.

FT NON_TER 119 119

SQ SEQUENCE 119 AA; 12658 MW; D6338098794DCF5E CRC64;

Query Match 57.6%; Score 53; DB 1; Length 119;

Best Local Similarity 69.2%; Pred. No. 0.057;

Matches 9; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 5 DGSNKHYADSVYK 17

DB 54 NGNDKHYADSVYK 66

RESULT 8

HV3B HUMAN

ID HV3B HUMAN STANDARD; PRT; 114 AA.

AC P01763;

DT 21-JUL-1986 (Rel. 01, Created)

DT 21-JUL-1986 (Rel. 01, Last sequence update)

DT 15-JUL-1999 (Rel. 38, Last annotation update)

DE Ig heavy chain V-III region WEA.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

NCBI_TaxID=9606;

[1]

SEQUENCE.

RX MEDLINE=63273707; PubMed=6410398;

Goni F., Frangione B.;

RT "Amino acid sequence of the Fv region of a human monoclonal IgM (protein MEA) with antibody activity against 3,4-pyruvylated galactose in Klebsiella polysaccharides K30 and K33." RT Proc. Natl. Acad. Sci. U.S.A. 80:4837-4841(1983).

CC -1- MISCELLANEOUS: THIS CHAIN WAS OBTAINED FROM A MONOCLONAL ANTIBODY AGAINST 3,4-PYRUVYLATED GALACTOSE AND ISOLATED FROM A PATIENT WITH WALDENSTROM'S MACROGLOBULINEMIA.

DR PIR: A02046; M3HME.

DR HSSP: P01772; 2PB4.

DR InterPro: IPR003006; Ig_MHC.

DR InterPro: IPR003596; Ig_V.

DR Pfam: PF00047; Ig_1.

DR SMART: SM00406; IgV_1.

KW Immunoglobulin V region.

FT MOD_RES 1 1

FT NON_TER 114 114

SO SEQUENCE 114 AA; 12256 MW; D88234FB418A0787 CRC64;

Query Match 56.5%; Score 52; DB 1; Length 114; Best Local Similarity 64.7%; Pred. No. 0.079; Matches 11; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 1 ISYDGSNKHYADSVKG 17

DB 50 FIGSGSTYYADSVKG 66

RESULT 9

HV05_CARAU STANDARD; PRT; 116 AA.

ID HV05_CARAU

AC P191B1;

DT 01-NOV-1990 (Rel. 16, Created)

DT 01-NOV-1990 (Rel. 16, Last sequence update)

DT 15-JUL-1999 (Rel. 38, Last annotation update)

DE Ig heavy chain V region 5A precursor.

OS Carassius auratus (Goldfish).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes; Cyprinidae; Carassius.

OC NCBI_TaxID=7957;

OX [1]

RN MEDLINE=8144476; PubMed=3125551;

RP SEQUENCE FROM N.A.

RA Wilson M.R., Middleton D., Warr G.W.;

RT "Immunoglobulin heavy chain variable region gene evolution: structure and family relationships of two genes and a pseudogene in a teleost fish."

RT Proc. Natl. Acad. Sci. U.S.A. 85:1566-1570(1988).

RL PIR: B28966; B28966.

DR HSSP: P01772; 2PB4.

DR InterPro: IPR003006; Ig_MHC.

DR InterPro: IPR003596; Ig_V.

DR Pfam: PF00047; Ig_1.

DR SMART: SM00406; IgV_1.

KW Immunoglobulin V region; signal.

FT SIGNAL 1 19

FT CHAIN 20 116

FT DOMAIN 20 49

FT DOMAIN 50 54

FT DOMAIN 55 68

FT DOMAIN 69 84

FT DOMAIN 85 116

FT DISUFID 41 114

FT NON_TER 116 116

SO SEQUENCE 116 AA; 12808 MW; 9C2279E2DF199B12 CRC64;

Query Match 56.5%; Score 52; DB 1; Length 116; Best Local Similarity 56.2%; Pred. No. 0.081; Matches 9; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 2 ISYDGSNKHYADSVKG 17

DB 69, VIYSGSTYYADSVKG 84

RESULT 10

HV3J_HUMAN STANDARD; PRT; 121 AA.

ID HV3J_HUMAN

AC P01771;

DT 21-JUL-1986 (Rel. 01, Created)

DT 21-JUL-1986 (Rel. 01, Last sequence update)

DT 15-JUL-1999 (Rel. 38, Last annotation update)

DE Ig heavy chain V-III region HIL.

OS Homo sapiens (human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

OC NCBI_TaxID=9606;

OX [1]

RN MEDLINE=79124695; PubMed=420800;

RP SEQUENCE.

RA Chiu Y.-Y.H., Lopez de Castro J.A., Poljak R.J.;

RT "Amino acid sequence of the VH region of human myeloma cryoimmunoglobulin IgG H1."

RT Biochemistry 18:553-560(1979).

CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGG1 MYELOMA PROTEIN.

DR PIR: A02054; G1HMH.

DR HSSP: P01772; 2PB4.

DR InterPro: IPR003006; Ig_MHC.

DR InterPro: IPR003596; Ig_V.

DR Pfam: PF00047; Ig_1.

DR SMART: SM00406; IgV_1.

KW Immunoglobulin V region.

FT MOD_RES 1 1

FT NON_TER 121 121

SO SEQUENCE 121 AA; 13566 MW; 480FC5610EFD5AB CRC64;

Query Match 56.5%; Score 52; DB 1; Length 121; Best Local Similarity 62.5%; Pred. No. 0.085; Matches 10; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 2 ISYDGSNKHYADSVKG 17

DB 51 IYNGSRITYGDSVKG 66

RESULT 11

HV16_MOUSE STANDARD; PRT; 136 AA.

ID HV16_MOUSE

AC P01783;

DT 21-JUL-1986 (Rel. 01, Created)

DT 21-JUL-1986 (Rel. 01, Last sequence update)

DT 15-JUL-1999 (Rel. 38, Last annotation update)

DE Ig heavy chain V region MOPC 21 precursor (fragment).

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OC NCBI_TaxID=10090;

OX [1]

RN MEDLINE=81234548; PubMed=6788376;

RP SEQUENCE FROM N.A.

RA Bothwell A.L.M., Paekind M., Reck M., Imanishi-Kari T., Rajewsky K., Baltimore D.;

RT "Heavy chain variable region contribution to the NPb family of antibodies: somatic mutation evident in a gamma 2a variable region."

RT Cell 24:625-637(1981).

RL [2]

SO SEQUENCE OF 17-136.

RX MEDLINE=77100368; PubMed=401950;

RX Adegugbo K., Milstein C., Secher D.S.;

RA "Molecular analysis of spontaneous somatic mutants."

RL Nature 265:299-304(1977).

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DR EMBL/J00522; AAD15290.1; ..
 DR PIR: A02066; G1M321.

DR HSSP: P01772; 2FB4.

DR InterPro: IPR003006; Ig_MHC.

DR InterPro: IPR003596; Ig_V.

DR Pfam: PF00047; Ig; 1.

DR SMART: SM00406; IgV; 1.

KW Immunoglobulin V region; Signal.

FT NON_TER 1 1

FT SIGNAL <1 16

FT CHAIN 17 136

FT DOMAIN 115 119 IG HEAVY CHAIN V REGION MOPC 21.

FT DISULFID 120 136 D SEGMENT.

FT CONFLICT 75 112 JH4 SEGMENT.

FT CONFLICT 89 78 HYAD -> DYAH (IN REF. 2).

FT CONFLICT 115 115 DN -> ND (IN REF. 2).

FT CONFLICT 120 120 W -> H (IN REF. 2).

FT NON_TER 136 136 Y -> W (IN REF. 2).

SQ SEQUENCE 136 AA; 15071 MW; 2276A98DBDF016 CRC64;

Query Match 55.4%; Score 51; DB 1; Length 136;
 Best Local Similarity 58.8%; Pred. No. 0.14;
 Matches 10; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

OY 1 F1SYDGSNKHVADSVKG 17

Db 66 Y1SGSGSTLHYADTVKG 82

RESULT 12

ID HV3A_HUMAN

AC P01762; STANDARD; PRT; 122 AA.

DT 21-JUL-1986 (Rel. 01, Created)

DT 21-JUL-1986 (Rel. 01, Last sequence update)

DT 15-JUL-1999 (Rel. 38, Last annotation update)

DE Ig heavy chain V-III region TRO.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE (MYELOMA PROTEIN TRO).

RX MEDLINE=76023781; PubMed=809331;

RA Kratzin H., Altevogt P., Ruban E., Kortt A., Starosck K.,

RA Hilschmann N.;

RT "The primary structure of a monoclonal IgA-immunoglobulin (IgA Tro.),

RT structure of the complete IgA-molecule."

RT Hope-seyler's Z. Physiol. Chem. 356:1337-1342(1975).

CC -1- MISCELLANEOUS: THE SEQUENCE OF THE C REGION IS ALSO GIVEN.

DR PIR: A02045; A1HUTR.

DR HSSP: P01772; 2FB4.

DR InterPro: IPR003006; Ig_MHC.

DR InterPro: IPR003596; Ig_V.

DR Pfam: PF00047; Ig; 1.

DR SMART: SM00406; IgV; 1.

KW Immunoglobulin V region.

FT MOD_RES 1 1

FT NON_TER 122 122

SQ SEQUENCE 122 AA; 13472 MW; 2E21A11DA04D80F9 CRC64;

Query Match 54.3%; Score 50; DB 1; Length 122;
 Best Local Similarity 58.8%; Pred. No. 0.18;
 Matches 10; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

OY 1 F1SYDGSNKHVADSVKG 17

Db 50 Y1SGSGSTLHYADTVKG 66

RESULT 13

ID HV3T_HUMAN

AC P01781; STANDARD; PRT; 116 AA.

DT 21-JUL-1986 (Rel. 01, Created)

DT 21-JUL-1986 (Rel. 01, Last sequence update)

DT 15-JUN-2002 (Rel. 41, Last annotation update)

DE Ig heavy chain V-III region GAL.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE.

RX MEDLINE=75059123; PubMed=4803843;

RA Watanabe S., Barnickol H.U., Horn J., Berttram J., Hilschmann N.;

RT "The primary structure of a monoclonal IgM-immunoglobulin

RT (macroglobulin Gal.), II: the amino acid sequence of the H-chain (mu-

RT type) subgroup H III. Architecture of the complete IgM-molecule."

RT Hope-seyler's Z. Physiol. Chem. 354:1505-1509(1973).

RL [2]

RP REVISION TO 28-33.

RA Hilschmann N.;

RL Submitted (JUN-1975) to the PIR data bank.

CC -1- MISCELLANEOUS: THIS MU CHAIN WAS ISOLATED FROM A WALDENSTROM'S

CC MACROGLOBULIN.

DR PIR: A02064; M3HUGL.

DR HSSP: P01772; 2FB4.

DR InterPro: IPR003006; Ig_MHC.

DR InterPro: IPR003596; Ig_V.

DR Pfam: PF00047; Ig; 1.

DR SMART: SM00406; IgV; 1.

KW Immunoglobulin V region.

FT NON_TER 116 116

SQ SEQUENCE 116 AA; 12730 MW; 2C67CA9AAAAA1282 CRC64;

Query Match 53.3%; Score 49; DB 1; Length 116;
 Best Local Similarity 56.2%; Pred. No. 0.26;
 Matches 9; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

OY 2 ISYDGSNKHVADSVKG 17

Db 51 IKZBSGZBYVDVYKG 66

RESULT 14

ID HV3F_HUMAN

AC P01767; STANDARD; PRT; 115 AA.

DT 21-JUL-1986 (Rel. 01, Created)

DT 21-JUL-1986 (Rel. 01, Last sequence update)

DT 15-JUL-1999 (Rel. 38, Last annotation update)

DE Ig heavy chain V-III region BUT.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE.

RX MEDLINE=78137069; PubMed=416441;

RA Torano A., Putnam F.W.;

RT "Complete amino acid sequence of the alpha 2 heavy chain of a human

RT IgA2 immunoglobulin of the A2m (2) allotype."

RT Proc. Natl. Acad. Sci. U.S.A. 75:966-969(1978).

CC -1- MISCELLANEOUS: THE SEQUENCE OF THE ALPHA-2, A2M(2) ALLOTYPE, C

CC REGION OF THIS MYELOMA PROTEIN IS ALSO GIVEN.

DR PIR: A02050; A2HTBU.

DR HSSP: P01789; 1MCP.

DR InterPro: IPR003006; Ig_MHC.

DR InterPro; IPR003596; IG_V.
 DR Pfam; PF00047; IG_1.
 DR SMART; SM00406; IG_V_1.
 KW Immunoglobulin V region.
 FT NON TER 115 115
 SO SEQUENCE 115 AA; 12379 MW; 208876A7DE52DCF4 CRC64;

Query Match 52.2%; Score 48; DB 1; Length 115;
 Best Local Similarity 64.3%; Pred. No. 0.37;
 Matches 9; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

OY 4 YDGSNKHYADSVKG 17
 DB 52 YRGCTYYADSVKG 65

RESULT 15.

ID HV03 CARAU STANDARD; PRT; 117 AA.
 AC P19180;
 DT 01-NOV-1990 (Rel. 16, Created)
 DT 01-NOV-1990 (Rel. 16, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE 15 heavy chain V region 3 precursor.
 OS Carassius auratus (Goldfish).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
 CC Cyprinidae; Carassius.
 OX NCBI_TaxID=7957;

SEQUENCE FROM N.A.

RP MEDLINE=88144476; PubMed=312551;
 RA Wilson M.R., Middleton D., Warr G.W.;
 RT "Immunoglobulin heavy chain variable region gene evolution: structure
 fish.";
 RL Proc. Natl. Acad. Sci. U.S.A. 85:1566-1570(1988).

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CC EMBL; J03616; AAAS0807.1; -
 DR PIR; A28966; A28966.
 DR HSSP; P01772; 2PB4.
 DR InterPro; IPR003006; IG_MHC.
 DR InterPro; IPR003596; IG_V.
 DR Pfam; PF00047; IG_1.
 DR SMART; SM00406; IG_V_1.
 KW Immunoglobulin V region; Signal.
 FT SIGNAL 1 19
 FT CHAIN 20 117 IG HEAVY CHAIN V REGION 3.
 FT DOMAIN 20 49 FRAMEWORK-1.
 FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING-1.
 FT DOMAIN 55 68 FRAMEWORK-2.
 FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING-2.
 FT DOMAIN 86 117 FRAMEWORK-3.
 FT DISULFID 41 115 BY SIMILARITY.
 FT NON TER 117 117
 SO SEQUENCE 117 AA; 13220 MW; 512B625003FA6ECB CRC64;

Query Match 51.1%; Score 47; DB 1; Length 117;
 Best Local Similarity 69.2%; Pred. No. 0.56;
 Matches 9; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 5 DGSNKHYADSVKG 17
 DB 73 DGSVDVSYADTVKG 85

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 3, 2003, 08:07:54 ; Search time 8.47099 Seconds
(without alignments)
413.506 Million cell updates/sec

Title: US-09-644-668A-33
Sequence: 1 F1SYDGSNKHRYADSVKG 17

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

SPTREMBL.21.*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_virus:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_virus:*
16: sp_bacterioplasmid:*
17: sp_archaeoplasmid:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	81	88.0	113	4	Q9UL90
2	80	87.0	116	4	Q9UL93
3	80	87.0	613	4	Q8WUK1
4	68	73.9	122	4	Q9UL84
5	63	68.5	147	4	Q9Y509
6	58	63.0	95	4	Q9UL86
7	56	60.9	118	4	Q9UL72
8	55	59.8	121	4	Q9UL71
9	53	57.6	317	5	Q8WR58
10	53	57.6	326	5	Q8WP98
11	53	57.6	414	5	Q963G5
12	53	57.6	491	5	Q963G9
13	50	54.3	305	17	Q97CD6
14	49	53.3	597	4	Q96BB9
15	48	52.2	112	4	Q9HCL1
16	47	51.1	308	2	Q9SOK5

17	47	51.1	469	2	Q9FAR9	Q9FAR9 shewanella
18	47	51.1	576	13	Q8QHU1	Q8QHU1 brachydanio
19	46	50.0	1400	4	Q9UP67	Q9UP67 homo sapien
20	45	48.9	119	11	Q920B7	Q920B7 mus musculu
21	45	48.9	416	4	Q9NPP6	Q9NPP6 homo sapien
22	45	48.9	549	5	Q9NSM7	Q9NSM7 caenorhabdi
23	45	48.9	860	11	Q9JIS8	Q9JIS8 mus musculu
24	45	48.9	1011	4	Q9UP95	Q9UP95 homo sapien
25	45	48.9	1011	4	Q8TDD4	Q8TDD4 homo sapien
26	45	48.9	1014	4	Q9UFR2	Q9UFR2 homo sapien
27	45	48.9	1068	4	Q6O632	Q6O632 homo sapien
28	45	48.9	1085	4	Q13953	Q13953 homo sapien
29	45	48.9	1085	6	Q28677	Q28677 oryctolagus
30	45	48.9	1085	11	Q63632	Q63632 rattus norv
31	45	48.9	1085	11	Q55069	Q55069 mus musculu
32	45	48.9	1086	6	Q18887	Q18887 sus scrofa
33	45	48.9	1099	4	Q9Y642	Q9Y642 homo sapien
34	45	48.9	1099	11	Q924N3	Q924N3 mus musculu
35	45	48.9	1150	4	Q9Y665	Q9Y665 homo sapien
36	45	48.9	1150	4	Q9UHW9	Q9UHW9 homo sapien
37	45	48.9	1150	11	Q924N4	Q924N4 mus musculu
38	44.5	48.4	1100	2	Q9XGJ9	Q9XGJ9 klebsiella
39	44	47.8	71	7	Q9GJ71	Q9GJ71 salmo trutt
40	44	47.8	192	10	Q9SDR4	Q9SDR4 thupa plica
41	44	47.8	342	13	Q8QGW8	Q8QGW8 oryzae lat
42	44	47.8	470	16	Q97B81	Q97B81 clostridium
43	44	47.8	479	11	Q91WP5	Q91WP5 mus musculu
44	44	47.8	536	5	Q45994	Q45994 caenorhabdi
45	44	47.8	1000	3	Q74719	Q74719 debaryomyce

ALIGNMENTS

RESULT 1

Q9UL90 PRELIMINARY; PRT; 113 AA.
AC Q9UL90;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE Myosin-reactive Immunoglobulin heavy chain variable region (Fragment).
DE OS Homo sapiens (Human).
DE CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
DE OC Mammalia; Eutheria; Primates; Carnivora; Hominidae; Homo.
DE OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalle N.N., Berny S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal fetus."
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035024; AAD56260.1; -
DR HSSP; P01772; 2FB4.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF00047; IG_1.
DR SMART; SM00406; IGV_1.
FT NON_TER 1
FT NON_TER 113
SQ SEQUENCE 113 AA; 12437 MW; ED57FDD19086D07F CRC64;

Query Match 88.0%; Score 81; DB 4; Length 113;
Best Local Similarity 88.2%; Pred. No. 1.3e-05;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Cy 1 F1SYDGSNKHRYADSVKG 17
Db 50 F1SYDGSNKHRYADSVKG 66

RESULT 2

Q9UL93 PRELIMINARY; PRT; 116 AA.

AC Q9UL93; 01-MAY-2000 (TrEMBLrel. 13, Created)

DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)

DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)

DE Myosin-reactive immunoglobulin heavy chain variable region (Fragment).

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

NCBI_TaxID=9606;

RP SEQUENCE FROM N.A.

RX MEDLINE=9827139; PubMed=9614934;

RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M., Young D.C.;

RT "Myosin-reactive autoantibodies in rheumatic carditis and normal fetus";

RL Clin. Immunol. Immunopathol. 87:184-192(1998).

DR EMBL; AF035021; AAD56257.1; -.

DR HSSP; P01772; 2FB4.

DR InterPro; IPR003006; Ig_MHC.

DR Pfam; PF00047; Ig; 1.

DR SMART; SM00406; IgV; 1.

FT NON_TER 1 116

FT SEQUENCE 116 AA; 12434 MW; 0DA0348154DD6061 CRC64;

QY 2 ISYDGSNKHYADSVKG 17

Db 50 ISYDGSNKHYADSVKG 65

Query Match 87.0%; Score 80; DB 4; Length 116;

Best Local Similarity 93.8%; Pred. No. 2e-05;

Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

RESULT 3

Q8WUK1 PRELIMINARY; PRT; 613 AA.

AC Q8WUK1; 01-MAR-2002 (TrEMBLrel. 20, Created)

DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)

DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)

DE Hypothetical 67.3 kDa protein.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

NCBI_TaxID=9606;

RP SEQUENCE FROM N.A.

RX Strauberg R.;

DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)

DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)

DE InterPro; IPR003006; Ig_MHC.

DR Pfam; PF00047; Ig; 1.

DR SMART; SM00409; Ig; 2.

DR SMART; SM00407; Ig; 1.

DR SMART; SM00406; Ig; 1.

DR PROSITE; PS00290; IG_MHC; UNKNOWN_3.

KM Hypothetical protein.

SO SEQUENCE 613 AA; 67296 MW; 60C7F5950671E315 CRC64;

Query Match 87.0%; Score 80; DB 4; Length 613;

Best Local Similarity 93.8%; Pred. No. 0.00013;

Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 ISYDGSNKHYADSVKG 17

Db 70 ISYDGSNKHYADSVKG 85

RESULT 4

Q9UL84 PRELIMINARY; PRT; 122 AA.

AC Q9UL84; 01-MAY-2000 (TrEMBLrel. 13, Created)

DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)

DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)

DE Myosin-reactive immunoglobulin heavy chain variable region (Fragment).

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

NCBI_TaxID=9606;

RP SEQUENCE FROM N.A.

RX MEDLINE=9827139; PubMed=9614934;

RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M., Young D.C.;

RT "Myosin-reactive autoantibodies in rheumatic carditis and normal fetus";

RL Clin. Immunol. Immunopathol. 87:184-192(1998).

DR EMBL; AF035030; AAD56266.1; -.

DR HSSP; P01772; 2FB4.

DR InterPro; IPR003006; Ig_MHC.

DR Pfam; PF00047; Ig; 1.

DR SMART; SM00406; IgV; 1.

FT NON_TER 1 122

FT SEQUENCE 122 AA; 13579 MW; 36054D41366545B8 CRC64;

QY 2 ISYDGSNKHYADSVKG 17

Db 51 ISNDGSNKHYADSVKG 66

Query Match 73.9%; Score 68; DB 4; Length 122;

Best Local Similarity 87.5%; Pred. No. 0.0019;

Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

RESULT 5

Q9Y509 PRELIMINARY; PRT; 147 AA.

AC Q9Y509; 01-NOV-1999 (TrEMBLrel. 12, Created)

DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)

DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)

DE VHS protein (Fragment).

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

NCBI_TaxID=9606;

RP SEQUENCE FROM N.A.

RX MEDLINE=96071149; PubMed=7475288;

RA Cao J., Vescio R.A., Rettig M.B., Hong C.H., Kim A., Lee J.C., Lichtenstein A.K., Berenson J.R.;

RT "A CD10-positive subset of malignant cells is identified in multiple leukemia using PCR with patient-specific immunoglobulin gene primers";

RL EMBL; S80860; AAD14339.1; -.

DR HSSP; P01772; 2FB4.

DR InterPro; IPR003006; Ig_MHC.

DR Pfam; PF00047; Ig; 1.

DR SMART; SM00406; IGV; 1.
 FT NON TER 1
 SQ SEQUENCE 147 AA; 13768 MW; 8489FCAA7BC925C CRC64;

Query Match 68.5%; Score 63; DB 4; Length 147;
 Best Local Similarity 75.0%; Pred. No. 0.015;
 Matches 12; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 2 ISYDGNKHYADSVYK 17
 ||||| :|||
 51 ISYDGNKHYADSVYK 66

RESULT 6

ID Q9ULB6 PRELIMINARY; PRT; 95 AA.

AC Q9ULB6;
 DT 01-MAY-2000 (TREMBlrel. 13, Created)
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
 DE Immunoglobulin heavy chain (Fragment).
 GN VH.

OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 NX NCBI_TaxID=9606;

RP SEQUENCE FROM N.A.
 RA Tang Y., Kayano H.;
 RT "Human VH gene sequence."
 RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AB035268; BAAB7067.1; -.

DR HSSP; P01772; 2FB4.
 DR InterPro; IPR003006; IG_MHC.
 DR InterPro; IPR003596; IG_V.
 DR Pfam; PF00047; IG; 1.

DR SMART; SM00406; IGV; 1.

FT NON TER 1
 FT NON TER 95
 SQ SEQUENCE 95 AA; 10527 MW; 90A8C6D16D22574A CRC64;

Query Match 63.0%; Score 58; DB 4; Length 95;
 Best Local Similarity 68.8%; Pred. No. 0.06;
 Matches 11; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

OY 2 ISYDGNKHYADSVYK 17
 ||||| :|||
 50 IKODGSEKIVDSYK 65

RESULT 7

ID Q9UL72 PRELIMINARY; PRT; 118 AA.

AC Q9UL72;
 DT 01-MAY-2000 (TREMBlrel. 13, Created)
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
 DE Myosin-reactive immunoglobulin heavy chain variable region (Fragment).

OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 NX NCBI_TaxID=9606;

RP SEQUENCE FROM N.A.

RA MEDLINE=98277139; PubMed=9614934;
 RA Wu X., Liu B., Van der Merwe P.L., Kallis N.N., Berney S.M.,
 RA Young D.C.;
 RT "Myosin-reactive autoantibodies in rheumatic carditis and normal fetus";

RL Clin. Immunol. Immunopathol. 87:184-192(1998).
 DR EMBL; AF035042; AAD56278.1; -.
 DR HSSP; P01772; 2FB4.

DR InterPro; IPR003006; IG_MHC.
 DR InterPro; IPR003596; IG_V.
 DR Pfam; PF00047; IG; 1.
 DR SMART; SM00406; IGV; 1.
 FT NON TER 1
 FT NON TER 118
 SQ SEQUENCE 118 AA; 12872 MW; BAD1A5944B2D5CCA CRC64;

Query Match 60.9%; Score 56; DB 4; Length 118;
 Best Local Similarity 56.2%; Pred. No. 0.16;
 Matches 9; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

OY 2 ISYDGNKHYADSVYK 17
 ||||| :|||
 50 VYGGSGSYADSVYK 65

RESULT 8

ID Q9UL71 PRELIMINARY; PRT; 121 AA.

AC Q9UL71;
 DT 01-MAY-2000 (TREMBlrel. 13, Created)
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
 DE Myosin-reactive immunoglobulin heavy chain variable region (Fragment).

OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 NX NCBI_TaxID=9606;

RP SEQUENCE FROM N.A.
 RA Wu X., Liu B., Van der Merwe P.L., Kallis N.N., Berney S.M.,
 RA Young D.C.;
 RT "Myosin-reactive autoantibodies in rheumatic carditis and normal fetus";

RL Clin. Immunol. Immunopathol. 87:184-192(1998).
 DR EMBL; AF035043; AAD56279.1; -.

DR HSSP; P01772; 2FB4.
 DR InterPro; IPR003006; IG_MHC.
 DR InterPro; IPR003596; IG_V.

DR Pfam; PF00047; IG; 1.
 DR SMART; SM00406; IGV; 1.

FT NON TER 1
 FT NON TER 121
 SQ SEQUENCE 121 AA; 13154 MW; 2F045CFA5D50736 CRC64;

Query Match 59.8%; Score 55; DB 4; Length 121;
 Best Local Similarity 68.8%; Pred. No. 0.24;
 Matches 11; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

OY 2 ISYDGNKHYADSVYK 17
 ||||| :|||
 51 ISYDGNKHYADSVYK 66

RESULT 9

ID Q8WR58 PRELIMINARY; PRT; 317 AA.

AC Q8WR58;
 DT 01-MAR-2002 (TREMBlrel. 20, Created)
 DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)
 DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
 DE Surface antigen MB2 (Fragment).

OS Plasmodium falciparum (Isolate NF54).
 OC Eukaryota; Alveolata; Apicomplexa; Haemosporidia; Plasmodium.
 NX NCBI_TaxID=5843;

RP SEQUENCE FROM N.A.

RA STRAIN=NF54;
 RX MEDLINE=21336662; PubMed=11371568;
 RA Nguyen T.V., Fujiocka H., Kang A.S., Rogers W.O., Fidock D.A.,

RA James A.A.;
 RT "Stage-dependent localization of a novel gene product of the malaria parasite, Plasmodium falciparum."
 RL J. Biol. Chem. 276:26724-26731(2001).
 DR EMBL, AF454665; AAL57857.1; -.
 FT NON-TER 317 317
 SQ SEQUENCE 317 AA; 37333 MW; BF9760AB91ADEANF CRC64;

Query Match 57.6%; Score 53; DB 5; Length 317;
 Best Local Similarity 64.3%; Pred. No. 1.6;
 Matches 9; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 2 ISYDGSNKHVADSV 15
 DB 56 ISYDSSNSHYNDKI 69

RESULT 10

Q8WP98 PRELIMINARY; PRT; 326 AA.
 AC Q8WP98;
 DT 01-MAR-2002 (TREMBlrel. 20, Created)
 DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)
 DE Surface antigen MB2 (Fragment).
 OS Plasmodium falciparum.
 OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
 NCBI_Taxid=5833;

RP SEQUENCE FROM N.A.
 RC STRAIN=VEN-1S9, AND PNG-MU237;
 RX MEDLINE=21336662; PubMed=11371568;
 RA Nguyen T.V., Fujiooka H., Kang A.S., Rogers W.O., Fidock D.A.,
 RA James A.A.;
 RT "Stage-dependent localization of a novel gene product of the malaria parasite, Plasmodium falciparum."
 RL J. Biol. Chem. 276:26724-26731(2001).
 DR EMBL, AF454666; AAL57858.1; -.
 DR EMBL, AF454667; AAL57859.1; -.
 FT NON-TER 326 326
 SQ SEQUENCE 326 AA; 38349 MW; 7567623979D6112A CRC64;

Query Match 57.6%; Score 53; DB 5; Length 326;
 Best Local Similarity 64.3%; Pred. No. 1.6;
 Matches 9; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 2 ISYDGSNKHVADSV 15
 DB 56 ISYDSSNSHYNDKI 69

RESULT 11

ID Q963G5 PRELIMINARY; PRT; 414 AA.
 AC Q963G5;
 DT 01-DEC-2001 (TREMBlrel. 19, Created)
 DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
 DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
 DE MB2 (Fragment).
 OS Plasmodium falciparum.
 OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
 NCBI_Taxid=5833;

RP SEQUENCE FROM N.A.
 RC MEDLINE=21336662; PubMed=11371568;
 RA Nguyen T.V., Fujiooka H., Kang A.S., Rogers W.O., Fidock D.A.,
 RA James A.A.;
 RT "Stage-dependent localization of a novel gene product of the malaria parasite, Plasmodium falciparum."
 RL J. Biol. Chem. 276:26724-26731(2001).
 DR EMBL, AF378136; AAK72251.1; -.
 FT NON-TER 414 414
 SQ SEQUENCE 414 AA; 48711 MW; A76F62B773B5CC4D CRC64;

Query Match 57.6%; Score 53; DB 5; Length 414;
 Best Local Similarity 64.3%; Pred. No. 2.1;
 Matches 9; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 2 ISYDGSNKHVADSV 15
 DB 56 ISYDSSNSHYNDKI 69

RESULT 12

Q963G9 PRELIMINARY; PRT; 491 AA.
 AC Q963G9;
 DT 01-DEC-2001 (TREMBlrel. 19, Created)
 DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
 DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
 DE MB2 (Fragment).
 OS Plasmodium falciparum.
 OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
 NCBI_Taxid=5833;

RP SEQUENCE FROM N.A.
 RC MEDLINE=21336662; PubMed=11371568;
 RA Nguyen T.V., Fujiooka H., Kang A.S., Rogers W.O., Fidock D.A.,
 RA James A.A.;
 RT "Stage-dependent localization of a novel gene product of the malaria parasite, Plasmodium falciparum."
 RL J. Biol. Chem. 276:26724-26731(2001).
 DR EMBL, AF378132; AAK72247.1; -.
 DR InterPro; IPR003029; SI.
 FT NON-TER 491 491
 SQ SEQUENCE 491 AA; 57536 MW; E12D9219E0F6134C CRC64;

Query Match 57.6%; Score 53; DB 5; Length 491;
 Best Local Similarity 64.3%; Pred. No. 2.6;
 Matches 9; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 2 ISYDGSNKHVADSV 15
 DB 56 ISYDSSNSHYNDKI 69

RESULT 13

ID Q97CD6 PRELIMINARY; PRT; 305 AA.
 AC Q97CD6;
 DT 01-OCT-2001 (TREMBlrel. 18, Created)
 DT 01-OCT-2001 (TREMBlrel. 18, Last sequence update)
 DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
 DE ABC transport system ATP-binding protein.
 GN TV0166 OR TVG0175536.
 OS Thermoplasma volcanium.
 OC Archaea; Euryarchaeota; Thermoplasmata; Thermoplasmatales; Thermoplasmataceae; Thermoplasma.
 NCBI_Taxid=50339;

RP SEQUENCE FROM N.A.
 RC STRAIN=GSSI / DSM 4299 / JCM 9571;
 RX MEDLINE=20570466; PubMed=11121031;
 RA Kawashima T., Amano N., Koike H., Makino S.-I., Higuchi S.,
 RA Kawashima-Ohya Y., Watanabe K., Yamazaki M., Kanehori K., Kawamoto T.,
 RA Nunoshiba T., Yamamoto Y., Aramaki H., Makino K., Suzuki M.;
 RT "Archaeal adaptation to higher temperatures revealed by genomic sequence of Thermoplasma volcanium."
 RL Proc. Natl. Acad. Sci. U.S.A. 97:14257-14262(2000).
 DR EMBL, AP000991; BAB59308.1; -.
 DR InterPro; IPR003593; AAA_ATPase.
 DR InterPro; IPR003439; ABC_transport.
 DR InterPro; IPR001579; Chitinase_18/2.
 DR Pfam; PF00005; ABC_tran; 1.
 DR ProDom; PD000006; ABC_transport; 1.

DR SMART; SM00382; AAA; 1.
DR PROSITE; PS00211; ABC TRANSPORTER; UNKNOWN_1.
DR PROSITE; PS01095; CHITINASE 18; UNKNOWN_1.
KW ATP-binding; Complete proteome.
SQ SEQUENCE 305 AA; 33434 MW; A1BA9CB7D27B5755 CRC64;

Query Match 54.3%; Score 50; DB 17; Length 305;
Best Local Similarity 66.7%; Pred. No. 4.6;
Matches 10; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

OY 2 ISYDGSNKHVADSVK 16
|||::|:|:
Db 261 ISYDGSNERRADIK 275

RESULT 14

O96BB9 PRELIMINARY; PRT; 597 AA.
AC Q96BB9;
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
DE Hypothetical 65.0 kDa protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=B-CELL;
RA Strausberg R.;
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
EMBL: BC015760; AAH15760.1; -
DR InterPro; IPR003006; IG_MHC.
DR Pfam; PF00047; IG; 5.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_3.
KW Hypothetical protein.
SQ SEQUENCE 597 AA; 65039 MW; 4FCA3AD8CE263D9 CRC64;

Query Match 53.3%; Score 49; DB 4; Length 597;
Best Local Similarity 62.5%; Pred. No. 14;
Matches 10; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

OY 2 ISYDGSNKHVADSVK 17
|||::|:|:
Db 70 ISGSGSTYVADSVK 85

RESULT 15

O9HCC1 PRELIMINARY; PRT; 112 AA.
AC Q9HCC1;
DT 01-MAR-2001 (TREMBlrel. 16, Created)
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE Single chain Fv (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Kikuchi M., Takeda C., Tsujimoto Y., Asada S., Nagata K.;
RT "An antibody fragment2A3 specific for native lysozyme: Isolation from a
human synthetic phage display library and characterization.";
RL Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.
EMBL: AB049915; BAB16829.1; -
DR HSP; P01772; 2P84
DR InterPro; IPR003599; IG_
DR InterPro; IPR003600; IG_like.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; IG; 1.

DR SMART; SM00409; IG; 1.
DR SMART; SM00406; IGv; 1.
DR SMART; SM00410; IG_like; 1.
FT NON_TER 1 1
FT NON_TER 112 112
SQ SEQUENCE 112 AA; 12243 MW; 24F1A45EC3B84788 CRC64;

Query Match 52.2%; Score 48; DB 4; Length 112;
Best Local Similarity 56.2%; Pred. No. 3.1;
Matches 9; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

OY 2 ISYDGSNKHVADSVK 17
|||::|:|:
Db 51 INWNGSGTVADSVK 66

Search completed: June 3, 2003, 08:20:54
Job time : 9.47099 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 3, 2003, 08:02:14 ; Search time 7.6587 Seconds
(Without alignments)
295.776 Million cell updates/sec

Title: US-09-644-668a-33
Sequence: 1 FISYDGSNKHVADSVKG 17

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues
Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

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- 2: /SID2/gcgdata/geneseq/geneseq-emb1/AA1981.DAT:*
- 3: /SID2/gcgdata/geneseq/geneseq-emb1/AA1982.DAT:*
- 4: /SID2/gcgdata/geneseq/geneseq-emb1/AA1983.DAT:*
- 5: /SID2/gcgdata/geneseq/geneseq-emb1/AA1984.DAT:*
- 6: /SID2/gcgdata/geneseq/geneseq-emb1/AA1985.DAT:*
- 7: /SID2/gcgdata/geneseq/geneseq-emb1/AA1986.DAT:*
- 8: /SID2/gcgdata/geneseq/geneseq-emb1/AA1987.DAT:*
- 9: /SID2/gcgdata/geneseq/geneseq-emb1/AA1988.DAT:*
- 10: /SID2/gcgdata/geneseq/geneseq-emb1/AA1989.DAT:*
- 11: /SID2/gcgdata/geneseq/geneseq-emb1/AA1990.DAT:*
- 12: /SID2/gcgdata/geneseq/geneseq-emb1/AA1991.DAT:*
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- 14: /SID2/gcgdata/geneseq/geneseq-emb1/AA1993.DAT:*
- 15: /SID2/gcgdata/geneseq/geneseq-emb1/AA1994.DAT:*
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- 18: /SID2/gcgdata/geneseq/geneseq-emb1/AA1997.DAT:*
- 19: /SID2/gcgdata/geneseq/geneseq-emb1/AA1998.DAT:*
- 20: /SID2/gcgdata/geneseq/geneseq-emb1/AA1999.DAT:*
- 21: /SID2/gcgdata/geneseq/geneseq-emb1/AA2000.DAT:*
- 22: /SID2/gcgdata/geneseq/geneseq-emb1/AA2001.DAT:*
- 23: /SID2/gcgdata/geneseq/geneseq-emb1/AA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	92	100.0	17 22	AA867496 Human heavy chain
2	92	100.0	118 22	AA867509 light chain variab
3	92	100.0	118 22	AA867514 Heavy chain variab
4	86	93.5	17 21	AA839830 Anti-hi12 antibod
5	83	90.2	17 21	AA839836 Anti-hi12 antibod
6	83	90.2	17 21	AA839838 Anti-hi12 antibod
7	83	90.2	17 22	AA867491 Human heavy chain
8	83	90.2	118 22	AA867508 light chain variab
9	83	90.2	118 22	AA867513 Heavy chain variab
10	82	89.1	17 21	AA839829 Anti-hi12 antibod

11	82	89.1	17	21	AA839833	Anti-hi12 antibody
12	82	89.1	17	21	AA839835	Anti-hi12 antibody
13	82	89.1	17	21	AA839837	Anti-hi12 antibody
14	81	88.0	17	21	AA839847	Anti-hi12 antibody
15	81	88.0	17	21	AA839503	Anti-hi12 antibody
16	81	88.0	17	21	AA839511	Anti-hi12 antibody
17	81	88.0	17	21	AA839828	Anti-hi12 antibody
18	81	88.0	17	21	AA839832	Anti-hi12 antibody
19	81	88.0	17	21	AA839834	Anti-hi12 antibody
20	81	88.0	17	21	AA839842	Anti-hi12 antibody
21	81	88.0	17	21	AA839865	Anti-hi12 antibody
22	81	88.0	17	21	AA839871	Anti-hi12 antibody
23	81	88.0	17	21	AA839881	Anti-hi12 antibody
24	81	88.0	98	21	AA840123	Anti-hi12 antibody
25	81	88.0	98	21	AA840141	Anti-hi12 antibody
26	81	88.0	114	21	AA839499	Anti-hi12 antibody
27	81	88.0	115	21	AA839507	Anti-hi12 antibody
28	81	88.0	115	21	AA839515	Anti-hi12 antibody
29	81	88.0	115	21	AA839517	Anti-hi12 antibody
30	81	88.0	115	21	AA839519	Anti-hi12 antibody
31	81	88.0	115	21	AA839521	Anti-hi12 antibody
32	81	88.0	115	21	AA839523	Anti-hi12 antibody
33	81	88.0	115	21	AA839525	Anti-hi12 antibody
34	81	88.0	115	21	AA839527	Anti-hi12 antibody
35	81	88.0	115	21	AA839531	Anti-hi12 antibody
36	81	88.0	115	21	AA839533	Anti-hi12 antibody
37	81	88.0	115	21	AA839535	Anti-hi12 antibody
38	81	88.0	115	21	AA839537	Anti-hi12 antibody
39	81	88.0	115	21	AA839539	Anti-hi12 antibody
40	81	88.0	115	21	AA839541	Anti-hi12 antibody
41	81	88.0	115	21	AA839543	Anti-hi12 antibody
42	81	88.0	115	21	AA839545	Anti-hi12 antibody
43	81	88.0	115	21	AA839547	Anti-hi12 antibody
44	81	88.0	115	21	AA839549	Anti-hi12 antibody
45	81	88.0	115	21	AA839551	Anti-hi12 antibody

ALIGNMENTS

RESULT 1
ID AA867496 standard; peptide; 17 AA.
XX AA867496;
XX
AC
XX
XX
29-MAY-2001 (first entry)
XX
DE Human heavy chain complementarity determining region 2 (CDR2).
XX Complementarity determining region; CDR; immune response; antibody;
XX cytotoxic T lymphocyte associated antigen-4; CTLA-4; B7 ligand; cancer;
KW autoimmune disease; infectious disease; inflammation; allergy;
KW rheumatoid arthritis; myasthenia gravis; lupus erythematosus;
KW multiple sclerosis; insulin-dependent diabetes mellitus; inflammation;
KW transplant rejection; graft versus host disease.
XX
XX Homo sapiens.
XX WO200114424-A2.
XX
XX 01-MAR-2001.
XX
XX 24-AUG-2000; 2000MC-US23356.
XX
XX 24-AUG-1999; 99US-0150452.
XX
XX (MEDA-) MEDAREX INC.
XX
XX Kortman AJ, Halk EL, Lomberg N;
XX WPI; 2001-202933/20.
XX

PT Novel human sequence antibody that binds to human cytotoxic T
 PT lymphocyte associated antigen-4, useful for inducing, augmenting or
 PT prolonging immune response to antigen or for suppressing immune
 PT response in patient

PS Claim 31; Page 99; 127pp; English.

CC AAB67490-99 and AAB67501-06 represents complementarity determining
 CC regions (CDRs) of human antibodies. The antibodies specifically bind to
 CC human cytotoxic T lymphocyte associated antigen-4 (CTLA-4). Such
 CC antibodies are used in methods for inducing, augmenting or prolonging
 CC an immune response to an antigen in a patient, where the antibodies
 CC block binding of human CTLA-4 to human B7 ligands. The antibodies are
 CC also useful for treating autoimmune disease in a subject caused or
 CC exacerbated by increased activity of T cells and for treating prostate
 CC cancer, melanoma or epithelial cancer. A polyvalent or polyclonal
 CC antibody preparation comprising two antibodies of the invention are
 CC useful for suppressing a immune response in a patient. They are used for
 CC treating cancer, infectious diseases and promoting beneficial autoimmune
 CC reactions for the treatment of diseases with inflammatory or allergic
 CC components. The polyvalent or polyclonal preparations are useful for
 CC treating autoimmune diseases such as rheumatoid arthritis, myasthenia
 CC gravis and lupus erythematosus, multiple sclerosis, insulin-dependent
 CC diabetes mellitus, transplant rejection, and inflammation, graft versus
 CC host disease.

CC Sequence 17 AA;

Query Match 100.0%; Score 92; DB 22; Length 17;
 Best Local Similarity 100.0%; Pred. No. 2e-08;

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTSYDGSNKHVADSVKG 17
 Db 1 FTSYDGSNKHVADSVKG 17

RESULT 2
 AAB67509
 ID AAB67509 standard; peptide; 118 AA.

AC AAB67509;

DT 29-MAY-2001 (first entry)

XX Light chain variable region of anti-CTLA-4 antibody 4B6.

XX Complementarity determining region; CDR; immune response; antibody;
 KW cytotoxic T lymphocyte associated antigen-4; CTLA-4; B7 ligand; cancer;
 KW autoimmune disease; infectious disease; inflammation; allergy;
 KW rheumatoid arthritis; myasthenia gravis; lupus erythematosus;
 KW multiple sclerosis; insulin-dependent diabetes mellitus; inflammation;
 KW transplant rejection; graft versus host disease.

OS Homo sapiens.

XX Key Location/Qualifiers

XX Region 31..35

XX Region /note= "CDR1"

XX Region /note= "CDR2"

XX Region /note= "CDR3"

XX WO200114424-A2.

XX 01-MAR-2001.

XX 24-AUG-2000; 2000WO-US23356.

XX 24-AUG-1999; 99US-0150452.

XX (MEDA-) MEDAREX INC.

XX Korman AJ, Halk EL, Lonberg N;
 XX WPI; 2001-202933/20.

PT Novel human sequence antibody that binds to human cytotoxic T
 PT lymphocyte associated antigen-4, useful for inducing, augmenting or
 PT prolonging immune response to antigen or for suppressing immune
 PT response in patient

PS Claim 26; Fig 7; 127pp; English.

CC The present sequence represents the light chain variable region of
 CC human antibody 4B6. This antibody specifically binds to human
 CC cytotoxic T lymphocyte associated antigen-4 (CTLA-4). Such antibodies
 CC are used in methods for inducing, augmenting or prolonging an immune
 CC response to an antigen in a patient, where the antibodies block
 CC binding of human CTLA-4 to human B7 ligands. The antibodies are
 CC also useful for treating autoimmune disease in a subject caused or
 CC exacerbated by increased activity of T cells and for treating prostate
 CC cancer, melanoma or epithelial cancer. A polyvalent or polyclonal
 CC antibody preparation comprising two antibodies of the invention are
 CC useful for suppressing a immune response in a patient. They are used for
 CC treating cancer, infectious diseases and promoting beneficial autoimmune
 CC reactions for the treatment of diseases with inflammatory or allergic
 CC components. The polyvalent or polyclonal preparations are useful for
 CC treating autoimmune diseases such as rheumatoid arthritis, myasthenia
 CC gravis and lupus erythematosus, multiple sclerosis, insulin-dependent
 CC diabetes mellitus, transplant rejection, and inflammation, graft versus
 CC host disease.

CC Sequence 118 AA;

Query Match 100.0%; Score 92; DB 22; Length 118;
 Best Local Similarity 100.0%; Pred. No. 1.7e-07;

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTSYDGSNKHVADSVKG 17
 Db 50 FTSYDGSNKHVADSVKG 66

RESULT 3
 AAB67514
 ID AAB67514 standard; peptide; 118 AA.

AC AAB67514;

DT 29-MAY-2001 (first entry)

XX Heavy chain variable region of anti-CTLA-4 antibody 10D1.

XX Complementarity determining region; CDR; immune response; antibody;
 KW cytotoxic T lymphocyte associated antigen-4; CTLA-4; B7 ligand; cancer;
 KW autoimmune disease; infectious disease; inflammation; allergy;
 KW rheumatoid arthritis; myasthenia gravis; lupus erythematosus;
 KW multiple sclerosis; insulin-dependent diabetes mellitus; inflammation;
 KW transplant rejection; graft versus host disease.

OS Homo sapiens.

XX Key Location/Qualifiers

XX Region 31..35

XX Region /note= "CDR1"

XX Region /note= "CDR2"

XX Region /note= "CDR3"

XX WO200114424-A2.

XX 01-MAR-2001.

PF 24-AUG-2000; 2000MO-US23356.
 XX 24-AUG-1999; 99US-0150452.
 XX (MEDA-) MEDAREX INC.
 PA Korman AJ, Halk EL, Lomborg N;
 PI WPI; 2001-202933/20.
 DR
 XX Novel human sequence antibody that binds to human cytotoxic T
 PT lymphocyte associated antigen-4, useful for inducing, augmenting or
 PT prolonging immune response to antigen or for suppressing immune
 PT response in patient -

XX Claim 26; Fig 8; 127pp; English.

XX The present sequence represents the heavy chain variable region of
 CC human antibody 10D1. This antibody specifically binds to human
 CC cytotoxic T lymphocyte associated antigen-4 (CTLA-4). Such antibodies
 CC are used in methods for inducing, augmenting or prolonging an immune
 CC response to an antigen in a patient, where the antibodies block
 CC binding of human CTLA-4 to human B7 ligands. The antibodies are
 CC also useful for treating autoimmune disease in a subject caused or
 CC exacerbated by increased activity of T cells and for treating prostate
 CC cancer, melanoma or epithelial cancer. A polyvalent or polyclonal
 CC antibody preparation comprising two antibodies of the invention are
 CC useful for suppressing an immune response in a patient. They are used for
 CC treating cancer, infectious diseases and promoting beneficial autoimmune
 CC reactions for the treatment of diseases with inflammatory or allergic
 CC components. The polyvalent or polyclonal preparations are useful for
 CC treating autoimmune diseases such as rheumatoid arthritis, myasthenia
 CC gravis and lupus erythematosus, multiple sclerosis, insulin-dependent
 CC diabetes mellitus, transplant rejection, and inflammation, graft versus
 CC host disease.

XX Sequence 118 AA;

Query Match 100.0%; Score 92; DB 22; Length 118;

Best Local Similarity 100.0%; Pred. No. 1.7e-07;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FISTYDGSNKKYADSVKG 17
 |||
 DB 50 FISTYDGSNKKYADSVKG 66

RESULT 4

AAB39830
 ID AAB39830 standard; Peptide; 17 AA.

XX AAB39830;

DT 05-FEB-2001 (first entry)

DE Anti-IL12 antibody heavy chain CDR2 amino acid sequence SEQ ID 346.

XX Human; neutralizing antibody; interleukin-12; IL-12; antiinflammatory;
 KM complementarity determining region; CDR; antirheumatic; antiarthritic;
 KM antileukemic; neuroprotective; antiproliferative; antitumor; cardiant;
 KM antiparasitic; antibacterial; immunosuppressive; Crohn's disease;
 KM multiple sclerosis; rheumatoid arthritis.

OS Homo sapiens.

PN WO200056772-A1.

PD 28-SEP-2000.

PF 24-MAR-2000; 2000MO-US07946.

PR 25-MAR-1999; 99US-0126603.

PA (BADI) BASF AG.
 PA (GENT) GENETICS INST INC.
 XX Salfield JG, Roguska M, Paskind M, Banerjee S, Tracey DE, White M;
 PI Kaymakalan Z, Labkovsky B, Sakorafas P, Friedrich S, Wyles A;
 PI Veldman GM, Venturini A, Warne NW, Widom A, Rivin JG, Duncan AR;
 PI Derbyshire EJ, Carmen S, Smith S, Holter TL, Du Fou SL;
 DR WPI; 2000-638250/61.
 XX
 XX New human antibody specific for human interleukin-12 (IL-12) used to
 PT treat disorders characterized by aberrant IL-12 expression e.g. Crohn's
 PT disease and multiple sclerosis -

XX Claim 33; Figure 2B; 377pp; English.

XX This invention relates to a new human antibody specific for human
 CC interleukin-12 (IL-12). The invention also includes antigen binding
 CC portions that bind to IL-12. Sequences AAB39485-B39516 represent human
 CC anti-IL-12 antibody heavy and light chain complementarity determining
 CC region (CDR) amino acid sequences, and also includes variable region
 CC amino acid sequences. Other variable region amino acid sequences are
 CC given in AAB39517-B39560 and AAB40068-B40149. Sequences AAB39561-B39771
 CC represent anti-IL-12 CDR3 related amino acid sequences, AAB39772-B40063
 CC represent other CDR sequences. Light chain CDR3 consensus sequences are
 CC given in AAB40064-B40067. Primers used in the identification and
 CC construction of the antibodies of the invention are given in
 CC A061062-C61071. The antibody of the invention is a neutralizing
 CC antibody and has antirheumatic; antiarthritic; antileukemic;
 CC antiparasitic; neuroprotective; antiproliferative; antitumor;
 CC cardiant; antiparasitic; antibacterial and immunosuppressive activity.
 CC The antibodies or antigen-binding fragments are useful in the treatment
 CC of disorders associated with detrimental release of human IL-12,
 CC especially Crohn's disease, multiple sclerosis and rheumatoid arthritis.
 CC They can also be used in the manufacture of a pharmaceutical composition
 CC to treat human IL-12 disorders.

XX Sequence 17 AA;

Query Match 93.5%; Score 86; DB 21; Length 17;

Best Local Similarity 94.1%; Pred. No. 1.9e-07;
 Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 FISTYDGSNKKYADSVKG 17
 |||
 DB 1 FISTYDGSNKKYADSVKG 17

RESULT 5

AAB39836
 ID AAB39836 standard; Peptide; 17 AA.

XX AAB39836;

DT 05-FEB-2001 (first entry)

DE Anti-IL12 antibody heavy chain CDR2 amino acid sequence SEQ ID 352.

XX Human; neutralizing antibody; interleukin-12; IL-12; antiinflammatory;
 KM complementarity determining region; CDR; antirheumatic; antiarthritic;
 KM antileukemic; neuroprotective; antiproliferative; antitumor; cardiant;
 KM antiparasitic; antibacterial; immunosuppressive; Crohn's disease;
 KM multiple sclerosis; rheumatoid arthritis.

OS Homo sapiens.

PN WO200056772-A1.

PD 28-SEP-2000.

PF 24-MAR-2000; 2000MO-US07946.

PR 25-MAR-1999; 99US-0126603.

XX (BAD) BASF AG.
 PA (GEM) GENETICS INST INC.
 XX
 PI Salfeld JG, Roguoka M, Paekind M, Banerjee S, Tracey DE, White M,
 PI Kaymakcalan Z, Labkovsky B, Sakorafas P, Friedrich S, Myles A,
 PI Veldman GM, Venturini A, Warne NW, Widom A, Elvin JG, Duncan AR,
 PI Derbyshire EJ, Carmen S, Smith S, Hollet TL, Du Fou SL,
 XX WPI; 2000-638250/61.

XX New human antibody specific for human interleukin-12 (IL-12) used to
 PT treat disorders characterized by aberrant IL-12 expression e.g. Crohn's
 PT disease and multiple sclerosis -
 XX

PS Claim 33; Figure 2B; 377pp; English.

XX This invention relates to a new human antibody specific for human
 CC interleukin-12 (IL-12). The invention also includes antigen binding
 CC portions that bind to IL-12. Sequences AAB39485-B39516 represent human
 CC anti-IL-12 antibody heavy and light chain complementarity determining
 CC region (CDR) amino acid sequences, and also includes variable region
 CC amino acid sequences. Other variable region amino acid sequences are
 CC given in AAB39517-B39560 and AAB40068-B40149. Sequences AAB39561-B39771
 CC represent anti-IL-12 CDR3 related amino acid sequences. AAB39772-B40063
 CC represent other CDR sequences. Light chain CDR3 consensus sequences are
 CC given in AAB40064-B40067. Primers used in the identification and
 CC construction of the antibodies of the invention are given in
 CC AAC61065-C61071. The antibody of the invention is a neutralizing
 CC antibody and has antirheumatic; antiarthritic; antisclerotic;
 CC antiinflammatory; neuroprotective; antiparastitic; antiaesthetic;
 CC cardiant; antiparasitic; antibacterial and immunosuppressive activity.
 CC The antibodies or antigen-binding fragments are useful in the treatment
 CC of disorders associated with detrimental release of human IL-12,
 CC especially Crohn's disease, multiple sclerosis and rheumatoid arthritis.
 CC They can also be used in the manufacture of a pharmaceutical composition
 CC to treat human IL-12 disorders.
 CC

SO Sequence 17 AA;

Query Match 90.2%; Score 83; DB 21; Length 17;
 Best Local Similarity 88.2%; Pred. No. 5.9e-07;
 Matches 15; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 FTSYDGNKHYADSVYKG 17
 ||:|||||:|||||
 Db 1 FIAYDGNKHYADSVYKG 17

RESULT 6
 AAB39838

ID AAB39838 standard; peptide; 17 AA.

AC AAB39838;

DT 05-FEB-2001 (first entry)

DE Anti-hIL12 antibody heavy chain CDR2 amino acid sequence SEQ ID 354.

XX Human; neutralizing antibody; interleukin-12; IL-12; antiinflammatory;
 KW complementarity determining region; CDR; antirheumatic; antiaesthetic;
 KW antisclerotic; neuroprotective; antiparastitic; antiaesthetic; cardiant;
 KW antiparasitic; antibacterial; immunosuppressive; Crohn's disease;
 KW multiple sclerosis; rheumatoid arthritis.

OS Homo sapiens.

PN WO200056772-A1.

PD 28-SEP-2000.

PF 24-MAR-2000; 2000WO-US07946.

PR 25-MAR-1999; 99US-0126603.

PA (BAD) BASF AG.
 PA (GEM) GENETICS INST INC.

XX Salfeld JG, Roguoka M, Paekind M, Banerjee S, Tracey DE, White M,
 PI Kaymakcalan Z, Labkovsky B, Sakorafas P, Friedrich S, Myles A,
 PI Veldman GM, Venturini A, Warne NW, Widom A, Elvin JG, Duncan AR,
 PI Derbyshire EJ, Carmen S, Smith S, Hollet TL, Du Fou SL,
 XX WPI; 2000-638250/61.

XX New human antibody specific for human interleukin-12 (IL-12) used to
 PT treat disorders characterized by aberrant IL-12 expression e.g. Crohn's
 PT disease and multiple sclerosis -
 XX

PS Claim 33; Figure 2B; 377pp; English.

XX This invention relates to a new human antibody specific for human
 CC interleukin-12 (IL-12). The invention also includes antigen binding
 CC portions that bind to IL-12. Sequences AAB39485-B39516 represent human
 CC anti-IL-12 antibody heavy and light chain complementarity determining
 CC region (CDR) amino acid sequences, and also includes variable region
 CC amino acid sequences. Other variable region amino acid sequences are
 CC given in AAB39517-B39560 and AAB40068-B40149. Sequences AAB39561-B39771
 CC represent anti-IL-12 CDR3 related amino acid sequences. AAB39772-B40063
 CC represent other CDR sequences. Light chain CDR3 consensus sequences are
 CC given in AAB40064-B40067. Primers used in the identification and
 CC construction of the antibodies of the invention are given in
 CC AAC61065-C61071. The antibody of the invention is a neutralizing
 CC antibody and has antirheumatic; antiarthritic; antisclerotic;
 CC antiinflammatory; neuroprotective; antiparastitic; antiaesthetic;
 CC cardiant; antiparasitic; antibacterial and immunosuppressive activity.
 CC The antibodies or antigen-binding fragments are useful in the treatment
 CC of disorders associated with detrimental release of human IL-12,
 CC especially Crohn's disease, multiple sclerosis and rheumatoid arthritis.
 CC They can also be used in the manufacture of a pharmaceutical composition
 CC to treat human IL-12 disorders.
 CC

SO Sequence 17 AA;

Query Match 90.2%; Score 83; DB 21; Length 17;
 Best Local Similarity 88.2%; Pred. No. 5.9e-07;
 Matches 15; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 FTSYDGNKHYADSVYKG 17
 ||:|||||:|||||
 Db 1 FIAYDGNKHYADSVYKG 17

RESULT 7
 AAB67491

ID AAB67491 standard; peptide; 17 AA.

AC AAB67491;

DT 29-MAY-2001 (first entry)

DE Human heavy chain complementarity determining region 2 (CDR2).

XX Complementarity determining region; CDR; immune response; antibody;
 KW cytotoxic T lymphocyte associated antigen-4; CTLA-4; B7 ligand; cancer;
 KW autoimmune disease; infectious disease; inflammation; allergy;
 KW rheumatoid arthritis; myosclerosis; lupus erythematosus;
 KW multiple sclerosis; insulin-dependent diabetes mellitus; inflammation;
 KW transplant rejection; graft versus host disease.

OS Homo sapiens.

PN WO200114424-A2.

PD 01-MAR-2001.

PF 24-AUG-2000; 2000WO-US23356.
XX 24-AUG-1999; 99US-0150452.
XX (MEDA-) MEDAREX INC.
XX Korman AJ, Halk EL, Lomborg N;
XX WPI; 2001-202933/20.
XX Novel human sequence antibody that binds to human cytotoxic T
PT lymphocyte associated antigen-4, useful for inducing, augmenting or
PT prolonging immune response to antigen or for suppressing immune
PT response in patient
XX
PS Claim 30; Page 99; 127pp; English.
XX AAB6790-99 and AAB67501-06 represents complementarity determining
CC regions (CDRs) of human antibodies. The antibodies specifically bind to
CC human cytotoxic T lymphocyte associated antigen-4 (CTLA-4). Such
CC antibodies are used in methods for inducing, augmenting or prolonging
CC an immune response to an antigen in a patient, where the antibodies
CC block binding of human CTLA-4 to human B7 ligands. The antibodies are
CC also useful for treating autoimmune disease in a subject caused or
CC exacerbated by increased activity of T cells and for treating prostate
CC cancer, melanoma or epithelial cancer. A polyvalent or polyclonal
CC antibody preparation comprising two antibodies of the invention are
CC useful for suppressing an immune response in a patient. They are used for
CC treating cancer, infectious diseases and promoting beneficial autoimmune
CC reactions for the treatment of diseases with inflammatory or allergic
CC components. The polyvalent or polyclonal preparations are useful for
CC treating autoimmune diseases such as rheumatoid arthritis, myasthenia
CC gravis and lupus erythematosus, multiple sclerosis, insulin-dependent
CC diabetes mellitus, transplant rejection, and inflammation, graft versus
CC host disease.
XX
SQ Sequence 17 AA;
XX
XX Query Match 90.2%; Score 83; DB 22; Length 17;
Best Local Similarity 88.2%; Pred. No. 5.9e-07;
Matches 15; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
XX
OY 1 FISYDGSNKKHYADSVKG 17
|||:|:|:|:|:|:|
1 FISYDGNKKYADSVKG 17
XX
ID AAB67508 standard; peptide; 118 AA.
XX AAB67508;
XX
DT 29-MAY-2001 (first entry)
XX
DE Light chain variable region of anti-CTLA-4 antibody 10D1.
XX
XX Complementarity determining region; CDR; immune response; antibody;
KW cytotoxic T lymphocyte associated antigen-4; CTLA-4; B7 ligand; cancer;
KW autoimmune disease; infectious disease; inflammation; allergy;
KW rheumatoid arthritis; myasthenia gravis; lupus erythematosus;
KW multiple sclerosis; insulin-dependent diabetes mellitus; inflammation;
KW transplant rejection; graft versus host disease.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT 31..35 /note= "CDR1"
FT 50..66 /note= "CDR2"
FT 99..107 /note= "CDR3"
FT Region

XX
FN W0200114424-A2.
XX 01-MAR-2001.
XX 24-AUG-2000; 2000WO-US23356.
XX 24-AUG-1999; 99US-0150452.
XX (MEDA-) MEDAREX INC.
XX Korman AJ, Halk EL, Lomborg N;
XX WPI; 2001-202933/20.
XX Novel human sequence antibody that binds to human cytotoxic T
PT lymphocyte associated antigen-4, useful for inducing, augmenting or
PT prolonging immune response to antigen or for suppressing immune
PT response in patient
XX
PS Claim 25; Fig 7; 127pp; English.
XX
XX The present sequence represents the light chain variable region of
CC human antibody 10D1. This antibody specifically binds to human
CC cytotoxic T lymphocyte associated antigen-4 (CTLA-4). Such antibodies
CC are used in methods for inducing, augmenting or prolonging an immune
CC response to an antigen in a patient, where the antibodies block
CC binding of human CTLA-4 to human B7 ligands. The antibodies are
CC also useful for treating autoimmune disease in a subject caused or
CC exacerbated by increased activity of T cells and for treating prostate
CC cancer, melanoma or epithelial cancer. A polyvalent or polyclonal
CC antibody preparation comprising two antibodies of the invention are
CC useful for suppressing an immune response in a patient. They are used for
CC treating cancer, infectious diseases and promoting beneficial autoimmune
CC reactions for the treatment of diseases with inflammatory or allergic
CC components. The polyvalent or polyclonal preparations are useful for
CC treating autoimmune diseases such as rheumatoid arthritis, myasthenia
CC gravis and lupus erythematosus, multiple sclerosis, insulin-dependent
CC diabetes mellitus, transplant rejection, and inflammation, graft versus
CC host disease.
XX
SQ Sequence 118 AA;
XX
XX Query Match 90.2%; Score 83; DB 22; Length 118;
Best Local Similarity 88.2%; Pred. No. 5.3e-06;
Matches 15; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
XX
OY 1 FISYDGSNKKHYADSVKG 17
|||:|:|:|:|:|:|
50 FISYDGNKKYADSVKG 66
XX
ID AAB67513 standard; peptide; 118 AA.
XX AAB67513;
XX
DT 29-MAY-2001 (first entry)
XX
DE Heavy chain variable region of anti-CTLA-4 antibody 10D1.
XX
XX Complementarity determining region; CDR; immune response; antibody;
KW cytotoxic T lymphocyte associated antigen-4; CTLA-4; B7 ligand; cancer;
KW autoimmune disease; infectious disease; inflammation; allergy;
KW rheumatoid arthritis; myasthenia gravis; lupus erythematosus;
KW multiple sclerosis; insulin-dependent diabetes mellitus; inflammation;
KW transplant rejection; graft versus host disease.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT 31..35

FT	/note= "CDR1"	
FT	50.66	
FT	/note= "CDR2"	
FT	99.107	
FT	/note= "CDR3"	
XX		
PN	WO200114424-A2.	
XX		
PD	01-MAR-2001.	
XX		
PP	24-AUG-2000; 2000WO-US23356.	
XX		
PR	24-AUG-1999; 99US-0150452.	
PA	(MEDA-) MEDAREX INC.	
XX		
PI	Korman AJ, Halk EL, Lonberg N;	
DR	WPI; 2001-202933/20.	
XX		
PT	Novel human sequence antibody that binds to human cytotoxic T	
PT	lymphocyte associated antigen-4, useful for inducing, augmenting or	
PT	prolonging immune response to antigen or for suppressing immune	
XX	response in patient	
PS	Claim 25; Fig 8; 127bp; English.	
XX		
CC	The present sequence represents the heavy chain variable region of	
CC	human antibody 10D1. This antibody specifically binds to human	
CC	cytotoxic T lymphocyte associated antigen-4 (CTLA-4). Such antibodies	
CC	are used in methods for inducing, augmenting or prolonging an immune	
CC	response to an antigen in a patient, where the antibodies block	
CC	binding of human CTLA-4 to human B7 ligands. The antibodies are	
CC	also useful for treating autoimmune disease in a subject caused or	
CC	exacerbated by increased activity of T cells and for treating prostate	
CC	cancer, melanoma or epithelial cancer. A polyvalent or polyclonal	
CC	antibody preparation comprising two antibodies of the invention are	
CC	useful for suppressing a immune response in a patient. They are used for	
CC	treating cancer, infectious diseases and promoting beneficial autoimmune	
CC	reactions for the treatment of diseases with inflammatory or allergic	
CC	components. The polyvalent or polyclonal preparations are useful for	
CC	treating autoimmune diseases such as rheumatoid arthritis, myasthenia	
CC	gravis and lupus erythematosus, multiple sclerosis, insulin-dependent	
CC	diabetes mellitus, transplant rejection, and inflammation, graft versus	
CC	host disease.	
SO	Sequence 118 AA;	
QY	1 F1SYDGSNKHADSVKG 17	
DB	50 F1SYDGNKKYADSVKG 66	
RESULT 10		
AAB39829		
ID	AAB39829 standard; Peptide; 17 AA.	
XX		
AC	AAB39829;	
XX		
DT	05-FEB-2001 (first entry)	
XX		
DB	Anti-hIL12 antibody heavy chain CDR2 amino acid sequence SEQ ID 345.	
XX		
XX	Human; neutralizing antibody; interleukin-12; IL-12; antiinflammatory;	
KM	complementarity determining region; CDR; antirheumatic; antiarthritis;	
KM	antisclerotic; neuroprotective; antipsoriatic; antiaesthetic; cardiant;	
KM	antiparasitic; antibacterial; immunosuppressive; Crohn's disease;	
XX	multiple sclerosis; rheumatoid arthritis.	

OS Homo sapiens.
XX
XX WO20056772-A1.
XX
XX 28-SEP-2000.
XX
XX 24-MAR-2000; 2000WO-US07946.
XX
XX 25-MAR-1999; 99US-0126603.
XX
XX (BADI) BASF AG.
XX (GEMY) GENETICS INST INC.
XX
XX Salfield JG, Roguska M, Paskind M, Banerjee S, Tracey DE, White M,
XX Kaymakcalan Z, Labkovsky B, Sakorafas P, Friedrich S, Wyles A,
XX Veldman GM, Venturini A, Wane NW, Widom A, Elvin JG, Duncan AR,
XX Deryshire EJ, Carmen S, Smith S, Holtet TL, Du Fou SL;
XX WPI, 2000-638250/61.
XX
XX New human antibody specific for human interleukin-12 (IL-12) used to
XX treat disorders characterized by aberrant IL-12 expression e.g. Crohn's
XX disease and multiple sclerosis -
XX
XX Claim 33; Figure 2B; 377pp; English.
XX
XX This invention relates to a new human antibody specific for human
XX interleukin-12 (IL-12). The invention also includes antigen binding
XX portions that bind to IL-12. Sequences AAB39485-839516 represent human
XX anti-IL-12 antibody heavy and light chain complementarity determining
XX region (CDR) amino acid sequences, and also includes variable region
XX amino acid sequences. Other variable region amino acid sequences are
XX given in AAB39517-839560 and AAB40068-B40149. Sequences AAB39561-839771
XX represent anti-IL-12 CDR3 related amino acid sequences, AAB39772-840063
XX represent other CDR sequences, light chain CDR3 consensus sequences are
XX given in AAB40064-B40067. Primers used in the identification and
XX construction of the antibodies of the invention are given in
XX AAB61062-661071. The antibody of the invention is a neutralising
XX antibody and has antineumatic, antiarthritic, antisclerotic,
XX antiinflammatory, neuroprotective, antipsoiatric, antiasthmatic,
XX cardiant, antiaplastic, antibacterial and immunosuppressive activity.
XX The antibodies or antigen-binding fragments are useful in the treatment
XX of disorders associated with detrimental release of human IL-12,
XX especially Crohn's disease, multiple sclerosis and rheumatoid arthritis.
XX They can also be used in the manufacture of a pharmaceutical composition
XX to treat human IL-12 disorders.
XX
XX Sequence 17 AA;
XX
XX Query Match 89.1%; Score 82; DB 21; Length 17;
XX Best Local Similarity 88.2%; Pred. No. 8.7e-07;
XX Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
XX
XX 1 FIFDGSNKHAYADSVKG 17
XX ||| ||||| ||||| |||||
XX 1 FIFDGSNKKYADSVKG 17
XX
XX RESULT 11
XX AAB39833
XX ID AAB39833 standard; Peptide; 17 AA.
XX
XX AAB39833;
XX
XX 05-FEB-2001 (first entry)
XX
XX Anti-IL12 antibody heavy chain CDR2 amino acid sequence SEQ ID 349.
XX
XX Human; neutralising antibody; interleukin-12; IL-12; antiinflammatory;
XX Complementarity determining region; CDR; antineumatic; antiarthritic;
XX antisclerotic; neuroprotective; antipsoiatric; antiasthmatic; cardiant;
XX antiaplastic; antibacterial; immunosuppressive; Crohn's disease;
XX multiple sclerosis; rheumatoid arthritis.

XX OS Homo sapiens.
 XX PN WO200056772-A1.
 XX PD 28-SEP-2000.
 XX PF 24-MAR-2000; 2000MO-US07946.
 XX PR 25-MAR-1999; 99US-0126603.
 XX PA (BADI) BASF AG.
 XX PA (GEMT) GENETICS INST INC.
 XX PI Salfeld JG, Roguska M, Paekind M, Banerjee S, Tracey DE, White M,
 XX PI Kaymakalan Z, Labkovsky B, Sakorafas P, Friedrich S, Myles A,
 XX PI Veldman GM, Venturini A, Warne NW, Widom A, Elyin JG, Duncan AR,
 XX PI Derbyshire EJ, Carmen S, Smith S, Holter TL, Du Fou SL,
 XX WPI; 2000-638250/61.
 XX DR
 XX PT New human antibody specific for human interleukin-12 (IL-12) used to
 XX PT treat disorders characterized by aberrant IL-12 expression e.g. Crohn's
 XX PT disease and multiple sclerosis -
 XX PS Claim 33; Figure 2B; 377pp; English.
 XX CC This invention relates to a new human antibody specific for human
 XX CC interleukin-12 (IL-12). The invention also includes antigen binding
 XX CC portions that bind to IL-12. Sequences AAB39485-B39516 represent human
 XX CC anti-IL-12 antibody heavy and light chain complementarity determining
 XX CC region (CDR) amino acid sequences, and also includes variable region
 XX CC amino acid sequences. Other variable region amino acid sequences are
 XX CC given in AAB39517-B39560 and AAB40068-B40149. Sequences AAB39561-B39771
 XX CC represent anti-IL-12 CDR3 related amino acid sequences, AAB39772-B40063
 XX CC represent other CDR sequences. Light chain CDR3 consensus sequences are
 XX CC given in AAB40064-B40067. Primers used in the identification and
 XX CC construction of the antibodies of the invention are given in
 XX CC AAB61062-661071. The antibody of the invention is a neutralizing
 XX CC antiinflammatory; neuroprotective; antiproliferative; antisclerotic;
 XX CC cardiatic; antiparasitic; antibacterial and immunosuppressive activity.
 XX CC The antibodies or antigen-binding fragments are useful in the treatment
 XX CC of disorders associated with detrimental release of human IL-12,
 XX CC especially Crohn's disease, multiple sclerosis and rheumatoid arthritis.
 XX CC They can also be used in the manufacture of a pharmaceutical composition
 XX CC to treat human IL-12 disorders.
 XX SQ Sequence 17 AA;
 XX
 XX Query Match 89.1%; Score 82; DB 21; Length 17;
 XX Best Local Similarity 88.2%; Pred. No. 8.7e-07;
 XX Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 1 FSYDGSNKHYADSVYKG 17
 DB 1 FIKYDGSNKHYADSVYKG 17
 XX
 XX RESULT 12
 XX AAB39835
 XX ID AAB39835 standard; Peptide; 17 AA.
 XX AC AAB39835;
 XX DT 05-FEB-2001 (first entry)
 XX DE Anti-hIL12 antibody heavy chain CDR2 amino acid sequence SEQ ID 351.
 XX XX Human; neutralizing antibody; interleukin-12; IL-12; antiinflammatory;
 XX KW complementarity determining region; CDR; antirheumatic; antiarthritic;
 XX KW antisclerotic; neuroprotective; antiproliferative; antiasclerotic; cardiatic;
 XX KW antiparasitic; antibacterial; immunosuppressive; Crohn's disease;

KW multiple sclerosis; rheumatoid arthritis.
 XX OS Homo sapiens.
 XX PN WO200056772-A1.
 XX PD 28-SEP-2000.
 XX PF 24-MAR-2000; 2000MO-US07946.
 XX PR 25-MAR-1999; 99US-0126603.
 XX PA (BADI) BASF AG.
 XX PA (GEMT) GENETICS INST INC.
 XX PI Salfeld JG, Roguska M, Paekind M, Banerjee S, Tracey DE, White M,
 XX PI Kaymakalan Z, Labkovsky B, Sakorafas P, Friedrich S, Myles A,
 XX PI Veldman GM, Venturini A, Warne NW, Widom A, Elyin JG, Duncan AR,
 XX PI Derbyshire EJ, Carmen S, Smith S, Holter TL, Du Fou SL,
 XX WPI; 2000-638250/61.
 XX DR
 XX PT New human antibody specific for human interleukin-12 (IL-12) used to
 XX PT treat disorders characterized by aberrant IL-12 expression e.g. Crohn's
 XX PT disease and multiple sclerosis -
 XX PS Claim 33; Figure 2B; 377pp; English.
 XX CC This invention relates to a new human antibody specific for human
 XX CC interleukin-12 (IL-12). The invention also includes antigen binding
 XX CC portions that bind to IL-12. Sequences AAB39485-B39516 represent human
 XX CC anti-IL-12 antibody heavy and light chain complementarity determining
 XX CC region (CDR) amino acid sequences, and also includes variable region
 XX CC amino acid sequences. Other variable region amino acid sequences are
 XX CC given in AAB39517-B39560 and AAB40068-B40149. Sequences AAB39561-B39771
 XX CC represent anti-IL-12 CDR3 related amino acid sequences, AAB39772-B40063
 XX CC represent other CDR sequences. Light chain CDR3 consensus sequences are
 XX CC given in AAB40064-B40067. Primers used in the identification and
 XX CC construction of the antibodies of the invention are given in
 XX CC AAB61062-661071. The antibody of the invention is a neutralizing
 XX CC antiinflammatory; neuroprotective; antiproliferative; antisclerotic;
 XX CC cardiatic; antiparasitic; antibacterial and immunosuppressive activity.
 XX CC The antibodies or antigen-binding fragments are useful in the treatment
 XX CC of disorders associated with detrimental release of human IL-12,
 XX CC especially Crohn's disease, multiple sclerosis and rheumatoid arthritis.
 XX CC They can also be used in the manufacture of a pharmaceutical composition
 XX CC to treat human IL-12 disorders.
 XX SQ Sequence 17 AA;
 XX
 XX Query Match 89.1%; Score 82; DB 21; Length 17;
 XX Best Local Similarity 88.2%; Pred. No. 8.7e-07;
 XX Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 1 FSYDGSNKHYADSVYKG 17
 DB 1 FIKYDGSNKHYADSVYKG 17
 XX
 XX RESULT 13
 XX AAB39837
 XX ID AAB39837 standard; Peptide; 17 AA.
 XX AC AAB39837;
 XX DT 05-FEB-2001 (first entry)
 XX DE Anti-hIL12 antibody heavy chain CDR2 amino acid sequence SEQ ID 353.
 XX XX Human; neutralizing antibody; interleukin-12; IL-12; antiinflammatory;
 XX KW complementarity determining region; CDR; antirheumatic; antiarthritic;
 XX KW antisclerotic; neuroprotective; antiproliferative; antiasclerotic; cardiatic;
 XX KW antiparasitic; antibacterial; immunosuppressive; Crohn's disease;

KW antiparasitic; antibacterial; immunosuppressive; Crohn's disease;
 KM multiple sclerosis; rheumatoid arthritis.
 XX Homo sapiens.
 XX WO200056772-A1.
 XX 28-SEP-2000.
 XX 24-MAR-2000; 2000WO-US07946.
 XX 25-MAR-1999; 99US-0126603.
 XX (BADI) BASF AG.
 XX (GEMV) GENETICS INST. INC.
 XX Salfeld JG, Roguska M, Paskind M, Banerjee S, Tracey DE, White M,
 PI Kaymakcalan Z, Labkovsky B, Sakorafas P, Friedrich S, Myles A,
 PI Veldman GM, Venturini A, Warne NW, Widom A, Rivin JG, Duncan AR,
 PI Derbyshire EJ, Carmen S, Smith S, Holter TL, Du Fou SL,
 DR WPI, 2000-638250/61.
 XX New human antibody specific for human interleukin-12 (IL-12) used to
 PT treat disorders characterized by aberrant IL-12 expression e.g. Crohn's
 PT disease and multiple sclerosis -
 XX Claim 33; Figure 28; 37pp; English.
 XX This invention relates to a new human antibody specific for human
 CC interleukin-12 (IL-12). The invention also includes antigen binding
 CC portions that bind to IL-12. Sequences AAB39485-B39516 represent human
 CC anti-IL-12 antibody heavy and light chain complementarity determining
 CC region (CDR) amino acid sequences, and also includes variable region
 CC given in AAB39517-B39560 and AAB40068-B40149. Sequences AAB39561-B39771
 CC represent anti-IL-12 CDR3 related amino acid sequences, AAB39772-B40063
 CC represent other CDR sequences. Light chain CDR3 consensus sequences are
 CC given in AAB40064-B40067. Primers used in the identification and
 CC construction of the antibodies of the invention are given in
 CC AAC61062-C61071. The antibody of the invention is a neutralizing
 CC antibody and has antirheumatic; antiarthritic; antisclerotic;
 CC antiinflammatory; neuroprotective; antiparasitic; antisthmatic;
 CC cardiant; antiparasitic; antibacterial and immunosuppressive activity.
 CC The antibodies or antigen-binding fragments are useful in the treatment
 CC of disorders associated with detrimental release of human IL-12,
 CC especially Crohn's disease, multiple sclerosis and rheumatoid arthritis.
 CC They can also be used in the manufacture of a pharmaceutical composition
 CC to treat human IL-12 disorders.
 XX Sequence 17 AA;
 SQ
 Query Match 89.1%; Score 82; DB 21; Length 17;
 Best Local Similarity 88.2%; Pred. No. 8.7e-07;
 Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 1 F1SYDGSNKGHYADSVKG 17
 DB 1 F1SYDGSNKGHYADSVKG 17
 RESULT 14
 AAB39487
 ID AAB39487 standard; Protein; 17 AA.
 AC AAB39487;
 XX 05-FEB-2001 (first entry)
 XX Anti-hIL-12 antibody heavy chain CDR2 amino acid sequence SEQ ID 3.
 DB Human; neutralizing antibody; interleukin-12; IL-12; antiinflammatory;
 KM complementarity determining region; CDR; antirheumatic; antisthmatic;

KW antisclerotic; neuroprotective; antiparasitic; antisthmatic; cardiant;
 KM antiparasitic; antibacterial; immunosuppressive; Crohn's disease;
 KM multiple sclerosis; rheumatoid arthritis.
 XX Homo sapiens.
 XX WO200056772-A1.
 XX 28-SEP-2000.
 XX 24-MAR-2000; 2000WO-US07946.
 XX 25-MAR-1999; 99US-0126603.
 XX (BADI) BASF AG.
 XX (GEMV) GENETICS INST. INC.
 XX Salfeld JG, Roguska M, Paskind M, Banerjee S, Tracey DE, White M,
 PI Kaymakcalan Z, Labkovsky B, Sakorafas P, Friedrich S, Myles A,
 PI Veldman GM, Venturini A, Warne NW, Widom A, Rivin JG, Duncan AR,
 PI Derbyshire EJ, Carmen S, Smith S, Holter TL, Du Fou SL,
 DR WPI, 2000-638250/61.
 XX New human antibody specific for human interleukin-12 (IL-12) used to
 PT treat disorders characterized by aberrant IL-12 expression e.g. Crohn's
 PT disease and multiple sclerosis -
 XX Claim 16; Page 225; 37pp; English.
 XX This invention relates to a new human antibody specific for human
 CC interleukin-12 (IL-12). The invention also includes antigen binding
 CC portions that bind to IL-12. Sequences AAB39485-B39516 represent human
 CC anti-IL-12 antibody heavy and light chain complementarity determining
 CC region (CDR) amino acid sequences, and also includes variable region
 CC amino acid sequences. Other variable region amino acid sequences are
 CC given in AAB39517-B39560 and AAB40068-B40149. Sequences AAB39561-B39771
 CC represent anti-IL-12 CDR3 related amino acid sequences, AAB39772-B40063
 CC represent other CDR sequences. Light chain CDR3 consensus sequences are
 CC given in AAB40064-B40067. Primers used in the identification and
 CC construction of the antibodies of the invention are given in
 CC AAC61062-C61071. The antibody of the invention is a neutralizing
 CC antibody and has antirheumatic; antiarthritic; antisclerotic;
 CC antiinflammatory; neuroprotective; antiparasitic; antisthmatic;
 CC cardiant; antiparasitic; antibacterial and immunosuppressive activity.
 CC The antibodies or antigen-binding fragments are useful in the treatment
 CC of disorders associated with detrimental release of human IL-12,
 CC especially Crohn's disease, multiple sclerosis and rheumatoid arthritis.
 CC They can also be used in the manufacture of a pharmaceutical composition
 CC to treat human IL-12 disorders.
 XX Sequence 17 AA;
 SQ
 Query Match 88.0%; Score 81; DB 21; Length 17;
 Best Local Similarity 88.2%; Pred. No. 1.3e-06;
 Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 1 F1SYDGSNKGHYADSVKG 17
 DB 1 F1SYDGSNKGHYADSVKG 17
 RESULT 15
 AAB39503
 ID AAB39503 standard; Protein; 17 AA.
 AC AAB39503;
 XX 05-FEB-2001 (first entry)
 XX Anti-hIL-12 antibody heavy chain CDR2 amino acid sequence SEQ ID 19.
 DB Human; neutralizing antibody; interleukin-12; IL-12; antiinflammatory;

complementarity determining region; CDR; antirheumatic; antiarthritic;
antisclerotic; neuroprotective; antipoxiatic; antiaesthetic; cardiant;
antiparasitic; antibacterial; immunosuppressive; Crohn's disease;
multiple sclerosis; rheumatoid arthritis.

Homo sapiens.

WO200056772-A1.

28-SEP-2000.

24-MAR-2000; 2000WO-US07946.

25-MAR-1999; 99US-0126603.

(BADI) BASF AG.
(GEMY) GENETICS INST INC.

Salfeld JG, Roguska M, Paskind M, Banerjee S, Tracey DE, White M,
Kaymakcalan Z, Labkovsky B, Sakorafas P, Friedlich S, Myles A,
Veldman GM, Venturini A, Warne NW, Widom A, Elvin JG, Duncan AR,
Derbyshire EJ, Carmen S, Smith S, Hollet TL, Du Fou SL,
WPI; 2000-638250/61.

New human antibody specific for human interleukin-12 (IL-12) used to
treat disorders characterized by aberrant IL-12 expression e.g. Crohn's
disease and multiple sclerosis -

Claim 24; Page 232; 377pp; English.

This invention relates to a new human antibody specific for human
interleukin-12 (IL-12). The invention also includes antigen binding
portions that bind to IL-12. Sequences AAB39485-839516 represent human
anti-IL-12 antibody heavy and light chain complementarity determining
region (CDR) amino acid sequences, and also includes variable region
amino acid sequences. Other variable region amino acid sequences are
given in AAB39517-839560 and AAB40068-840149. Sequences AAB39561-839771
represent anti-IL-12 CDR3 related amino acid sequences, AAB39772-840063
represent other CDR sequences, light chain CDR3 consensus sequences are
given in AAB40064-840067. Primers used in the identification and
construction of the antibodies of the invention are given in
AAB61062-C61071. The antibody of the invention is a neutralizing
antibody and has antirheumatic; antiarthritic; antisclerotic;
antiinflammatory; neuroprotective; antipoxiatic; antiaesthetic;
cardiant; antiparasitic; antibacterial and immunosuppressive activity.
The antibodies or antigen-binding fragments are useful in the treatment
of disorders associated with detrimental release of human IL-12,
especially Crohn's disease, multiple sclerosis and rheumatoid arthritis.
They can also be used in the manufacture of a pharmaceutical composition
to treat human IL-12 disorders.

Sequence 17 AA;

Query Match 88.0%; Score 81; DB 21; Length 17;

Best Local Similarity 88.2%; Pred. No. 1.3e-06;

Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 FISTYGSNKHVADSVKG 17
|||:|||||
Db 1 FIRYDSNKKYVADSVKG 17

Search completed: June 3, 2003, 08:14:50
Job time : 8.6587 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 3, 2003, 08:21:07 ; Search time 4.03242 Seconds

(Without alignments)

426.742 Million cell updates/sec

Title: US-09-644-668a-33

Sequence: 1 F1SYDGSNKHRYADSVKG 17

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 383519 seqs, 101223694 residues

Total number of hits satisfying chosen parameters: 383519

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	81	88.0	249	9	US-09-880-748-1956 Sequence 1956, App
2	81	88.0	251	9	US-09-880-748-952 Sequence 952, App
3	81	88.0	251	9	US-09-880-748-982 Sequence 982, App
4	80	87.0	83	9	US-10-078-958-7 Sequence 7, Appl
5	80	87.0	98	9	US-10-194-975-23 Sequence 23, Appl
6	80	87.0	98	9	US-10-194-975-24 Sequence 24, Appl
7	80	87.0	98	9	US-10-194-975-25 Sequence 25, Appl
8	80	87.0	122	9	US-09-144-886-68 Sequence 68, Appl
9	80	87.0	122	9	US-09-144-886-69 Sequence 69, Appl
10	80	87.0	128	10	US-09-850-165-104 Sequence 104, Appl
11	80	87.0	225	9	US-09-453-234-102 Sequence 102, App
12	80	87.0	225	9	US-09-453-234-108 Sequence 108, App
13	80	87.0	225	9	US-09-453-234-110 Sequence 110, App
14	80	87.0	238	9	US-09-880-748-11931 Sequence 1931, App
15	80	87.0	241	9	US-09-880-748-11931 Sequence 1931, App
16	80	87.0	247	9	US-09-880-748-12055 Sequence 2055, App
17	80	87.0	247	9	US-09-880-748-12055 Sequence 2055, App
18	80	87.0	248	9	US-09-880-748-1330 Sequence 1330, App
19	80	87.0	249	9	US-09-880-748-1421 Sequence 1421, App

20	80	87.0	249	9	US-09-880-748-397 Sequence 397, App
21	80	87.0	249	9	US-09-880-748-512 Sequence 512, App
22	80	87.0	249	9	US-09-880-748-892 Sequence 892, App
23	80	87.0	249	9	US-09-880-748-911 Sequence 911, App
24	80	87.0	249	9	US-09-880-748-1102 Sequence 1102, App
25	80	87.0	249	9	US-09-880-748-1108 Sequence 1108, App
26	80	87.0	249	9	US-09-880-748-1110 Sequence 1110, App
27	80	87.0	249	9	US-09-880-748-1111 Sequence 1111, App
28	80	87.0	249	9	US-09-880-748-1113 Sequence 1113, App
29	80	87.0	249	9	US-09-880-748-1115 Sequence 1115, App
30	80	87.0	249	9	US-09-880-748-1117 Sequence 1117, App
31	80	87.0	249	9	US-09-880-748-1119 Sequence 1119, App
32	80	87.0	249	9	US-09-880-748-1124 Sequence 1124, App
33	80	87.0	249	9	US-09-880-748-1725 Sequence 1725, App
34	80	87.0	252	9	US-09-880-748-1201 Sequence 1201, App
35	80	87.0	252	9	US-09-880-748-1394 Sequence 1394, App
36	80	87.0	252	9	US-09-880-748-1519 Sequence 1519, App
37	80	87.0	252	9	US-09-880-748-1627 Sequence 1627, App
38	80	87.0	252	9	US-09-880-748-1731 Sequence 1731, App
39	80	87.0	254	9	US-09-880-748-981 Sequence 981, App
40	80	87.0	254	9	US-09-880-748-983 Sequence 983, App
41	80	87.0	256	9	US-09-880-748-839 Sequence 839, App
42	80	87.0	256	9	US-09-880-748-1935 Sequence 1935, App
43	80	87.0	256	9	US-09-880-748-1935 Sequence 1935, App
44	79	85.9	243	9	US-09-880-748-1935 Sequence 1935, App
45	77	83.7	17	10	US-09-798-058-6 Sequence 6, Appl

ALIGNMENTS

RESULT 1
US-09-880-748-1956
; Sequence 1956, Application US/09880748
; Publication No. US2003005937A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunoselectively Bind Blys
; FILE REFERENCE: P5523
; CURRENT APPLICATION NUMBER: US/09/880,748
; CURRENT FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1956
; LENGTH: 249
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-1956
Query Match 88.0%; Score 81; DB 9; Length 249;
Best Local Similarity 88.2%; Pred. No. 4.5e-05;
Matches 15; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 1 F1SYDGSNKHRYADSVKG 17
DB 50 F1SYDGSNKHRYADSVKG 66
RESULT 2
US-09-880-748-952
; Sequence 952, Application US/09880748
; Publication No. US2003005937A1
; GENERAL INFORMATION:

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; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523
; CURRENT APPLICATION NUMBER: US/09/880,748
; CURRENT FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 952
; LENGTH: 251
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-952

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Query Match      88.0%; Score 81; DB 9; Length 251;
Best Local Similarity 88.2%; Pred. No. 4.5e-05;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

```

```

QY      1 F1SYDGSNKRYADSVYKG 17
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DB      50 F1RYDGSNKRYADSVYKG 66

```

```

RESULT 3
US-09-880-748-982
; Sequence 982, Application US/09880748
; Publication No. US2003005937A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523
; CURRENT APPLICATION NUMBER: US/09/880,748
; CURRENT FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 982
; LENGTH: 251
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-982

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Query Match      88.0%; Score 81; DB 9; Length 251;
Best Local Similarity 88.2%; Pred. No. 4.5e-05;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

```

```

QY      1 F1SYDGSNKRYADSVYKG 17
      |||||||:|||||
DB      50 F1RYDGSNKRYADSVYKG 66

```

```

RESULT 4
US-10-078-958-7
; Sequence 7, Application US/10078958
; Publication No. US20030070185A1

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; GENERAL INFORMATION:
; APPLICANT: JAKOBOVITS, AYA
; APPLICANT: KUCHERLAPATI, RAJU
; APPLICANT: KLAPHOLZ, SUSAN
; APPLICANT: MENDEZ, MICHAEL J.
; APPLICANT: GREEN, LARRY
; TITLE OF INVENTION: TRANSGENIC MAMMALS HAVING HUMAN Ig LOCI INCLUDING
; TITLE OF INVENTION: PLURAL VH AND VK REGIONS AND ANTIBODIES PRODUCED
; FILE REFERENCE: CELL 4.18 CON
; CURRENT APPLICATION NUMBER: US/10/078,958
; CURRENT FILING DATE: 2002-02-19
; PRIOR APPLICATION NUMBER: 08/759,620
; PRIOR FILING DATE: 1996-12-03
; NUMBER OF SEQ ID NOS: 79
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 83
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MOD RES
; LOCATION: (22)
; OTHER INFORMATION: Variable amino acid
US-10-078-958-7

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Query Match      87.0%; Score 80; DB 9; Length 83;
Best Local Similarity 93.8%; Pred. No. 2.1e-05;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```

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QY      2 ISYDGSNKRYADSVYKG 17
      |||||||:|||||
DB      36 ISYDGSNKRYADSVYKG 51

```

```

RESULT 5
US-10-194-975-23
; Sequence 23, Application US/10194975
; Publication No. US20030039649A1
; GENERAL INFORMATION:
; APPLICANT: Foote, Jefferson
; TITLE OF INVENTION: Super Humanized Antibodies
; FILE REFERENCE: 501231.01
; CURRENT APPLICATION NUMBER: US/10/194,975
; CURRENT FILING DATE: 2002-10-10
; PRIOR APPLICATION NUMBER: US 60/305,111
; PRIOR FILING DATE: 2001-07-12
; NUMBER OF SEQ ID NOS: 122
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 23
; LENGTH: 98
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-194-975-23

```

```

Query Match      87.0%; Score 80; DB 9; Length 98;
Best Local Similarity 93.8%; Pred. No. 2.5e-05;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      2 ISYDGSNKRYADSVYKG 17
      |||||||:|||||
DB      51 ISYDGSNKRYADSVYKG 66

```

```

RESULT 6
US-10-194-975-24
; Sequence 24, Application US/10194975
; Publication No. US20030039649A1
; GENERAL INFORMATION:
; APPLICANT: Foote, Jefferson
; TITLE OF INVENTION: Super Humanized Antibodies
; FILE REFERENCE: 501231.01
; CURRENT APPLICATION NUMBER: US/10/194,975

```



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OTHER INFORMATION: Ile or Val
FEATURE:
NAME/KEY: MOD RES
LOCATION: (23)
OTHER INFORMATION: Ser, Val or Ala
FEATURE:
NAME/KEY: MOD_RES
LOCATION: (49)
OTHER INFORMATION: Any amino acid, preferably Gly, Ser or Ala
FEATURE:
NAME/KEY: MOD_RES
LOCATION: (74)
OTHER INFORMATION: Asn or Asp
FEATURE:
NAME/KEY: MOD_RES
LOCATION: (75)
OTHER INFORMATION: Ala or Ser
FEATURE:
NAME/KEY: MOD_RES
LOCATION: (78)
OTHER INFORMATION: Met, Ser or Thr
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LOCATION: (79)
OTHER INFORMATION: Val, Ala or Leu
FEATURE:
NAME/KEY: MOD_RES
LOCATION: (84)
OTHER INFORMATION: Ser, Asp or Asn
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NAME/KEY: MOD_RES
LOCATION: (87)
OTHER INFORMATION: Lys, Glu or Arg
FEATURE:
NAME/KEY: MOD_RES
LOCATION: (88)
OTHER INFORMATION: Thr, Pro or Ala
FEATURE:
NAME/KEY: MOD_RES
LOCATION: (93)
OTHER INFORMATION: Leu or Val
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NAME/KEY: MOD_RES
LOCATION: (95)
OTHER INFORMATION: Phe or Tyr
FEATURE:
NAME/KEY: MOD_RES
LOCATION: (97)
OTHER INFORMATION: Thr or Ala
US-09-850-165-104
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Best Local Similarity 93.8%; Pred. No. 3.3e-05;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
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```
Qy 2 ISYDGSNKHYADSVKG 17
Db 51 ISYDGSNKHYADSVKG 66
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RESULT 11
US-09-453-234-102
; Sequence 102, Application US/09453234
; Publication No. US20030091995A1
; GENERAL INFORMATION:
; APPLICANT: Buechler, Joe
; APPLICANT: Walkiers, Gunars
; APPLICANT: Gray, Jeff
; APPLICANT: Lomborg, Nils
; APPLICANT: Biosite Diagnostics, Inc.
; APPLICANT: Genpharm International
; TITLE OF INVENTION: Human Antibodies
; FILE REFERENCE: 020015-000110US
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CURRENT APPLICATION NUMBER: US/09/453,234
CURRENT FILING DATE: 1999-12-01
PRIOR APPLICATION NUMBER: US 60/157,415
PRIOR FILING DATE: 1999-10-02
NUMBER OF SEQ ID NOS: 112
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 102
LENGTH: 225
TYPE: PRT
ORGANISM: Homo sapiens
OTHER INFORMATION: M2-31H
US-09-453-234-102
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Query Match      87.0%; Score 80; DB 9; Length 225;
Best Local Similarity 93.8%; Pred. No. 5.8e-05;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
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Qy 2 ISYDGSNKHYADSVKG 17
Db 51 ISYDGSNKHYADSVKG 66
```

```
RESULT 12
US-09-453-234-108
; Sequence 108, Application US/09453234
; Publication No. US20030091995A1
; GENERAL INFORMATION:
; APPLICANT: Buechler, Joe
; APPLICANT: Walkiers, Gunars
; APPLICANT: Gray, Jeff
; APPLICANT: Lomborg, Nils
; APPLICANT: Biosite Diagnostics, Inc.
; APPLICANT: Genpharm International
; TITLE OF INVENTION: Human Antibodies
; FILE REFERENCE: 020015-000110US
; CURRENT APPLICATION NUMBER: US/09/453,234
; CURRENT FILING DATE: 1999-12-01
; PRIOR APPLICATION NUMBER: US 60/157,415
; PRIOR FILING DATE: 1999-10-02
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 108
; LENGTH: 225
; TYPE: PRT
; ORGANISM: Homo sapiens
; OTHER INFORMATION: M2-34H
US-09-453-234-108
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Query Match      87.0%; Score 80; DB 9; Length 225;
Best Local Similarity 93.8%; Pred. No. 5.8e-05;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
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```
Qy 2 ISYDGSNKHYADSVKG 17
Db 51 ISYDGSNKHYADSVKG 66
```

```
RESULT 13
US-09-453-234-110
; Sequence 110, Application US/09453234
; Publication No. US20030091995A1
; GENERAL INFORMATION:
; APPLICANT: Buechler, Joe
; APPLICANT: Walkiers, Gunars
; APPLICANT: Gray, Jeff
; APPLICANT: Lomborg, Nils
; APPLICANT: Biosite Diagnostics, Inc.
; APPLICANT: Genpharm International
; TITLE OF INVENTION: Human Antibodies
; FILE REFERENCE: 020015-000110US
; CURRENT APPLICATION NUMBER: US/09/453,234
; CURRENT FILING DATE: 1999-12-01
; PRIOR APPLICATION NUMBER: US 60/157,415
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PRIOR FILING DATE: 1999-10-02
NUMBER OF SEQ ID NOS: 112
SOFTWARE: Patentln Ver. 2.1
SEQ ID NO 110
LENGTH: 225
TYPE: PRT
ORGANISM: Homo sapiens
OTHER INFORMATION: M2-35H
US-09-453-234-110

Query Match 87.0%; Score 80; DB 9; Length 225;
Best Local Similarity 93.8%; Pred. No. 5.8e-05;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 ISYDGNKHYADSVKG 17
DB 51 ISYDGNKHYADSVKG 66

RESULT 14

US-09-880-748-1931
Sequence 1931, Application US/09880748
Publication No. US20030059937A1
GENERAL INFORMATION:
APPLICANT: Ruben et al.
TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
FILE REFERENCE: PF523
CURRENT APPLICATION NUMBER: US/09/880,748
CURRENT FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: 60/212,210
PRIOR FILING DATE: 2000-06-15
PRIOR APPLICATION NUMBER: 60/240,816
PRIOR FILING DATE: 2000-10-17
PRIOR APPLICATION NUMBER: 60/276,248
PRIOR FILING DATE: 2001-03-16
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/293,499
PRIOR FILING DATE: 2001-05-25
NUMBER OF SEQ ID NOS: 3239
SOFTWARE: Patentln Ver. 2.0
SEQ ID NO 1931
LENGTH: 238
TYPE: PRT
ORGANISM: Homo sapiens
US-09-880-748-1931

Query Match 87.0%; Score 80; DB 9; Length 238;
Best Local Similarity 93.8%; Pred. No. 6.1e-05;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 ISYDGNKHYADSVKG 17
DB 51 ISYDGNKHYADSVKG 66

RESULT 15

US-09-880-748-2055
Sequence 2055, Application US/09880748
Publication No. US20030059937A1
GENERAL INFORMATION:

APPLICANT: Ruden et al.
TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
FILE REFERENCE: PF523

CURRENT APPLICATION NUMBER: US/09/880,748
CURRENT FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: 60/212,210
PRIOR FILING DATE: 2000-06-15
PRIOR APPLICATION NUMBER: 60/240,816
PRIOR FILING DATE: 2000-10-17
PRIOR APPLICATION NUMBER: 60/276,248
PRIOR FILING DATE: 2001-03-16
PRIOR APPLICATION NUMBER: 60/277,379

PRIOR FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/293,499
PRIOR FILING DATE: 2001-05-25
NUMBER OF SEQ ID NOS: 3239
SOFTWARE: Patentln Ver. 2.0
SEQ ID NO 2055
LENGTH: 241
TYPE: PRT
ORGANISM: Homo sapiens
US-09-880-748-2055

Query Match 87.0%; Score 80; DB 9; Length 241;
Best Local Similarity 93.8%; Pred. No. 6.2e-05;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 ISYDGNKHYADSVKG 17
DB 51 ISYDGNKHYADSVKG 66

Search completed: June 3, 2003, 08:52:55
Job time: 5.03242 secs

GenCore version 5.1.6
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OW protein - protein search, using sw model

Run on: June 3, 2003, 08:10:19 ; Search time 2.58191 Seconds

(without alignments)
193.728 Million cell updates/sec

Title: US-09-644-668a-33

Perfect score: 92
Sequence: 1 F1SYDGSNMKHYADSVKG 17

Scoring table: BLOSUM62

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Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : Issued Patents AA:*

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

No.	Score	Query Match	length	DB	ID	Description
1	80	87.0	98	1	US-08-211-202-118	Sequence 118, Appl
2	80	87.0	116	1	US-08-211-202-141	Sequence 141, Appl
3	80	87.0	117	3	US-08-545-809A-115	Sequence 115, Appl
4	80	87.0	119	1	US-08-331-398A-46	Sequence 46, Appl
5	80	87.0	119	2	US-08-331-397B-46	Sequence 46, Appl
6	80	87.0	119	2	US-08-759-804A-46	Sequence 46, Appl
7	80	87.0	119	4	US-09-227-693A-46	Sequence 46, Appl
8	80	87.0	120	1	US-08-211-202-135	Sequence 135, Appl
9	80	87.0	120	1	US-07-942-245-35	Sequence 35, Appl
10	80	87.0	123	4	US-08-983-607-38	Sequence 38, Appl
11	80	87.0	128	1	US-08-478-039-96	Sequence 38, Appl
12	80	87.0	128	1	US-08-476-349A-96	Sequence 96, Appl
13	80	87.0	126	4	US-09-240-274-25	Sequence 96, Appl
14	80	87.0	126	4	US-09-240-274-25	Sequence 25, Appl
15	80	87.0	126	4	US-09-240-274-25	Sequence 25, Appl
16	80	87.0	126	4	US-09-240-274-25	Sequence 153, Appl
17	80	87.0	141	1	US-08-259-372A-2	Sequence 2, Appl
18	80	87.0	141	1	US-08-468-671-2	Sequence 2, Appl
19	80	87.0	126	4	US-09-240-274-16	Sequence 16, Appl
20	80	87.0	126	4	US-09-240-274-152	Sequence 152, Appl
21	80	87.0	127	4	US-09-240-274-139	Sequence 139, Appl
22	80	87.0	124	4	US-09-240-274-4	Sequence 4, Appl
23	80	87.0	179	4	US-08-862-124-2	Sequence 2, Appl
24	80	87.0	287	4	US-08-862-124-17	Sequence 17, Appl
25	80	87.0	304	4	US-08-862-124-14	Sequence 14, Appl
26	80	87.0	124	4	US-09-240-274-5	Sequence 5, Appl
27	72	78.3	123	1	US-09-240-274-6	Sequence 6, Appl
					US-08-478-039-94	Sequence 94, Appl

28	72	78.3	123	1	US-08-476-349A-94	Sequence 94, App1
29	71	77.2	125	1	US-08-276-852-72	Sequence 72, App1
30	71	77.2	125	1	US-08-276-852-73	Sequence 74, App1
31	71	77.2	125	1	US-08-276-852-74	Sequence 75, App1
32	71	77.2	125	1	US-08-276-852-75	Sequence 76, App1
33	71	77.2	125	1	US-08-276-852-76	Sequence 77, App1
34	71	77.2	125	1	US-08-276-852-77	Sequence 78, App1
35	71	77.2	125	1	US-08-899-575-72	Sequence 72, App1
36	71	77.2	125	1	US-08-899-575-73	Sequence 74, App1
37	71	77.2	125	1	US-08-899-575-74	Sequence 75, App1
38	71	77.2	125	1	US-08-899-575-75	Sequence 76, App1
39	71	77.2	125	1	US-08-899-575-76	Sequence 77, App1
40	71	77.2	125	1	US-08-899-575-77	Sequence 78, App1
41	71	77.2	125	1	US-08-899-575-72	Sequence 72, App1
42	71	77.2	125	1	US-08-899-575-73	Sequence 74, App1
43	71	77.2	125	1	US-08-899-575-74	Sequence 75, App1
44	71	77.2	125	1	US-08-899-575-75	Sequence 76, App1
45	71	77.2	125	1	US-08-899-575-76	Sequence 77, App1

ALIGNMENTS

RESULT 1
US-08-211-202-118
Sequence 118, Application US/08211202
Patent No. 5565332
GENERAL INFORMATION:
APPLICANT: HOOGENBOOM, Hendricus Renerus Jacobus Mattheus
APPLICANT: BAIER, Michael
APPLICANT: JESPER, Laurent Stephane Anne Therese
APPLICANT: WINTER, Gregory Paul
TITLE OF INVENTION: Production of chimeric antibodies - a
NUMBER OF SEQUENCES: 144
CORRESPONDENCE ADDRESS:
ADDRESSER: David W. Clough, Marshall O'Toole Gerstein Murray &
ADDRESSER: Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION NUMBER: US/08/211,202
FILING DATE: 23-SEP-1992
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9120252.3
FILING DATE: 23-SEP-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9120377.8
FILING DATE: 25-SEP-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9206318.9
FILING DATE: 24-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9206372.6
FILING DATE: 24-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB92/00883
FILING DATE: 15-MAY-1992
ATTORNEY/AGENT INFORMATION:
NAME: David W. Clough
REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 28111/31960
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300

TELEFAX: 312-474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 118:
SEQUENCE CHARACTERISTICS:
LENGTH: 98 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-211-202-118

Query Match 87.0%; Score 80; DB 1; Length 98;
Best Local Similarity 93.8%; Pred. No. 4.7e-06;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 ISYDGSNKRYADSVKG 17
|||||:|||||
DB 51 ISYDGSNKRYADSVKG 66

RESULT 2

US-08-211-202-141
Sequence 141, Application US/08211202
Patent No. 5565332

GENERAL INFORMATION:

APPLICANT: HOOGENBOOM, Hendricus Renerus Jacobus Matheus
APPLICANT: BAIER, Michael
APPLICANT: JESPER, Laurent Stephane Anne Therese
APPLICANT: WINTER, Gregory Paul
TITLE OF INVENTION: Production of chimeric antibodies - a
NUMBER OF SEQUENCES: 144
CORRESPONDENCE ADDRESS:
ADDRESSER: David W. Clough, Marshall O'Toole Gerstein Murray &
ADDRESSER: Boston
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606-6402

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/211,202
FILING DATE: 23-SEP-1992
CLASSIFICATION: 435

PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9120252.3
FILING DATE: 23-SEP-1991

PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9120377.8
FILING DATE: 25-SEP-1991

PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9206318.9
FILING DATE: 24-MAR-1992

PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9206372.6
FILING DATE: 24-MAR-1992

PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB92/00883
FILING DATE: 15-MAY-1992

ATTORNEY/AGENT INFORMATION:
NAME: David W. Clough
REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 28111/31960
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
TELEFAX: 312-474-0448

TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 141:
SEQUENCE CHARACTERISTICS:

LENGTH: 116 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-211-202-141

Query Match 87.0%; Score 80; DB 1; Length 116;
Best Local Similarity 93.8%; Pred. No. 5.6e-06;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 ISYDGSNKRYADSVKG 17
|||||:|||||
DB 51 ISYDGSNKRYADSVKG 66

RESULT 3

US-08-545-809A-115
Sequence 115, Application US/08545809A
Patent No. 6096878

GENERAL INFORMATION:

APPLICANT: Honjo, Tasuku
APPLICANT: Matsuda, Fumihiko
TITLE OF INVENTION: HUMAN IMMUNOGLOBULIN VH GENE
NUMBER OF SEQUENCES: 145
CORRESPONDENCE ADDRESS:
ADDRESSER: Fish & Richardson, P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02110-2804

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/545,809A
FILING DATE: 27-MAR-1996

PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/JP93/00603
FILING DATE: 10-MAY-1993

ATTORNEY/AGENT INFORMATION:
NAME: Freeman, John W.
REGISTRATION NUMBER: 29,066
REFERENCE/DOCKET NUMBER: 06501/004001

TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-542-5070
TELEFAX: 617-542-8906

TELEX: 200154
INFORMATION FOR SEQ ID NO: 115:
SEQUENCE CHARACTERISTICS:
LENGTH: 117 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-545-809A-115

Query Match 87.0%; Score 80; DB 3; Length 117;
Best Local Similarity 93.8%; Pred. No. 5.6e-06;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 ISYDGSNKRYADSVKG 17
|||||:|||||
DB 70 ISYDGSNKRYADSVKG 85

RESULT 4

US-08-331-398A-46
Sequence 46, Application US/08331398A
Patent No. 5608039

GENERAL INFORMATION:

APPLICANT: Pastan, Ira
 APPLICANT: Willingham, Mark
 APPLICANT: Fitzgerald, David
 APPLICANT: Brinkmann, Ulrich
 APPLICANT: Pal, Lee
 TITLE OF INVENTION: Single Chain B3 Antibody Fusion Proteins
 TITLE OF INVENTION: and Their Uses (as amended)
 NUMBER OF SEQUENCES: 68
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Townsend and Townsend and Crew
 STREET: One Market Plaza, Stewart Street Plaza
 CITY: San Francisco
 STATE: California
 COUNTRY: USA
 ZIP: 94105-1492
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/331,398A
 FILING DATE: 28-OCT-1994
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/767,331
 FILING DATE: 30-SEP-1991
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/596,289
 FILING DATE: 12-OCT-1990
 ATTORNEY/AGENT INFORMATION:
 NAME: Hunter, Tom
 REGISTRATION NUMBER: 38,498
 REFERENCE/DOCKET NUMBER: 015280-126110US
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 543-9600
 TELEFAX: (415) 543-5043
 INFORMATION FOR SEQ ID NO: 46:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 119 amino acids
 TYPE: amino acid
 STRANDEDNESS:
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 FEATURE:
 NAME/KEY: Protein
 LOCATION: 1..119
 OTHER INFORMATION: /note="Human fetal immunoglobulin
 OTHER INFORMATION: 56P1/CL Variable Heavy chain (V-H)"

```

Query Match          87.0% Score 80; DB 1; Length 119;
Best Local Similarity 93.8%; Pred. NO. 5.7e-06;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      2 ISYDGSNKRYADSVYGK 17
        |||||:|||||
Db       51 ISYDGSNKRYADSVYGK 66

RESULT 5
US-08-311-397B-46
Sequence 46, Application US/08311397B
Patent No. 5981726
GENERAL INFORMATION:
APPLICANT: Pastan, Ira
APPLICANT: Benhar, Itai
TITLE OF INVENTION: Chimeric and Mutationally Stabilized Tumor-Specific Antibody Fragments, Fusion Proteins, and Uses Thereof
TITLE OF INVENTION:
NUMBER OF SEQUENCES: 68
CORRESPONDENCE ADDRESS:
ADDRESSSE: townsend and Townsend and Crew
```

STREET: One Market Plaza, Stewart Street Plaza
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94105-1492
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/331,397B
FILING DATE: 28-OCT-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/767,331
FILING DATE: 30-SEP-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/596,289
FILING DATE: 12-OCT-1990
ATTORNEY/AGENT INFORMATION:
NAME: Hunter, Tom
REGISTRATION NUMBER: 38,498
REFERENCE/DOCKET NUMBER: 015280-126120US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 543-9600
TELEFAX: (415) 543-5043
INFORMATION FOR SRD ID NO: 46:
SEQUENCE CHARACTERISTICS:
LENGTH: 119 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURE:
NAME/KEY: Protein
LOCATION: 1..119
OTHER INFORMATION: /note= "Human fetal immunoglobulin
OTHER INFORMATION: 56P1'CL Variable Heavy chain (V-H)"
US-08-331-397B-46

```

Query Match          87.0%; Score 80; DB 2; Length 119;
Best Local Similarity 93.8%; Pred. No. 5.7e-06;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY      2  ISYDGSNKHYADSVYKG 17
      |||||:|||||
Db      51  ISYDGSNKYYADSVYKG 66

RESULT 6
US-08-759-804A-46
Sequence 46; Application US/08759804A
Patent No. 5990296
GENERAL INFORMATION:
APPLICANT: Pastan, Ira
APPLICANT: Willingham, Mark
APPLICANT: Fitzgerald, David J.
APPLICANT: Brinkmann, Ulrich
APPLICANT: Pal, Lee
TITLE OF INVENTION: Tumor-Specific Antibody Fragments,
TITLE OF INVENTION: Fusion Proteins, and Uses Thereof
NUMBER OF SEQUENCES: 68
CORRESPONDENCE ADDRESS:
ADDRESSRE: Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible

```

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/759,804A
FILING DATE: 03-DEC-1996
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/331,398
FILING DATE: 28-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/767,331
FILING DATE: 30-SEP-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/596,289
FILING DATE: 12-OCT-1990
ATTORNEY/AGENT INFORMATION:
NAME: Weber, Ellen L.
REGISTRATION NUMBER: 32,762
REFERENCE/DOCKET NUMBER: 015280-126140US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 46:
SEQUENCE CHARACTERISTICS:
LENGTH: 119 amino acids
TYPE: amino acid
STRANDEDNESS: linear
TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURE:
NAME/KEY: Protein
LOCATION: 1..119
OTHER INFORMATION: /note="Human fetal immunoglobulin
OTHER INFORMATION: 56p1/CL Variable Heavy chain (V-H)"
US-08-759-804A-46

Query Match 87.0%; Score 80; DB 2; Length 119;
Best Local Similarity 93.8%; Pred. No. 5.7e-06;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 ISYDSNKHVADSVKG 17
DB 51 ISYDSNKHVADSVKG 66

RESULT 7
US-09-227-693-46
Sequence 46, Application US/09227693
Patent No. 6287562
GENERAL INFORMATION:
APPLICANT: PASTAN, Ira
APPLICANT: BENHAR, Itai
APPLICANT: PADIAN, Eduardo A.
APPLICANT: JUNG, Sun-Hee
APPLICANT: LEE, Byungkook
TITLE OF INVENTION: HUMANIZED TUMOR-SPECIFIC ANTIBODY
TITLE OF INVENTION: FRAGMENTS, FUSION PROTEINS, AND USES THEREOF
NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
ADDRESSER: Townsend and Townsend Kourie and Crew
STREET: Stewart Street Tower, One Market Plaza
CITY: San Francisco
STATE: California
COUNTRY: US
ZIP: 94105-1493
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/227,693
FILING DATE:

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/331,396
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/767,331
FILING DATE: 30-SEP-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/596,289
FILING DATE: 12-OCT-1990
ATTORNEY/AGENT INFORMATION:
NAME: Weber, Ellen Lauver
REGISTRATION NUMBER: 32,762
REFERENCE/DOCKET NUMBER: 15280-126-1-3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 543-9600
TELEFAX: (415) 543-5043
INFORMATION FOR SEQ ID NO: 46:
SEQUENCE CHARACTERISTICS:
LENGTH: 119 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Protein
LOCATION: 1..119
OTHER INFORMATION: /note="Human fetal immunoglobulin
OTHER INFORMATION: 56p1/CL VH region"
US-09-227-693-46

Query Match 87.0%; Score 80; DB 4; Length 119;
Best Local Similarity 93.8%; Pred. No. 5.7e-06;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 ISYDSNKHVADSVKG 17
DB 51 ISYDSNKHVADSVKG 66

RESULT 8
US-08-211-202-135
Sequence 135, Application US/08211202
Patent No. 5565332
GENERAL INFORMATION:
APPLICANT: HOOGENBOOM, Hendricus Reneus Jacobus Matreus
APPLICANT: BAIER, Michael
APPLICANT: JESPER, Laurent Stephane Anne Therese
APPLICANT: WINTER, Gregory Paul
TITLE OF INVENTION: Production of chimeric antibodies - a
TITLE OF INVENTION: Combinatorial approach
NUMBER OF SEQUENCES: 144
CORRESPONDENCE ADDRESS:
ADDRESSER: David W. Clough, Marshall O'Toole Gerstein Murray &
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/211,202
FILING DATE: 23-SEP-1992
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9120252.3
FILING DATE: 23-SEP-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9120377.8

FILED DATE: 25-SEP-1991
PRIOR APPLICATION DATA: GB 9206318.9
FILING DATE: 24-MAR-1992
PRIOR APPLICATION DATA: GB 9206372.6
FILING DATE: 24-MAR-1992
PRIOR APPLICATION DATA: PCT/GB92/00883
FILING DATE: 15-MAY-1992
ATTORNEY/AGENT INFORMATION:
NAME: David W. Clough
REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 28111/31960
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
TELEFAX: 312-474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 135:
SEQUENCE CHARACTERISTICS:
LENGTH: 120 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-211-202-135

Query Match 87.0%; Score 80; DB 1; Length 120;
Best Local Similarity 93.8%; Pred. No. 5.8e-06;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 ISYDSNKHVADSVKG 17
DB 51 ISYDSNKHVADSVKG 66

RESULT 9
US-07-942-245-35
Sequence 35, Application US/07942245
Patent No. 5639641
GENERAL INFORMATION:
APPLICANT: PEDERSEN, Jan T.
APPLICANT: SEARLE, Stephen M.J.
APPLICANT: REES, Anthony R.
APPLICANT: ROGUSKA, Michael A.
APPLICANT: GUILD, Braydon C.
TITLE OF INVENTION: SURFACE RESIDUE VENERING OF RODENT
TITLE OF INVENTION: ANTIBODIES
NUMBER OF SEQUENCES: 522
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sughrie, Mlon, Zim, Macpeak & Seas
STREET: 2100 Pennsylvania Avenue, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: United States
ZIP: 20037-3202
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: HP 9000/700 Workstation
OPERATING SYSTEM: UNIX
SOFTWARE: in house
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/942.245
FILING DATE: 09-SEP-1992
CLASSIFICATION: 530
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 293-7060
TELEFAX: (202) 293-7860
TELEX: 6491103
INFORMATION FOR SEQ ID NO: 35:
SEQUENCE CHARACTERISTICS:
LENGTH: 120 amino acids
TYPE: amino acid
TOPOLOGY: linear

MOLECULE TYPE: peptide
US-07-942-245-35

Query Match 87.0%; Score 80; DB 1; Length 120;
Best Local Similarity 93.8%; Pred. No. 5.8e-06;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 ISYDSNKHVADSVKG 17
DB 51 ISYDSNKHVADSVKG 66

RESULT 10
US-08-983-607-38
Sequence 38, Application US/08983607
Patent No. 6140470
GENERAL INFORMATION:
APPLICANT: Alan Garten
APPLICANT: Xiaohong Cai
TITLE OF INVENTION: Human Anti-Tumor Monoclonal Anti-
TITLE OF INVENTION: bodies
NUMBER OF SEQUENCES: 51
CORRESPONDENCE ADDRESS:
ADDRESSEE: Department of Molecular Biophysics
ADDRESSEE: and Biochemistry, Yale University
STREET: 266 Whitney Avenue
CITY: New Haven
STATE: Connecticut
COUNTRY: United States of America
ZIP: 06520-8114
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" 1.44 Mb diskette
COMPUTER: IBM PC
OPERATING SYSTEM: MS DOS
SOFTWARE: word processing
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/983.607
FILING DATE: April 27, 1998
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/IB96/01032
FILING DATE: June 28, 1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Mary M. Kinsey
REGISTRATION NUMBER: 32423
REFERENCE/DOCKET NUMBER: OCR-679
TELECOMMUNICATION INFORMATION:
TELEPHONE: 203-773-9544
TELEFAX: 203-773-1183
INFORMATION FOR SEQ ID NO: 38:
SEQUENCE CHARACTERISTICS:
LENGTH: 123 residues
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: polypeptide
DESCRIPTION: polypeptide
ORIGINAL SOURCE:
ORGANISM: Homo sapiens (melanoma patient
ORGANISM: immunized with autologous tumor cells)
INDIVIDUAL ISOLATE: peripheral blood lympho-
INDIVIDUAL ISOLATE: cytes
IMMEDIATE SOURCE:
LIBRARY: DM414 scFv antibodies obtained from
LIBRARY: fuses fusion phage construct
CLONE: V575
FEATURE:
NAME/KEY: heavy chain
US-08-983-607-38

Query Match 87.0%; Score 80; DB 4; Length 123;
Best Local Similarity 93.8%; Pred. No. 5.9e-06;

Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 2 ISYDGNKRYADSVKG 17
|||||:|||||
Db 51 ISYDGNKRYADSVKG 66

RESULT 11
US-08-478-039-96
; Sequence 96, Application US/08478039
; Patent No. 5681722
; GENERAL INFORMATION:
; APPLICANT: Newman, Roland A.
; APPLICANT: Hanna, Nabil
; APPLICANT: Raab, Ronald W.
; TITLE OF INVENTION: Recombinant Antibodies for Human Therapy
; NUMBER OF SEQUENCES: 114
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
; STREET: 699 Prince St.
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/478,039
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/379,072
; FILING DATE: 25-JAN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/912,292
; FILING DATE: 10-JUL-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/856,281
; FILING DATE: 23-MAR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/735,064
; FILING DATE: 25-JUL-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Teskin Esq., Robin L.
; REGISTRATION NUMBER: 35,030
; REFERENCE/DOCKET NUMBER: 012712-160
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-836-6620
; TELEFAX: 703-836-2021
; INFORMATION FOR SEQ ID NO: 96:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 128 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: not relevant
; MOLECULE TYPE: peptide
; POSITION IN GENOME:
; CHROMOSOME/SEGMENT: RF SJ2
US-08-478-039-96

Query Match 87.0%; Score 80; DB 1; Length 128;
Best Local Similarity 93.8%; Pred. No. 6.2e-06;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 2 ISYDGNKRYADSVKG 17
|||||:|||||
Db 51 ISYDGNKRYADSVKG 66

RESULT 12

US-08-476-349A-96
; Sequence 96, Application US/08476349A
; Patent No. 5750105
; GENERAL INFORMATION:
; APPLICANT: Newman, Roland A.
; APPLICANT: Hanna, Nabil
; APPLICANT: Raab, Ronald W.
; TITLE OF INVENTION: Recombinant Antibodies for Human Therapy
; NUMBER OF SEQUENCES: 114
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
; STREET: 699 Prince St.
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/476,349A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/379,072
; FILING DATE: 25-JAN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/912,292
; FILING DATE: 10-JUL-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/856,281
; FILING DATE: 23-MAR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/735,064
; FILING DATE: 25-JUL-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Teskin Esq., Robin L.
; REGISTRATION NUMBER: 35,030
; REFERENCE/DOCKET NUMBER: 012712-161
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-836-6620
; TELEFAX: 703-836-2021
; INFORMATION FOR SEQ ID NO: 96:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 128 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: not relevant
; MOLECULE TYPE: peptide
; POSITION IN GENOME:
; CHROMOSOME/SEGMENT: RF SJ2
US-08-476-349A-96

Query Match 87.0%; Score 80; DB 1; Length 128;
Best Local Similarity 93.8%; Pred. No. 6.2e-06;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 2 ISYDGNKRYADSVKG 17
|||||:|||||
Db 51 ISYDGNKRYADSVKG 66

RESULT 13
US-09-240-274-25
; Sequence 25, Application US/09240274
; Patent No. 6253455
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: RH(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; FILE REFERENCE: 09596-4202

/ CURRENT APPLICATION NUMBER: US/09/240,274
/ CURRENT FILING DATE: 1999-01-29
/ EARLIER APPLICATION NUMBER: 60/081,380
/ EARLIER FILING DATE: 1998-04-10
/ EARLIER APPLICATION NUMBER: 60/028,550
/ EARLIER FILING DATE: 1996-10-11
/ NUMBER OF SEQ ID NOS: 224
/ SOFTWARE: Patentin Ver. 2.0
/ SEQ ID NO 25
/ LENGTH: 126
/ TYPE: PRT
/ ORGANISM: Homo sapiens
/ FEATURE:
/ OTHER INFORMATION: anti-Rh(D) chain D30
US-09-240-274-25

Query Match 82.6%; Score 76; DB 4; Length 126;
Best Local Similarity 81.2%; Pred. No. 2,7e-05;
Matches 13; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 ISYDGSNKHVADSVKG 17
:|||||:|||||
Db 51 VYDGSNKHVDSVKG 66

RESULT 14
US-09-240-274-26
/ Sequence 26, Application US/09240274
/ Patent No. 6255455
/ GENERAL INFORMATION:
/ APPLICANT: Siegel, Donald L.
/ TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
/ FILE REFERENCE: 09596-4202
/ CURRENT APPLICATION NUMBER: US/09/240,274
/ CURRENT FILING DATE: 1999-01-29
/ EARLIER APPLICATION NUMBER: 60/081,380
/ EARLIER FILING DATE: 1998-04-10
/ EARLIER APPLICATION NUMBER: 60/028,550
/ EARLIER FILING DATE: 1996-10-11
/ NUMBER OF SEQ ID NOS: 224
/ SOFTWARE: Patentin Ver. 2.0
/ SEQ ID NO 26
/ LENGTH: 126
/ TYPE: PRT
/ ORGANISM: Homo sapiens
/ FEATURE:
/ OTHER INFORMATION: anti-Rh(D) chain D31
US-09-240-274-26

Query Match 82.6%; Score 76; DB 4; Length 126;
Best Local Similarity 81.2%; Pred. No. 2,7e-05;
Matches 13; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 ISYDGSNKHVADSVKG 17
:|||||:|||||
Db 51 VYDGSNKHVDSVKG 66

RESULT 15
US-09-240-274-153
/ Sequence 153, Application US/09240274
/ Patent No. 6255455
/ GENERAL INFORMATION:
/ APPLICANT: Siegel, Donald L.
/ TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
/ FILE REFERENCE: 09596-4202
/ CURRENT APPLICATION NUMBER: US/09/240,274
/ CURRENT FILING DATE: 1999-01-29
/ EARLIER APPLICATION NUMBER: 60/081,380
/ EARLIER FILING DATE: 1998-04-10
/ EARLIER APPLICATION NUMBER: 60/028,550

/ EARLIER FILING DATE: 1996-10-11
/ NUMBER OF SEQ ID NOS: 224
/ SOFTWARE: Patentin Ver. 2.0
/ SEQ ID NO 153
/ LENGTH: 126
/ TYPE: PRT
/ ORGANISM: Homo sapiens
/ FEATURE:
/ OTHER INFORMATION: anti-Rh(D) antibody clone SH56
US-09-240-274-153

Query Match 82.6%; Score 76; DB 4; Length 126;
Best Local Similarity 81.2%; Pred. No. 2,7e-05;
Matches 13; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 ISYDGSNKHVADSVKG 17
:|||||:|||||
Db 51 VYDGSNKHVDSVKG 66

Search completed: June 3, 2003, 08:24:19
Job time : 2.58191 secs

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OM protein - protein search, using sw model

Run on: June 3, 2003, 08:02:44 / Search time 9.03072 Seconds
(without alignments)

450.095 Million cell updates/sec

Title: US-09-644-668a-15

Perfect score: 512
Sequence: 1 QVQLVESGGGVQVQPSRLRL.....LYLQNNSLRAEDTAVYYCAR 98

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	480	93.8	122	1 HV3G_HUMAN	P01768 homo sapien
2	454	88.7	119	1 HV3I_HUMAN	P01770 homo sapien
3	450	87.9	122	1 HV3H_HUMAN	P01769 homo sapien
4	448	87.5	121	1 HV3J_HUMAN	P01771 homo sapien
5	442	86.3	117	1 HV3C_HUMAN	P01764 homo sapien
6	440	85.9	126	1 HV3K_HUMAN	P01772 homo sapien
7	423.5	82.7	116	1 HV05_CARAU	P19181 carassius a
8	418	81.6	119	1 HV3L_HUMAN	P01773 homo sapien
9	406	79.3	114	1 HV3B_HUMAN	P01763 homo sapien
10	403	78.7	116	1 HV3T_HUMAN	P01783 mus musculu
11	403	78.4	136	1 HV16_MOUSE	P01766 mus musculu
12	401.5	77.9	120	1 HV3E_HUMAN	P01774 homo sapien
13	399	77.9	119	1 HV3M_HUMAN	P01777 mus musculu
14	397.5	77.6	115	1 HV3F_HUMAN	P01767 mus musculu
15	394	77.0	98	1 HV57_MOUSE	P18528 mus musculu
16	393	76.8	117	1 HV54_MOUSE	P18526 mus musculu
17	391	76.4	117	1 HV55_MOUSE	P18525 mus musculu
18	390	76.2	117	1 HV3O_HUMAN	P01776 homo sapien
19	388	75.8	119	1 HV3N_HUMAN	P01775 mus musculu
20	387.5	75.7	97	1 HV56_MOUSE	P18527 mus musculu
21	381	74.4	120	1 HV3U_HUMAN	P19180 carassius a
22	380	74.2	117	1 HV03_CARAU	P18529 mus musculu
23	377	73.6	117	1 HV58_MOUSE	P01762 mus musculu
24	376	73.4	122	1 HV3A_HUMAN	P01765 mus musculu
25	375	73.2	115	1 HV3D_HUMAN	P01762 mus musculu
26	373	72.9	117	1 HV3J_HUMAN	P01813 catman croc
27	371	72.5	119	1 HV3P_HUMAN	P01777 mus musculu
28	368.5	72.0	117	1 HV02_CANFA	P01785 mus musculu
29	367	71.7	117	1 HV53_MOUSE	P18524 mus musculu
30	367	71.7	117	1 HV59_MOUSE	P18530 mus musculu
31	362	70.7	113	1 HV34_MOUSE	P01803 mus musculu
32	360	70.3	113	1 HV30_MOUSE	P01799 mus musculu
33	358	69.9	114	1 HV01_CANFA	P01784 canis faml

34	358	69.9	116	1 HV36_MOUSE	P01806 mus musculu
35	358	69.9	119	1 HV37_MOUSE	P01807 mus musculu
36	358	69.9	119	1 HV38_MOUSE	P01808 mus musculu
37	357	69.7	115	1 HV32_MOUSE	P01801 mus musculu
38	357	69.7	145	1 HV01_RAT	P01805 ractus norv
39	356	69.5	122	1 HV20_MOUSE	P01789 mus musculu
40	355	69.3	113	1 HV27_MOUSE	P01796 mus musculu
41	355	69.3	113	1 HV28_MOUSE	P01797 mus musculu
42	355	69.3	116	1 HV3R_HUMAN	P01779 mus musculu
43	353	68.9	122	1 HV21_MOUSE	P01790 mus musculu
44	352	68.8	113	1 HV31_MOUSE	P01800 mus musculu
45	351	68.6	123	1 HV18_MOUSE	P01787 mus musculu

ALIGNMENTS

RESULT 1					
HV3G_HUMAN		STANDARD;	PRT;	122 AA.	
ID HV3G_HUMAN					
AC P01768:					
DT 21-JUL-1986 (Rel. 01, Created)					
DT 21-JUL-1986 (Rel. 01, Last sequence update)					
DT 15-JUL-1999 (Rel. 38, Last annotation update)					
DE Ig heavy chain V-II region CAM.					
OS Homo sapiens (Human)					
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;					
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.					
OX NCBI_TaxID=9606;					
RP [1]					
RP MEDLINE=81013859; PubMed=6774332;					
RX Lehman D.W., Putnam P.W.,					
RT "Amino acid sequence of the variable region of a human mu chain:					
RT location of a possible JH segment."					
RT Proc. Natl. Acad. Sci. U.S.A. 77:3239-3243(1980).					
CC -1- MISCELLANEOUS: THIS MU CHAIN WAS ISOLATED FROM THE PLASMA OF A					
CC PATIENT WITH MACROGLOBULINEMIA.					
DR PIR, A02051, M3HUM.					
DR HSSP, P01772, 2EB4.					
DR InterPro; IPR003006; IG_MHC.					
DR InterPro; IPR003596; IG_V.					
DR Pfam; PF00047; Ig; 1.					
DR SMART; SM00406; IGV; 1.					
KW Immunoglobulin V region.					
FT MOD_RES 1					
FT NON_TER 122					
FT SEQUENCE 122 AA; 13668 MW; A42D0F17D252P1C2 CRC64;					
Query Match					
Best Local Similarity	93.8%;	Score 480;	DB 1;	Length 122;	
Matches	87;	Pred. No. 2.6e-45;			
	Conservative	9;	Mismatches	2;	Indels 0; Gaps 0;
Oy	1 QVQLVESGGGVQVQPSRLRLSCAASGFTSSYAMHWVQAPGKLEWYAVISYQSSNXY 60				
Db	1 QVQLVESGGGVVZFGSRSLRLSCAASGFTSSYAMHWVQAPGKLEWYAVISYQSSNXY 60				
Oy	61 ADSVKGRTISRDNKNTLYLQNNSLRAEDTAVYYCAR 98				
Db	61 ABSVKGRTISRDNKNTLYLQNNSLRAEDTAVYYCAR 98				
RESULT 2					
HV3I_HUMAN		STANDARD;	PRT;	119 AA.	
ID HV3I_HUMAN					
AC P01770:					
DT 21-JUL-1986 (Rel. 01, Created)					
DT 21-JUL-1986 (Rel. 01, Last sequence update)					
DT 15-JUL-1999 (Rel. 38, Last annotation update)					
DE Ig heavy chain V-II region NIB.					
OS Homo sapiens (Human)					
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;					
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.					

[illegible]

OX NCBI_TaxID=9606;
 RN (1)
 RP SEQUENCE FROM N.A.
 RX MEDLINE=81101090; PubMed=6450418;
 RA Matthyssens G., Rabbits T.H.;
 RT "Structure and multiplicity of genes for the human immunoglobulin heavy chain variable region";
 RL Proc. Natl. Acad. Sci. U.S.A. 77:6561-6565(1980).
 CC -----
 CC This SWISS-PROT entry is copyrighted. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to license@sib-sib.ch).
 CC -----
 DR EMBL, J00236; AAA51516.1; -
 DR EMBL, M35415; AAA58735.1; -
 DR PIR, A02047; H3H26.
 DR HSSP, P01772; 2PB4.
 DR Genew; HGNC:5545; IGHV.
 DR InterPro; IPR003006; IG_MHC.
 DR InterPro; IPR003596; IG_V.
 DR Pfam; PF00047; Ig; 1.
 DR SMART; SM00406; IGV; 1.
 DR Immunoglobulin V region; Signal.
 FT SIGNAL 1 19
 FT CHAIN 20 117 IG HEAVY CHAIN V-II1 REGION VH26.
 FT NON_TER 117 117
 FT SEQUENCE 117 AA; 12582 MW; E826733F1A3CB0F1 CRC64;
 SQ
 Query Match 86.3%; Score 442; DB 1; Length 117;
 Best Local Similarity 85.7%; Pred. No. 3.3e-41;
 Matches 84; Conservative 6; Mismatches 8; Indels 0; Gaps 0;
 QY 1 QVLTSSGGGVQVQPSRLSCAAGFTFSSYAMHWKQAPGKLEWVAIVSYDGSNKY 60
 DB 20 EVOLSSGGGLVQPGSLRLSCAAGFTFSSYAMSWVROAPGKLEWVAIVSYDGSSTY 79
 QY 61 ADVKGRFTISRDNKNTLYIQMNSLRADPTAVYVCAR 98
 DB 80 GDSVKGRTISRDNKNTLYIQMNSLRADPTAVYVCAR 117
 RESULT 6
 HV3K_HUMAN STANDARD; PRT; 126 AA.
 ID HV3K_HUMAN
 AC P01772;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Ig heavy chain V-II1 region KOL.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Euteria; Primates; Carnivora; Hominoidea; Homo.
 NCBI_TaxID=9606;
 RN (1)
 RP SEQUENCE, AND DISULFIDE BONDS.
 RX MEDLINE=83289131; PubMed=6884994;
 RA Schmidt W.E., Jung H.-D., Palm W., Hilschmann N.;
 RT "Three-dimensional structure determination of antibodies. Primary structure of crystallized monoclonal immunoglobulin IgG1 KOL, I.",
 RL Hoppe-seyer's Z. Physiol. Chem. 364:713-747(1983).
 CC -----
 CC X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS).
 RX MEDLINE=81072295; PubMed=7441755;
 RA Marquardt M., Deisenhofer J., Huber R., Palm W.;
 RT "Crystallographic refinement and atomic models of the intact immunoglobulin molecule KOL and its antigen-binding fragment at 3.0 A and 1.0-A resolution.",
 RL J. Mol. Biol. 141:369-391(1980).
 DR PIR, A02055; G1HUKL.

DR PDB, 2PB4; 12-JUL-89.
 DR PDB, 2IG2; 12-JUL-89.
 DR InterPro; IPR003006; IG_MHC.
 DR InterPro; IPR003596; IG_V.
 DR Pfam; PF00047; Ig; 1.
 DR SMART; SM00406; IGV; 1.
 KW Immunoglobulin V region; 3D-structure.
 FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
 FT DISULFID 22 96
 FT DISULFID 105 110
 FT STRAND 3 7
 FT STRAND 11 12
 FT TURN 14 15
 FT STRAND 18 25
 FT HELIX 29 31
 FT STRAND 34 39
 FT TURN 41 42
 FT STRAND 46 51
 FT TURN 53 54
 FT STRAND 58 60
 FT TURN 62 67
 FT STRAND 68 73
 FT TURN 74 77
 FT STRAND 78 83
 FT HELIX 88 90
 FT STRAND 92 99
 FT STRAND 106 106
 FT TURN 107 108
 FT STRAND 109 109
 FT STRAND 113 113
 FT STRAND 120 124
 FT NON_TER 126 126
 FT SEQUENCE 126 AA; 13718 MW; E4D71B52B16F876 CRC64;
 SQ
 Query Match 85.9%; Score 440; DB 1; Length 126;
 Best Local Similarity 84.7%; Pred. No. 5.9e-41;
 Matches 83; Conservative 10; Mismatches 5; Indels 0; Gaps 0;
 QY 1 QVLTSSGGGVQVQPSRLSCAAGFTFSSYAMHWKQAPGKLEWVAIVSYDGSNKY 60
 DB 1 QVLTSSGGGVQVQPSRLSCAAGFTFSSYAMHWKQAPGKLEWVAIVSYDGSSTY 79
 QY 61 ADVKGRFTISRDNKNTLYIQMNSLRADPTAVYVCAR 98
 DB 61 ADVKGRFTISRDNKNTLYIQMNSLRADPTAVYVCAR 98
 RESULT 7
 HV05_CARAU STANDARD; PRT; 116 AA.
 ID HV05_CARAU
 AC P19181;
 DT 01-NOV-1990 (Rel. 16, Created)
 DT 01-NOV-1990 (Rel. 16, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Ig heavy chain V region 5A precursor.
 OS Carassius auratus (Goldfish).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes; Cyprinidae; Carassius.
 NCBI_TaxID=7957;
 RN (1)
 RP SEQUENCE FROM N.A.
 RX MEDLINE=88144476; PubMed=3125551;
 RA Wilson M.R., Middleton D., Watt G.W.;
 RT "Immunoglobulin heavy chain variable region gene evolution: structure and family relationships of two genes and a pseudogene in a teleost fish.",
 RL Proc. Natl. Acad. Sci. U.S.A. 85:1566-1570(1988).
 CC -----
 CC HSSP, P01772; 2PB4.
 DR PIR, B28966; B28966.
 DR HSSP, P01772; 2PB4.
 DR InterPro; IPR003006; IG_MHC.
 DR InterPro; IPR003596; IG_V.
 DR Pfam; PF00047; Ig; 1.

DR SMART; SM00406; IGV; 1.
 KW Immunoglobulin V region; Signal.
 FT CHAIN 1 19 IG HEAVY CHAIN V REGION SA.
 FT SIGNAL 20 116
 FT CHAIN 20 49 FRAMEWORK-1.
 FT DOMAIN 20 49
 FT DOMAIN 50 54 FRAMEWORK-1.
 FT DOMAIN 50 54 FRAMEWORK-2.
 FT DOMAIN 55 68
 FT DOMAIN 69 84 COMPLEMENTARITY-DETERMINING-2.
 FT DOMAIN 85 116 FRAMEWORK-3.
 FT DISULFID 41 114 BY SIMILARITY.
 FT NON TER 116
 SQ SEQUENCE 116 AA; 12808 MW; 9C2279E2DF199B12 CRC64;

Query Match 82.7%; Score 423.5; DB 1; Length 116;
 Best Local Similarity 84.7%; Pred. No. 3.3e-39;
 Matches 83; Conservative 5; Mismatches 9; Indels 1; Gaps 1;

QY 1 QVQLVSGGQVQPGKSLRLSCAASGFTSSYAMHWVROAPKGLKLEWVAIVSYDGSNKYY 60
 DB 20 EVQLVESGGGLVQPGGSLRLSCAASGFTSSYAMHWVROAPKGLKLEWVAIVSYDGSNKYY 78
 QY 61 ADVSKGRFTISRDNKNTLYLQMSLRAEDTAVYYCAR 98
 DB 79 ADVSKGRFTISRDNKNTLYLQMSLRAEDTAVYYCAR 116

RESULT 8

HV3L HUMAN

ID HV3L HUMAN STANDARD; PRT; 119 AA.

AC P01773;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Ig heavy chain V-III region BUR.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE (WEILOMA PROTEIN BUR).
 RX MEDLINE=79151016; PubMed=107164;
 RA Putnam F.W., Liu Y.-S.V., Low T.L.K.;
 RT "Primary structure of a human IgM immunoglobulin. IV. Streptococcal
 RT IgM protease, digestion, Fab and Fc fragments, and the complete
 RT amino acid sequence of the alpha 1 heavy chain."
 RL J. Biol. Chem. 254:2865-2874(1979).
 DR PIR; A02056; A1HUBR.
 DR HSSP; P01772; 2FB4.
 DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR003596; Ig_V.
 DR Pfam; PF00047; Ig_V.
 DR SMART; SM00406; IGV; 1.
 DR Immunoglobulin V region; Glycoprotein.
 FT MOD RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
 FT DISULFID 22 96
 FT CARBOHYD 28 28
 FT NON TER 119 119 N-LINKED (GLCNAC. . .).
 SQ SEQUENCE 119 AA; 12981 MW; 12A709A75344D024 CRC64;

Query Match 81.6%; Score 418; DB 1; Length 119;
 Best Local Similarity 78.6%; Pred. No. 1.3e-38;
 Matches 77; Conservative 9; Mismatches 12; Indels 0; Gaps 0;

QY 1 QVQLVSGGQVQPGKSLRLSCAASGFTSSYAMHWVROAPKGLKLEWVAIVSYDGSNKYY 60
 DB 1 QVQLVESGGGLVQPGGSLRLSCAASGFTSSYAMHWVROAPKGLKLEWVAIVSYDGSNKYY 60
 QY 61 ADVSKGRFTISRDNKNTLYLQMSLRAEDTAVYYCAR 98
 DB 61 ADVSKGRFTISRDNKNTLYLQMSLRAEDTAVYYCAR 98

RESULT 9

HV3B HUMAN
 ID HV3B HUMAN STANDARD; PRT; 114 AA.

AC P01763;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Ig heavy chain V-III region WEA.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]

RP SEQUENCE.
 RX MEDLINE=63273707; PubMed=6410398;
 RA Goni F., Frangione B.;
 RT "Amino acid sequence of the Fv region of a human monoclonal IgM
 RT (protein WEA) with antibody activity against 3,4-pyruvylated
 RT galactose in Klebsiella polysaccharides K30 and K33."
 RL Proc. Natl. Acad. Sci. U.S.A. 80:4837-4841(1983).
 CC -1- MISCELLANEOUS: THIS CHAIN WAS OBTAINED FROM A MONOCLONAL ANTIBODY
 CC AGAINST 3,4-PYRUVYLATED GALACTOSE AND ISOLATED FROM A PATIENT WITH
 CC WALDENSTROM'S MACROGLOBULINEMIA.

DR PIR; A02046; M3HWE.
 DR HSSP; P01772; 2FB4.
 DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR003596; Ig_V.
 DR Pfam; PF00047; Ig_V.
 DR SMART; SM00406; IGV; 1.
 DR Immunoglobulin V region.
 FT MOD RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
 FT NON TER 114 114
 SQ SEQUENCE 114 AA; 12256 MW; D88294FBA18A07B7 CRC64;

Query Match 79.3%; Score 406; DB 1; Length 114;
 Best Local Similarity 78.6%; Pred. No. 2.6e-37;
 Matches 77; Conservative 12; Mismatches 9; Indels 0; Gaps 0;

QY 1 QVQLVSGGQVQPGKSLRLSCAASGFTSSYAMHWVROAPKGLKLEWVAIVSYDGSNKYY 60
 DB 1 QVQLVSGGGLVQPGGSLRLSCAASGFTSSYAMHWVROAPKGLKLEWVAIVSYDGSNKYY 60
 QY 61 ADVSKGRFTISRDNKNTLYLQMSLRAEDTAVYYCAR 98
 DB 61 ADVSKGRFTISRDNKNTLYLQMSLRAEDTAVYYCAR 98

RESULT 10

HV3T HUMAN

ID HV3T HUMAN STANDARD; PRT; 116 AA.

AC P01781;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Ig heavy chain V-III region GAL.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]

RP SEQUENCE.
 RX MEDLINE=75059123; PubMed=4803843;
 RA Watanabe S., Barnikol H.U., Horn J., Berttram J., Hilschmann N.;
 RT "The primary structure of a monoclonal IgM-immunoglobulin
 RT (macroglobulin Gal.), II: the amino acid sequence of the H-chain (mu-
 RT type), subgroup H III. Architecture of the complete IgM-molecule."
 RL Hoppe-Seyler's Z. Physiol. Chem. 354:1505-1509(1973).
 RN [2]

REVISION TO 28-33.
 RP Hilschmann N.;
 RA Submitted (JUN-1975) to the PIR data bank.
 RL -1- MISCELLANEOUS: THIS MU CHAIN WAS ISOLATED FROM A WALDENSTROM'S
 CC MACROGLOBULIN.
 DR PIR; A02064; M3HUGL.

```

DR HSP: P01772; 2PB4.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR Immunoglobulin V region.
FT NON TER 116
SQ SEQUENCE 116 AA; 12730 MW; 2C67CA9AAAAA1282 CRC64;

Query Match
Best Local Similarity 78.7%; Score 403; DB 1; Length 116;
Matches 77; Conservative 7; Mismatches 14; Indels 0; Gaps 0;

QY 1 QVAVSGGGVQVQPGSRSLRLSCAASGFTSSYAMHWRAQPGKLEWVAVISYDGSNKTY 60
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 1 EVQVAVSGGDLVQPGSRSLRLSCAASGFTSSYAMHWRAQPGKLEWVAVISYDGSNKTY 60
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 61 ADVKGRFTISRDNKNTLYLQMSLRADPTAVYYCAR 98
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 61 VDSVKGRTISRDNKNTLYLQMSLRADPTAVYYCAR 98
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 11
HVL6_MOUSE STANDARD; PRT; 136 AA.
AC P01783;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V region MOPC 21 precursor (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_Taxid=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=81234548; PubMed=6788376;
RA Botwell A.L.M., Paskind M., Reith M., Imanishi-Kari T., Rajewsky K.,
RA Baltimore D.;
RT "Heavy chain variable region contribution to the NPD family of
RT antibodies: somatic mutation evident in a gamma 2a variable region.";
RL Cell 24:625-637(1981).
[2]
RN SEQUENCE OF 17-136.
RX MEDLINE=77100368; PubMed=401950;
RA Adergubo K., Milstein C., Secher D.S.;
RT "Molecular analysis of spontaneous somatic mutants.";
RL Nature. 265:299-304(1977).

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DR EMBL; J00522; AAD15290.1; -
DR PIR; A02066; G1M921.
DR HSP; P01772; 2PB4.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR Immunoglobulin V region; Signal.
FT NON TER 1
FT SIGNAL 1
FT CHAIN 17 16
FT DOMAIN 115 136 IG HEAVY CHAIN V REGION MOPC 21.
FT DOMAIN 120 136 D SEGMENT.
FT DISULFID 38 112 JH4 SEGMENT.
FT CONFLICT 75 78 HYAD -> DYAH (IN REF. 2).
FT CONFLICT 89 90 DN -> ND (IN REF. 2).

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FT CONFLICT 115 115 W -> H (IN REF. 2).
FT CONFLICT 120 120 Y -> W (IN REF. 2).
FT NON TER 136
SQ SEQUENCE 136 AA; 15071 MW; 2276A98DBDF7016 CRC64;

Query Match
Best Local Similarity 79.4%; Score 403; DB 1; Length 136;
Matches 77; Conservative 8; Mismatches 12; Indels 0; Gaps 0;

QY 2 QVAVSGGGVQVQPGSRSLRLSCAASGFTSSYAMHWRAQPGKLEWVAVISYDGSNKTYA 61
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 18 QVAVSGGGVQVQPGSRSLRLSCAASGFTSSYAMHWRAQPGKLEWVAVISYDGSNKTYA 77
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 62 DSVKGRFTISRDNKNTLYLQMSLRADPTAVYYCAR 98
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 78 DTVKGRFTISRDNKNTLYLQMSLRADPTAVYYCAR 114
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 12
HVL6_MOUSE STANDARD; PRT; 120 AA.
AC P01766;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V-III region BRO.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_Taxid=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=77117674; PubMed=65324;
RA Capra J.D., Hopper J.E.;
RT "Comparative studies on monotypic IGM lambda and IGG kappa from an
RT individual patient. III. The complete amino acid sequence of the VH
RT region of the IGM paraprotein.";
RL Immunochimistry 13:995-999(1976).
CC -1- MISCELLANEOUS: THIS CHAIN WAS OBTAINED FROM IGM ISOLATED FROM THE
CC SERUM OF A PATIENT WITH MALIGNANT LYMPHOMA OF THE WALDENSTROM
CC TYPE.
DR PIR; A02049; M3HUBM.
DR HSP; P01772; 2PB4.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR Immunoglobulin V region.
FT NON TER 120
SQ SEQUENCE 120 AA; 13227 MW; D3F0428F7C2B6410 CRC64;

Query Match
Best Local Similarity 80.6%; Score 401.5; DB 1; Length 120;
Matches 79; Conservative 8; Mismatches 10; Indels 1; Gaps 1;

QY 1 QVAVSGGGVQVQPGSRSLRLSCAASGFTSSYAMHWRAQPGKLEWVAVISYDGSNKTY 60
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 1 EVQVAVSGGGLVQPGSRSLRLSCAASGFTSSYAMHWRAQPGKLEWVAISGSGSTLHYA 59
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 61 ADVKGRFTISRDNKNTLYLQMSLRADPTAVYYCAR 98
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 60 ADVKGRFTISRDNKNTLYLQMSLRADPTAVYYCAR 97
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 13
HVL6_MOUSE STANDARD; PRT; 119 AA.
AC P01774;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V-III region POM.
OS Homo sapiens (Human).

```

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 ON NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE
 RX MEDLINE=75046755; PubMed=4139708;
 RA Capra J.D., Kehoe J.M.;
 RT "Structure of antibodies with shared idiotypy: the complete sequence
 RT of the heavy chain variable regions of two immunoglobulin M
 RT anti-gamma globulins".
 RL Proc. Natl. Acad. Sci. U.S.A. 71:4032-4036(1974).
 CC -I- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM IGM WITH ANTI-GAMMA
 CC GLOBULIN ACTIVITY.
 CC PIR; A02057; M3HUPM.
 DR HSSP; P01772; 2FB4.
 DR InterPro; IPR003006; IG_MHC.
 DR InterPro; IPR003596; IG_V.
 DR Pfam; PF00047; IG_1.
 DR SMART; SM00406; IGV_1.
 KW Immunoglobulin V region.
 FT VARIANT 54
 FT 54
 FT N -> D (PROBABLY DUE TO DEAMINATION
 FT DURING ISOLATION).
 FT /FTID=VAR_003966.
 FT NON TER 119 119
 SQ SEQUENCE 119 AA; 12953 MW; 2E018AF4DCB2610 CRC64;
 Query Match 77.9%; Score 399; DB 1; Length 119;
 Best Local Similarity 77.6%; Pred. No. 1.6e-36;
 Matches 76; Conservative 13; Mismatches 9; Indels 0; Gaps 0;
 QY 1 QVQLVESGGGVVPGQSRSLRSCAASGFTSSYAMHWROAPGKLEWVAIVSYDGSNKYY 60
 DB 1 EVQLVESGGGLVPGGSLRLSCAASGFTSSSMHWROAPGKLEWVAIVSYDGSNKYY 60
 QY 61 ADSVKGRFTISRDNKNTLYLQNMNLSRAEDTAVYYCAR 98
 DB 61 ADSVNGRFTISRDNKNTLYLQNMNLSRAEDTAVYYCAR 98
 RESULT 14
 ID HV3P_HUMAN STANDARD; PRT; 115 AA.
 AC P01767;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Ig heavy chain V-III region BDT.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 ON NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE
 RX MEDLINE=78137069; PubMed=416441;
 RA Torano A., Putnam F.W.;
 RT "Complete amino acid sequence of the alpha 2 heavy chain of a human
 RT IgA2 immunoglobulin of the A2m (2) allotype".
 RL Proc. Natl. Acad. Sci. U.S.A. 75:966-969(1978).
 CC -I- MISCELLANEOUS: THE SEQUENCE OF THE ALPHA-2, A2M(2) ALLOTYPE. C
 CC REGION OF THIS MYELOMA PROTEIN IS ALSO GIVEN.
 CC PIR; A02050; A2HUBU.
 DR HSSP; P01789; IMCP.
 DR InterPro; IPR003006; IG_MHC.
 DR InterPro; IPR003596; IG_V.
 DR Pfam; PF00047; IG_1.
 DR SMART; SM00406; IGV_1.
 KW Immunoglobulin V region.
 FT NON TER 115 115
 SQ SEQUENCE 115 AA; 12379 MW; 208876A7DF52DCF4 CRC64;
 Query Match 77.6%; Score 397.5; DB 1; Length 115;
 Best Local Similarity 75.5%; Pred. No. 2.2e-36;
 Matches 74; Conservative 13; Mismatches 10; Indels 1; Gaps 1;

QY 1 QVQLVESGGGVVPGQSRSLRSCAASGFTSSYAMHWROAPGKLEWVAIVSYDGSNKYY 60
 DB 1 EVQLVESGGGLVPGGSLRLSCAASGFTSSBHMHWROAPGKLEWVAIVSYDGSNKYY 59
 QY 61 ADSVKGRFTISRDNKNTLYLQNMNLSRAEDTAVYYCAR 98
 DB 60 ADSVNGRFTISRDNKNTLYLQNMNLSRAEDTAVYYCAR 97
 RESULT 15
 ID HV57_MOUSE STANDARD; PRT; 98 AA.
 AC P18528;
 DT 01-NOV-1990 (Rel. 16, Created)
 DT 01-NOV-1990 (Rel. 16, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Ig heavy chain V region 6.96.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 ON NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BA1B/CJ;
 RX MEDLINE=89279149; PubMed=2499654;
 RA Levy N.S., Malipiero U.V., Lebecque S.G., Gearhart P.J.;
 RT "Early onset of somatic mutation in immunoglobulin VH genes during
 RT the primary immune response".
 RL J. Exp. Med. 169:2007-2019(1989).
 CC -I- MISCELLANEOUS: THIS SEQUENCE BELONGS TO THE VH183 SUBFAMILY.
 CC PIR; U70501; HVM596.
 DR HSSP; P01772; 2FB4.
 DR InterPro; IPR003006; IG_MHC.
 DR InterPro; IPR003596; IG_V.
 DR Pfam; PF00047; IGV_1.
 DR SMART; SM00406; IGV_1.
 KW Immunoglobulin V region.
 FT NON TER 98 98
 SQ SEQUENCE 98 AA; 11007 MW; B8644F7F92FBF95B CRC64;
 Query Match 77.0%; Score 394; DB 1; Length 98;
 Best Local Similarity 76.5%; Pred. No. 4.4e-36;
 Matches 75; Conservative 10; Mismatches 13; Indels 0; Gaps 0;
 QY 1 QVQLVESGGGVVPGQSRSLRSCAASGFTSSYAMHWROAPGKLEWVAIVSYDGSNKYY 60
 DB 1 EVQLVESGGGLVPGGSLRLSCAASGFTSDYIMHWROAPGKLEWVAIVSYDGSNKYY 60
 QY 61 ADSVKGRFTISRDNKNTLYLQNMNLSRAEDTAVYYCAR 98
 DB 61 PDSVNGRFTISRDNKNTLYLQNMNLSRAEDTAVYYCAR 98
 Search completed: June 3, 2003, 08:15:44
 Job time : 9.03072 secs

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OM protein - protein search, using sw model

Run on: June 3, 2003, 08:07:54 / Search time 48.8328 Seconds
(without alignments)
413.506 Million cell updates/sec

Title: US-09-644-668a-15
Perfect score: 512
Sequence: 1. QVQLVSGGGVGPGRSLRL.....LYLQNNSLRAEDTAVYYCAR 98

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 671580 seqs, 206047115 residues
Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0
Maximum DB seq length: 200000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

SPTREMBL_21:*

- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mhc:*
- 8: sp_organelle:*
- 9: sp_phase:*
- 10: sp_plant:*
- 11: sp_prodent:*
- 12: sp_virus:*
- 13: sp_vertebrate:*
- 14: sp_unclassified:*
- 15: sp_virus:*
- 16: sp_bacteriap:*
- 17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	505	98.6	613	4 Q8WUK1	Q8WUK1 homo sapien
2	499	97.5	116	4 Q9UL93	Q9UL93 homo sapien
3	485	94.7	113	4 Q9UL90	Q9UL90 homo sapien
4	450	87.9	122	4 Q9UL84	Q9UL84 homo sapien
5	447	87.3	121	4 Q9UL71	Q9UL71 homo sapien
6	447	87.3	147	4 Q9Y509	Q9Y509 homo sapien
7	436	85.2	597	4 Q86B89	Q86B89 homo sapien
8	432	84.4	573	4 Q8WU38	Q8WU38 homo sapien
9	430	84.0	95	4 Q9UL86	Q9UL86 homo sapien
10	429	83.6	471	4 Q8TC77	Q8TC77 homo sapien
11	428	83.6	118	4 Q9UL91	Q9UL91 homo sapien
12	420	82.0	112	4 Q9UL72	Q9UL72 homo sapien
13	410.5	80.2	118	4 Q9UL72	Q9UL72 homo sapien
14	404	78.9	494	4 Q96K68	Q96K68 homo sapien
15	401	78.3	473	11 Q91205	Q91205 mus musculu
16	397	77.5	119	11 Q920E7	Q920E7 mus musculu

17	393	76.8	487	11 Q99KA4	Q99KA4 mus musculu
18	387	75.6	479	11 Q91WP5	Q91WP5 mus musculu
19	361	70.5	131	4 Q9UL88	Q9UL88 homo sapien
20	356	69.5	469	11 Q8R3V9	Q8R3V9 mus musculu
21	355.5	69.4	486	11 Q91Z07	Q91Z07 mus musculu
22	351	68.6	112	4 Q9UGP3	Q9UGP3 homo sapien
23	348.5	68.1	437	11 Q91IA4	Q91IA4 mus musculu
24	348	68.0	480	11 Q91XE1	Q91XE1 mus musculu
25	345	67.4	484	11 Q8VEA0	Q8VEA0 mus musculu
26	343	67.0	298	11 Q9QYF0	Q9QYF0 mus musculu
27	337	65.8	104	4 Q9UL87	Q9UL87 homo sapien
28	333	65.0	124	4 Q9UL92	Q9UL92 homo sapien
29	308	60.2	124	6 Q9N0M4	Q9N0M4 oryctolagus
30	306	59.8	159	4 Q96QSO	Q96QSO homo sapien
31	305	59.6	124	6 Q9N0M6	Q9N0M6 oryctolagus
32	304	59.4	125	4 Q9UL95	Q9UL95 homo sapien
33	300	58.6	484	11 Q91LA6	Q91LA6 mus musculu
34	293	57.2	119	4 Q9UL94	Q9UL94 homo sapien
35	290.5	56.7	121	11 Q99NG4	Q99NG4 mus musculu
36	286	55.9	143	11 Q91V67	Q91V67 mus musculu
37	286	55.9	500	4 Q9BRV0	Q9BRV0 homo sapien
38	282	55.1	473	11 Q9DBL4	Q9DBL4 mus musculu
39	281	54.9	614	4 Q96GA6	Q96GA6 homo sapien
40	280.5	54.8	482	11 Q91X92	Q91X92 mus musculu
41	278	54.3	142	11 Q924Q1	Q924Q1 mus musculu
42	278	54.3	241	11 Q921A6	Q921A6 mus musculu
43	278	54.3	463	11 Q93IC4	Q93IC4 mus musculu
44	277	54.1	119	5 Q9GYZ2	Q9GYZ2 schistosoma
45	276	53.9	137	11 Q924R6	Q924R6 mus musculu

ALIGNMENTS

RESULT 1

Q8WUK1 ID Q8WUK1 PRELIMINARY, PRT, 613 AA.
AC Q8WUK1;
DT 01-MAR-2002 (TREMBLrel. 20, Created)
DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Hypothetical 67.3 kDa protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
CC NCBI_TaxID=9606;
CX [1]
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=TONSIL;
RA Strauberg R;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC020240; AAH20240.1; -
DR InterPro; IPR003599; IG_1
DR InterPro; IPR003597; IG_CL
DR InterPro; IPR003006; IG_MHC
DR InterPro; IPR003596; IG_V
DR Pfam; PF0047; IG_5
DR SMART; SM00409; IG_2
DR SMART; SM00407; IGc1; 4
DR SMART; SM00406; IGv; 1
DR PROSITE; PS00290; IG_MHC; UNKNOWN_3
KW Hypothetical protein.
SQ SEQUENCE 613 AA; 67296 MW; 60C7F5950671E315 CRC64;

Query Match 98.6%; Score 505; DB 4; Length 613;
Best Local Similarity 98.0%; Pred. No. 1.3e-45;

Matches 96; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QVQLVSGGGVGPGRSLRLSCAASGFTSSVAMHWYRQAPGKLEWAVISIDGSKITY 60
Db 20 QVQLVSGGGVGPGRSLRLSCAASGFTSSVAMHWYRQAPGKLEWAVISIDGSKITY 79
Qy 61 ADVYKGRFTISRDNSKNTLYLQNNSLRAEDTAVYYCAR 98

Db 80 ADSVKGFTISRDNKNTLYLQNSLRPAEDTAVYYCAK 117

RESULT 2

Q9UL93

PRELIMINARY; PRT; 116 AA.

AC Q9UL93; 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DE 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE Myosin-reactive immunoglobulin heavy chain variable region (Fragment).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 NCBI_TaxID=9606;

RP SEQUENCE FROM N.A.
 RX MEDLINE=98277139; PubMed=9614934;
 RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
 RT "Myosin-reactive autoantibodies in rheumatic carditis and normal fetus."
 RL Clin. Immunol. Immunopathol. 87:184-192 (1998).
 DR EMBL; AF035021; AAD56257.1; -
 DR HSSP; P01772; 2F84.
 DR InterPro; IPR003006; IG_MHC.
 DR Pfam; PR00047; Ig_1.
 DR SMART; SM00406; IGV_1.
 FT NON_TER 1
 FT NON_TER 116
 SQ SEQUENCE 116 AA; 12434 MW; 0DA0348154DD6061 CRC64;

Query Match 97.5%; Score 499; DB 4; Length 116;
 Best Local Similarity 99.0%; Pred. No. 7e-46;
 Matches 95; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VOLVESGGGVQPGSRSLRLSCAAGFTFSYAMHWYQAPGKLEWVAVISYDGSNKYYA 61
 Db 1 VOLVESGGGVQPGSRSLRLSCAAGFTFSYAMHWYQAPGKLEWVAVISYDGSNKYYA 60
 Qy 62 DSVKGRFTISRDNKNTLYLQNSLRPAEDTAVYYCA 97
 Db 61 DSVKGRFTISRDNKNTLYLQNSLRPAEDTAVYYCA 96

RESULT 3

Q9UL90

PRELIMINARY; PRT; 113 AA.

AC Q9UL90; 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DE 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE Myosin-reactive immunoglobulin heavy chain variable region (Fragment).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 NCBI_TaxID=9606;

RP SEQUENCE FROM N.A.
 RX MEDLINE=98277139; PubMed=9614934;
 RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
 RT "Myosin-reactive autoantibodies in rheumatic carditis and normal fetus."
 RL Clin. Immunol. Immunopathol. 87:184-192 (1998).
 DR EMBL; AF035024; AAD56260.1; -
 DR HSSP; P01772; 2F84.
 DR InterPro; IPR003006; IG_MHC.
 DR SMART; SM00406; IGV_1.

DR Pfam; PF00047; Ig_1.
 DR SMART; SM00406; IGV_1.
 FT NON_TER 1
 FT NON_TER 113
 SQ SEQUENCE 113 AA; 12437 MW; ED57FDD19086D07F CRC64;

Query Match 94.7%; Score 485; DB 4; Length 113;
 Best Local Similarity 93.9%; Pred. No. 2.1e-44;
 Matches 92; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 1 QVOLVESGGGVQPGSRSLRLSCAAGFTFSYAMHWYQAPGKLEWVAVISYDGSNKYY 60
 Db 1 EVOLVESGGGVQPGSRSLRLSCAAGFTFSYAMHWYQAPGKLEWVAIFIRYDGSNKYY 60
 Qy 61 ADSVKGFTISRDNKNTLYLQNSLRPAEDTAVYYCA 98
 Db 61 ADSVKGFTISRDNKNTLYLQNSLRPAEDTAVYYCA 98

RESULT 4

Q9UL84

PRELIMINARY; PRT; 122 AA.

AC Q9UL84; 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DE 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE Myosin-reactive immunoglobulin heavy chain variable region (Fragment).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 NCBI_TaxID=9606;

RP SEQUENCE FROM N.A.
 RX MEDLINE=98277139; PubMed=9614934;
 RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
 RT "Myosin-reactive autoantibodies in rheumatic carditis and normal fetus."
 RL Clin. Immunol. Immunopathol. 87:184-192 (1998).
 DR EMBL; AF035030; AAD56266.1; -
 DR HSSP; P01772; 2F84.
 DR InterPro; IPR003006; IG_MHC.
 DR Pfam; PR00047; Ig_1.
 DR SMART; SM00406; IGV_1.
 FT NON_TER 1
 FT NON_TER 122
 SQ SEQUENCE 122 AA; 13579 MW; 36054D413654588 CRC64;

Query Match 87.9%; Score 450; DB 4; Length 122;
 Best Local Similarity 87.8%; Pred. No. 1.3e-40;
 Matches 86; Conservative 5; Mismatches 7; Indels 0; Gaps 0;

Qy 1 QVOLVESGGGVQPGSRSLRLSCAAGFTFSYAMHWYQAPGKLEWVAVISYDGSNKYY 60
 Db 1 EVOLVESGGGVQPGSRSLRLSCAAGFTFSYAMHWYQAPGKLEWVAALISDGSNKYY 60
 Qy 61 ADSVKGFTISRDNKNTLYLQNSLRPAEDTAVYYCA 98
 Db 61 ADSVKGFTISRDNKNTLYLQNSLRPAEDTAVYYCA 98

RESULT 5

Q9UL71

PRELIMINARY; PRT; 121 AA.

AC Q9UL71; 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DE 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE Myosin-reactive immunoglobulin heavy chain variable region (Fragment).
 OS Homo sapiens (Human).

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OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_Taxid=9606;
RN [1]
RN SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF030543; AAD56279.1; -.
DR HSSP; P01772; 2FB4.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; Igv; 1.
DR NON TER 1 1
FT NON TER 121 121
SO SEQUENCE 121 AA; 13154 MW; 2F045CCFA5D50736 CRC64;

Query Match 87.3%; Score 447; DB 4; Length 121;
Best Local Similarity 85.7%; Pred. No. 2.7e-40;
Matches 84; Conservative 7; Mismatches 7; Indels 0; Gaps 0;

Qy 1 QVQLVESGGGVQVQPGKSLRLTCAASGFFSSYAMHWVROAPKGLGIEWAVISYDGSNKTY 60
Db 1 EVQLVESGGGVQVQPGKSLRLTCAASGFFFDGVMHWVROAPKGLGIEWVSLISGDGSITY 60
Qy 61 ADSVKGRTTISRDNKNTLYIQMNSLRADPTAVYYCAR 98
Db 61 ADSVKGRTTISRDNKNSLYIQMNSLRADPTALYYCAK 98

RESULT 6
Q9Y509 PRELIMINARY; PRT; 147 AA.
ID Q9Y509;
AC Q9Y509;
DT 01-NOV-1999 (TREMBLrel. 12, Created)
DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE Vh3 protein (Fragment).
GN Vh3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_Taxid=9606;
RN [1]
RN SEQUENCE FROM N.A.
RX MEDLINE=96071149; PubMed=7475288;
RA Cao J., Vesicic R.A., Rettig M.B., Hong C.H., Kim A., Lee J.C.,
RL Lichtenstein A.K., Berenson J.R.;
RT "A CD10-positive subset of malignant cells is identified in multiple
RT myeloma using PCR with patient-specific immunoglobulin gene primers.";
RL Leukemia 9:1948-1953(1995).
DR EMBL; S80860; AAD14339.1; -.
DR HSSP; P01772; 2FB4.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; Igv; 1.
DR NON TER 1 1
SO SEQUENCE 147 AA; 15768 MW; 84899FCAA7BC925C CRC64;

Query Match 87.3%; Score 447; DB 4; Length 147;
Best Local Similarity 85.7%; Pred. No. 3.5e-40;
Matches 84; Conservative 6; Mismatches 8; Indels 0; Gaps 0;

Qy 1 QVQLVESGGGVQVQPGKSLRLTCAASGFFSSYAMHWVROAPKGLGIEWAVISYDGSNKTY 60
Db 1 QVHLVESGGGVQVQPGKSLRLTCAASGFFSTYGMHWVROAPKGLGIDVALLISDGSITY 60
Qy 61 ADSVKGRTTISRDNKNTLYIQMNSLRADPTAVYYCAR 98

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[illegible]

ID	Q8WU38	PRELIMINARY;	PRT;	573 AA.
AC	Q8WU38:			
DT	01-MAR-2002 (TrEMBLrel. 20, Created)			
DT	01-MAR-2002 (TrEMBLrel. 20, Last sequence update)			
DT	01-JUN-2002 (TrEMBLrel. 21, Last annotation update)			
DE	Hypothetical 63.0 kDa protein.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
OX	NCBI_TaxId=9606;			
RP	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=TONSIL;			
RL	Strausberg R.;			
RL	Submitted (JUN-2002) to the EMBL/GenBank/DBU databases.			
DR	EMBL; BC021276; AAH21276.1; -			
DR	InterPro; IPR003599; IG_1			
DR	InterPro; IPR003597; IG_C1			
DR	InterPro; IPR003006; IG_MHC.			
DR	InterPro; IPR003596; IG_V.			
DR	Pfam; PF00047; IG_4.			
DR	SMART; SM00409; IG_1.			
DR	SMART; SM00407; IG_C1.3.			
DR	SMART; SM00406; IG_1.			
DR	PROSITE; PS00290; IG_MHC; UNKNOWN_2.			
KW	Hypothetical protein_2			
SEQUENCE	573 AA; 62967 MW; FD072344033AC530 CRC64;			

Matches 81; Conservative 10; Mismatches 7; Indels 0; Gaps 0;

Qy 1 OVOLVSGGGVOPGSLRLSCAASGFTFSYAMHWROAPGKLEWVAIVSYDGSNKYY 60
Db 20 EVOLVSGGGVOPGSLRLSCAASGFTFDYAMHWROAPGKLEWVSGISMSGSIGY 79
Qy 61 ADVKGRFTISRDNKNTLYLQWNSLRADPTAVYYCAR 98
Db 80 ADVKGRFTISRDNKNTLYLQWNSLRADPTAVYYCAR 117

RESULT 9

QyULB6 PRELIMINARY; PRT; 95 AA.

ID QyULB6
AC QyULB6;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE Immunoglobulin heavy chain (Fragment).
GN VH.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Tange Y., Kayano H.;
RT "Human VH gene sequence."
RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB035268; BAA87067.1;
DR HSSP; P01772; 2F84.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF00047; IG; 1.
DR SMART; SM00406; IGv; 1.
FT NON_TER 1
FT NON_TER 95
SQ SEQUENCE 95 AA; 10527 MW; 90A8C6D16D2574A CRC64;

Query Match

Best Local Similarity 84.0%; Score 430; DB 4; Length 95;
Matches 83; Conservative 3; Mismatches 9; Indels 0; Gaps 0;

Qy 2 VOLVESGGGVOPGSLRLSCAASGFTFSYAMHWROAPGKLEWVAIVSYDGSNKYYA 61
Db 1 VOLVESGGGVOPGSLRLSCAASGFTFSYAMHWROAPGKLEWVAIVSYDGSNKYY 60
Qy 62 DSVKGRFTISRDNKNTLYLQWNSLRADPTAVYYC 96
Db 61 DSVKGRFTISRDNKNTLYLQWNSLRADPTAVYYC 95

RESULT 10

QyULC77 PRELIMINARY; PRT; 471 AA.

ID QyULC77
AC QyULC77;
DT 01-JUN-2002 (TREMBlrel. 21, Created)
DT 01-JUN-2002 (TREMBlrel. 21, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE Hypothetical 51.8 kDa protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Straussberg R.;
RT Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC024289; AAH24289.1;
KW Hypothetical protein.
SQ SEQUENCE 471 AA; 51791 MW; 388F7F4CF588660B CRC64;

Query Match 83.8%; Score 429; DB 4; Length 471;
Best Local Similarity 83.7%; Pred. No. 1.3e-37;
Matches 82; Conservative 9; Mismatches 7; Indels 0; Gaps 0;

Qy 1 OVOLVSGGGVOPGSLRLSCAASGFTFSYAMHWROAPGKLEWVAIVSYDGSNKYY 60
Db 20 EVOLVSGGGVOPGSLRLSCAASGFTFSYAMHWROAPGKLEWVSSSSSSSYIYY 79
Qy 61 ADVKGRFTISRDNKNTLYLQWNSLRADPTAVYYCAR 98
Db 80 ADVKGRFTISRDNKNTLYLQWNSLRADPTAVYYCAR 117

RESULT 11

QyULJ91 PRELIMINARY; PRT; 118 AA.

ID QyULJ91
AC QyULJ91;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE Myosin-reactive immunoglobulin heavy chain variable region (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Werf P.L., Kalis N.N., Berny S.M.,
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal fetus."
RL Clin. Immunol. Immunopathol. 87:184-192 (1998).
DR EMBL; AF035023; AAD56259.1;
DR HSSP; P01772; 2F84.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF00047; IG; 1.
DR SMART; SM00406; IGv; 1.
FT NON_TER 1
FT NON_TER 118
SQ SEQUENCE 118 AA; 12843 MW; D0633949F2AC149D CRC64;

Query Match

Best Local Similarity 83.6%; Score 428; DB 4; Length 118;
Matches 83; Conservative 7; Mismatches 8; Indels 0; Gaps 0;

Qy 1 OVOLVSGGGVOPGSLRLSCAASGFTFSYAMHWROAPGKLEWVAIVSYDGSNKYY 60
Db 1 EVOLVSGGGVOPGSLRLSCAASGFTFSYAMHWROAPGKLEWVSISSITITIIYY 60
Qy 61 ADVKGRFTISRDNKNTLYLQWNSLRADPTAVYYCAR 98
Db 61 ADVKGRFTISRDNKNTLYLQWNSLRADPTAVYYCAR 98

RESULT 12

QyHCC1 PRELIMINARY; PRT; 112 AA.

ID QyHCC1
AC QyHCC1;
DT 01-MAR-2001 (TREMBlrel. 16, Created)
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE Single chain Fv (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Kikuchi M., Takeda C., Tsujimoto Y., Asada S., Nagata K.;
RT "An antibody fragment2a3 specific for native lysozyme: isolation from a

```

RT human synthetic phage display library and characterization."
RL Submitted (OCT-2000) to the EMBL/Genbank/DBJ databases.
DR EMBL; AB049915; BAB16829.1; -
DR HSSP; P01772; 2FB4.
DR InterPro; IPR003599; 19.
DR InterPro; IPR003600; 19.
DR InterPro; IPR003606; 19_MHC.
DR InterPro; IPR003596; 19_V.
DR Pfam; PF00047; 19; 1.
DR SMART; SM00409; IG; 1.
DR SMART; SM00406; IG; 1.
DR SMART; SM00410; IG-like; 1.
FT NON_TER 1 112 1
SQ SEQUENCE 112 AA; 12243 MW; 24F1A45EC3B84788 CRC64;

Query Match 82.0%; Score 420; DB 4; Length 112;
Best Local Similarity 80.6%; Pred. No. 1.9e-37;
Matches 79; Conservative 10; Mismatches 9; Indels 0; Gaps 0;

QY 1 QVQLVESGGGVVQPGKSLRLSCAASGFTPSYAMHWVRQAPGKLEWVAIVSYDSNKKY 60
DB 1 EVQLVESGGGVVQPGKSLRLSCAASGFTDDYGMVSRQAPGKLEWVGIMNGGSTGY 60

QY 61 ADVSKGRFTISRDNKNTLYLQMSLRADDTAVYYCAR 98
DB 61 ADVSKGRFTISRDNKNTLYLQMSLRADDTAVYYCAR 98

RESULT 13
Q9UL72 PRELIMINARY; PRT; 118 AA.
ID Q9UL72;
AC Q9UL72;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DE 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE Myosin-reactive immunoglobulin heavy chain variable region
   (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
DE "Myosin-reactive autoantibodies in rheumatic carditis and normal
   fetus."
RL Clin. Immunol. Immunopathol. 87:184-192 (1998).
DR EMBL; AF035042; AAD56278.1; -
DR HSSP; P01772; 2FB4.
DR InterPro; IPR003006; 19_MHC.
DR InterPro; IPR003596; 19_V.
DR Pfam; PF00047; 19; 1.
DR SMART; SM00406; IG; 1.
FT NON_TER 1 118 1
SQ SEQUENCE 118 AA; 12872 MW; B4D1A5944B2D5CCA CRC64;

Query Match 80.2%; Score 410.5; DB 4; Length 118;
Best Local Similarity 83.7%; Pred. No. 2.1e-36;
Matches 82; Conservative 6; Mismatches 9; Indels 1; Gaps 1;

QY 1 QVQLVESGGGVVQPGKSLRLSCAASGFTPSYAMHWVRQAPGKLEWVAIVSYDSNKKY 60
DB 1 EVQLVESGGGVVQPGKSLRLSCAASGFTVSSYAMHWVRQAPGKLEWVAVSYDSNKKY 59

QY 61 ADVSKGRFTISRDNKNTLYLQMSLRADDTAVYYCAR 98
DB 61 ADVSKGRFTISRDNKNTLYLQMSLRADDTAVYYCAR 97

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RESULT 14
Q96K68 PRELIMINARY; PRT; 494 AA.
ID Q96K68;
AC Q96K68;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE CDNA FLJ14473 f18, clone MAMMA1001080, highly similar to Homo
   sapiens SNC73 protein (SNC73) mRNA.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=MAMMARY GLAND;
RA Isogai T., Ota T., Hayaashi K., Sugiyama T., Otsuki T., Suzuki Y.,
RA Nishikawa T., Nagai K., Sugano S., Shiraori A., Sudo H.,
RA Wagaitsuna M., Hosoi T., Kaku Y., Kodaira H., Kondo H., Sugawara M.,
RA Takahashi M., Chiba Y., Ishida S., Murakawa K., Ono Y., Takiguchi S.,
RA Yamamoto S., Kimura K., Murakami K., Ishii S., Kawai Y., Satou K.,
RA Yamamoto J., Makamatsu A., Nakamura Y., Nagahara K., Masuno Y.,
RA Ninomiya K., Iwayanagi T.;
RT "NEO Human cDNA sequencing project."
RL Submitted (May-2001) to the EMBL/Genbank/DBJ databases.
DR EMBL; AK027379; BAB55072.1; -
DR InterPro; IPR003006; 19_MHC.
DR Pfam; PF00047; 19; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
SQ SEQUENCE 494 AA; 53088 MW; 9A1D7AB5AEE4C0E CRC64;

Query Match 78.9%; Score 404; DB 4; Length 494;
Best Local Similarity 76.6%; Pred. No. 6.4e-35;
Matches 77; Conservative 10; Mismatches 11; Indels 0; Gaps 0;

QY 1 QVQLVESGGGVVQPGKSLRLSCAASGFTPSYAMHWVRQAPGKLEWVAIVSYDSNKKY 60
DB 20 EVQLVESGGGVVQPGKSLRLSCAASGFTSTYAMHWVRQAPGKLEWVSISSRSDDIY 79

QY 61 ADVSKGRFTISRDNKNTLYLQMSLRADDTAVYYCAR 98
DB 80 RDSVKGRTISRDNKNTLYLQMSLRADDTAVYYCAR 117

RESULT 15
Q91Z05 PRELIMINARY; PRT; 473 AA.
ID Q91Z05;
AC Q91Z05;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Hypothetical 51.9 kDa protein.
GN AU044919.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (JUL-2001) to the EMBL/Genbank/DBJ databases.
DR EMBL; BC010327; AAH10327.1; -
DR MGD; MGI:2144967; AU044919.
DR InterPro; IPR000345; Cyrc_heme_bind.
DR InterPro; IPR003006; 19_MHC.
DR Pfam; PF00047; 19; 3.
DR PROSITE; PS00190; CYTOCHROME C; UNKNOWN_1.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KV Hypothetical protein.
SQ SEQUENCE 473 AA; 51946 MW; CF625F008932AF12 CRC64;

Query Match 78.3%; Score 401; DB 11; Length 473;
Best Local Similarity 76.5%; Pred. No. 1.3e-34;

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PI Derbyshire EJ, Carmen S, Smith S, Holtet TL, Du Fou SL;

XX WPI; 2000-638250/61.

XX New human antibody specific for human interleukin-12 (IL-12) used to
PT treat disorders characterized by aberrant IL-12 expression e.g. Crohn's
PT disease and multiple sclerosis -

XX Claim 75; Page 121; 377pp; English.

XX This invention relates to a new human antibody specific for human
CC interleukin-12 (IL-12). The invention also includes antigen binding
CC portions that bind to IL-12. Sequences AAB39485-B39516 represent human
CC anti-IL-12 antibody heavy and light chain complementarity determining
CC region (CDR) amino acid sequences, and also includes variable region
CC amino acid sequences. Other variable region amino acid sequences are
CC given in AAB39517-B39560 and AAB40068-B40149. Sequences AAB39561-B39771
CC represent anti-IL-12 CDR3 related amino acid sequences, AAB39772-B40063
CC given in AAB40064-B40067. Primers used in the identification and
CC construction of the antibodies of the invention are given in
CC AAC61062-C61071. The antibody of the invention is a neutralizing
CC antibody and has antirheumatic; antiarthritic; antisclerotic;
CC antiinflammatory; neuroprotective; antipsoriatic; antiaesthetic;
CC cardiant; antiparasitic; antibacterial and immunosuppressive activity.
CC The antibodies or antigen-binding fragments are useful in the treatment
CC of disorders associated with detrimental release of human IL-12.
CC especially Crohn's disease, multiple sclerosis and rheumatoid arthritis.
CC They can also be used in the manufacture of a pharmaceutical composition
CC to treat human IL-12 disorders.

XX Sequence 98 AA;

Query Match 100.0%; Score 512; DB 21; Length 98;
Best Local Similarity 100.0%; Pred. No. 1.9e-41;
Matches 98; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QVQLVESGGGVQPGPGRSLRLSCAASGFTFSYAMHWROAPGKGLWVAIVSYGDSNKKY 60
DB 1 QVQLVESGGGVQPGPGRSLRLSCAASGFTFSYAMHWROAPGKGLWVAIVSYGDSNKKY 60
QY 61 ADSVKGRTTISRDNKNTLYLQMSLRAEDTAVYYCAR 98
DB 61 ADSVKGRTTISRDNKNTLYLQMSLRAEDTAVYYCAR 98

RESULT 2

ID AAB40101 standard; Protein; 98 AA.

AC AAB40101;

DT 05-FEB-2001 (first entry)

XX Anti-hIL12 antibody H chain V region amino acid sequence SEQ ID 627.

XX Human; neutralizing antibody; interleukin-12; IL-12; antiinflammatory;
KW complementarity determining region; CDR; antirheumatic; antiarthritic;
KW antisclerotic; neuroprotective; antipsoriatic; antiaesthetic; cardiant;
KW antiparasitic; antibacterial; immunosuppressive; Crohn's disease;
KW multiple sclerosis; rheumatoid arthritis.

OS Homo sapiens.

PN WO200056772-A1.

PD 28-SEP-2000.

PF 24-MAR-2000; 2000WO-US07946.

PR 25-MAR-1999; 99US-0126603.

PA (BADI) BASF AG.
PA (GENY) GENETICS INST INC.

XX Salfeld JG, Roguska M, Paskind M, Banerjee S, Tracey DE, White M;
PI Kaymakalan Z, Labkovsky B, Sakorafas P, Friedrich S, Myles A;
PI Velman GM, Venturini A, Warne NW, Widom A, Elyin JG, Duncan AR;
PI Deryshire EJ, Carmen S, Smith S, Holter TL, Du Fou SL;
XX WPI; 2000-638250/61.

XX New human antibody specific for human interleukin-12 (IL-12) used to
PT treat disorders characterized by aberrant IL-12 expression e.g. Crohn's
PT disease and multiple sclerosis -

XX Claim 75; Page 121; 377pp; English.

XX This invention relates to a new human antibody specific for human
CC interleukin-12 (IL-12). The invention also includes antigen binding
CC portions that bind to IL-12. Sequences AAB39485-B39516 represent human
CC anti-IL-12 antibody heavy and light chain complementarity determining
CC region (CDR) amino acid sequences, and also includes variable region
CC amino acid sequences. Other variable region amino acid sequences are
CC given in AAB39517-B39560 and AAB40068-B40149. Sequences AAB39561-B39771
CC represent anti-IL-12 CDR3 related amino acid sequences, AAB39772-B40063
CC given in AAB40064-B40067. Primers used in the identification and
CC construction of the antibodies of the invention are given in
CC AAC61062-C61071. The antibody of the invention is a neutralizing
CC antibody and has antirheumatic; antiarthritic; antisclerotic;
CC antiinflammatory; neuroprotective; antipsoriatic; antiaesthetic;
CC cardiant; antiparasitic; antibacterial and immunosuppressive activity.
CC The antibodies or antigen-binding fragments are useful in the treatment
CC of disorders associated with detrimental release of human IL-12.
CC especially Crohn's disease, multiple sclerosis and rheumatoid arthritis.
CC They can also be used in the manufacture of a pharmaceutical composition
CC to treat human IL-12 disorders.

XX Sequence 98 AA;

Query Match 100.0%; Score 512; DB 21; Length 98;
Best Local Similarity 100.0%; Pred. No. 1.9e-41;
Matches 98; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QVQLVESGGGVQPGPGRSLRLSCAASGFTFSYAMHWROAPGKGLWVAIVSYGDSNKKY 60
DB 1 QVQLVESGGGVQPGPGRSLRLSCAASGFTFSYAMHWROAPGKGLWVAIVSYGDSNKKY 60
QY 61 ADSVKGRTTISRDNKNTLYLQMSLRAEDTAVYYCAR 98
DB 61 ADSVKGRTTISRDNKNTLYLQMSLRAEDTAVYYCAR 98

RESULT 3

ID AAB40102 standard; Protein; 98 AA.

AC AAB40102;

DT 05-FEB-2001 (first entry)

XX Anti-hIL12 antibody H chain V region amino acid sequence SEQ ID 628.

XX Human; neutralizing antibody; interleukin-12; IL-12; antiinflammatory;
KW complementarity determining region; CDR; antirheumatic; antiarthritic;
KW antisclerotic; neuroprotective; antipsoriatic; antiaesthetic; cardiant;
KW antiparasitic; antibacterial; immunosuppressive; Crohn's disease;
KW multiple sclerosis; rheumatoid arthritis.

OS Homo sapiens.

PN WO200056772-A1.

PD 28-SEP-2000.

PF 24-MAR-2000; 2000WO-US07946.

XX 25-MAR-1999; 99US-0126603.
 XX (BADI) BASF AG.
 PA (GEM) GENETICS INST INC.
 XX
 PI Salfeld JG, Roguska M, Paskind M, Banerjee S, Tracey DE, White M;
 PI Kaymakcalan Z, Labkovsky B, Sakorafas P, Friedrich S, Myles A;
 PI Veldman GM, Venturini A, Warne NW, Widom A, Elvin JG, Duncan AR;
 PI Derbyshire EJ, Carmen S, Smith S, Hollet TL, Du Fou SL;
 DR WPI; 2000-638250/61.
 XX
 PT New human antibody specific for human interleukin-12 (IL-12) used to
 PT treat disorders characterized by aberrant IL-12 expression e.g. Crohn's
 PT disease and multiple sclerosis -
 PS
 PS Claim 75; Page 121; 377pp; English.
 XX
 CC This invention relates to a new human antibody specific for human
 CC interleukin-12 (IL-12). The invention also includes antigen binding
 CC portions that bind to IL-12. Sequences AAB39485-B39516 represent human
 CC anti-IL-12 antibody heavy and light chain complementarity determining
 CC region (CDR) amino acid sequences, and also includes variable region
 CC amino acid sequences. Other variable region amino acid sequences are
 CC given in AAB39517-B39560 and AAB40064-B40149. Sequences AAB39561-B39771
 CC represent anti-IL-12 CDR3 related amino acid sequences, AAB39772-B40063
 CC represent other CDR sequences. Light chain CDR3 consensus sequences are
 CC given in AAB40064-B40067. Primers used in the identification and
 CC construction of the antibodies of the invention are given in
 CC AAC61062-C61071. The antibody of the invention is a neutralising
 CC antibody and has antineumatic; antiarthritic; antisclerotic;
 CC antiinflammatory; neuroprotective; antipsoriatic; antiaesthetic;
 CC cardiant; antiparasitic; antibacterial and immunosuppressive activity.
 CC The antibodies or antigen-binding fragments are useful in the treatment
 CC of disorders associated with detrimental release of human IL-12,
 CC especially Crohn's disease, multiple sclerosis and rheumatoid arthritis.
 CC They can also be used in the manufacture of a pharmaceutical composition
 CC to treat human IL-12 disorders.
 XX
 SQ Sequence 98 AA;
 Query Match 100.0%; Score 512; DB 21; Length 98;
 Best Local Similarity 100.0%; Pred. No. 1.9e-41;
 Matches 98; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Db 1 QVQLVESGGGVQPGKSLRLSCAASGFTFSYAMHWVRQAPGKLEWYAVISYGSNKYY 60
 1 QVQLVESGGGVQPGKSLRLSCAASGFTFSYAMHWVRQAPGKLEWYAVISYGSNKYY 60
 QY 61 ADSYKGRFTISRDNKNTLYLQNNSLRAEDTAVYYCAR 98
 61 ADSYKGRFTISRDNKNTLYLQNNSLRAEDTAVYYCAR 98
 Db 61 ADSYKGRFTISRDNKNTLYLQNNSLRAEDTAVYYCAR 98
 RESULT 4
 AAB40103 standard; Protein; 98 AA.
 ID AAB40103
 AC AAB40103;
 DT 05-FEB-2001 (first entry)
 XX
 DE Anti-IL12 antibody H chain V region amino acid sequence SEQ ID 629.
 XX
 KW Human; neutralising antibody; interleukin-12; IL-12; antiinflammatory;
 KW complementarity determining region; CDR; antineumatic; antiarthritic;
 KW antisclerotic; neuroprotective; antipsoriatic; antiaesthetic; cardiant;
 KW antiparasitic; antibacterial; immunosuppressive; Crohn's disease;
 KW multiple sclerosis; rheumatoid arthritis.
 XX
 OS Homo sapiens.
 XX

PN WO200056772-A1.
 XX
 XX 28-SEP-2000.
 PD
 XX 24-MAR-2000; 2000WO-US07946.
 XX
 XX 25-MAR-1999; 99US-0126603.
 XX
 XX (BADI) BASF AG.
 PA (GEM) GENETICS INST INC.
 XX
 PI Salfeld JG, Roguska M, Paskind M, Banerjee S, Tracey DE, White M;
 PI Kaymakcalan Z, Labkovsky B, Sakorafas P, Friedrich S, Myles A;
 PI Veldman GM, Venturini A, Warne NW, Widom A, Elvin JG, Duncan AR;
 PI Derbyshire EJ, Carmen S, Smith S, Hollet TL, Du Fou SL;
 DR WPI; 2000-638250/61.
 XX
 PT New human antibody specific for human interleukin-12 (IL-12) used to
 PT treat disorders characterized by aberrant IL-12 expression e.g. Crohn's
 PT disease and multiple sclerosis -
 PS
 PS Claim 75; Page 121; 377pp; English.
 XX
 CC This invention relates to a new human antibody specific for human
 CC interleukin-12 (IL-12). The invention also includes antigen binding
 CC portions that bind to IL-12. Sequences AAB39485-B39516 represent human
 CC anti-IL-12 antibody heavy and light chain complementarity determining
 CC region (CDR) amino acid sequences, and also includes variable region
 CC amino acid sequences. Other variable region amino acid sequences are
 CC given in AAB39517-B39560 and AAB40064-B40149. Sequences AAB39561-B39771
 CC represent anti-IL-12 CDR3 related amino acid sequences, AAB39772-B40063
 CC represent other CDR sequences. Light chain CDR3 consensus sequences are
 CC given in AAB40064-B40067. Primers used in the identification and
 CC construction of the antibodies of the invention are given in
 CC AAC61062-C61071. The antibody of the invention is a neutralising
 CC antibody and has antineumatic; antiarthritic; antisclerotic;
 CC antiinflammatory; neuroprotective; antipsoriatic; antiaesthetic;
 CC cardiant; antiparasitic; antibacterial and immunosuppressive activity.
 CC The antibodies or antigen-binding fragments are useful in the treatment
 CC of disorders associated with detrimental release of human IL-12,
 CC especially Crohn's disease, multiple sclerosis and rheumatoid arthritis.
 CC They can also be used in the manufacture of a pharmaceutical composition
 CC to treat human IL-12 disorders.
 XX
 SQ Sequence 98 AA;
 Query Match 100.0%; Score 512; DB 21; Length 98;
 Best Local Similarity 100.0%; Pred. No. 1.9e-41;
 Matches 98; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Db 1 QVQLVESGGGVQPGKSLRLSCAASGFTFSYAMHWVRQAPGKLEWYAVISYGSNKYY 60
 1 QVQLVESGGGVQPGKSLRLSCAASGFTFSYAMHWVRQAPGKLEWYAVISYGSNKYY 60
 QY 61 ADSYKGRFTISRDNKNTLYLQNNSLRAEDTAVYYCAR 98
 61 ADSYKGRFTISRDNKNTLYLQNNSLRAEDTAVYYCAR 98
 Db 61 ADSYKGRFTISRDNKNTLYLQNNSLRAEDTAVYYCAR 98
 RESULT 5
 AAB40104 standard; Protein; 98 AA.
 ID AAB40104
 AC AAB40104;
 DT 05-FEB-2001 (first entry)
 XX
 DE Anti-IL12 antibody H chain V region amino acid sequence SEQ ID 630.
 XX
 KW Human; neutralising antibody; interleukin-12; IL-12; antiinflammatory;
 KW complementarity determining region; CDR; antineumatic; antiarthritic;
 KW antisclerotic; neuroprotective; antipsoriatic; antiaesthetic; cardiant;
 KW


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XX AAB40106;
XX
XX 05-FEB-2001 (first entry)
XX
DE Anti-IL12 antibody H chain V region amino acid sequence SEQ ID 632.
XX
XX Human, neutralizing antibody; interleukin-12; IL-12; antiinflammatory;
XX complementarity determining region; CDR; antirheumatic; antiarthritic;
XX antisclerotic; neutroprotective; antipsoaritic; antiaesthetic; cardiant;
XX antiparasitic; antibacterial; immunosuppressive; Crohn's disease;
XX multiple sclerosis; rheumatoid arthritis.
XX
XX Homo sapiens.
XX
XX WO200056772-A1.
XX
XX 28-SEP-2000.
XX
XX 24-MAR-2000; 2000MO-US07946.
XX
XX 25-MAR-1999; 99US-0126603.
XX
XX (BADI ) BASF AG.
XX (GEMV ) GENETICS INST INC.
XX
XX Salfeld JG, Roguska M, Paskind M, Banerjee S, Tracey DE, White M;
XX Kaymakcalan Z, Labkovsky B, Sakorafas P, Friedrich S, Myles A;
XX Veldman GM, Venturini A, Warne NW, Widom A, Elvin JG, Duncan AR;
XX Derbyshire EJ, Carmen S, Smith S, Holter TL, Du Fou SL;
XX WPI; 2000-638250/61.
XX
XX New human antibody specific for human interleukin-12 (IL-12) used to
XX treat disorders characterized by aberrant IL-12 expression e.g. Crohn's
XX disease and multiple sclerosis -
XX
XX Claim 75; Page 121; 377pp; English.
XX
XX This invention relates to a new human antibody specific for human
XX interleukin-12 (IL-12). The invention also includes antigen binding
XX portions that bind to IL-12. Sequences AAB39485-B39516 represent human
XX anti-IL-12 antibody heavy and light chain complementarity determining
XX region (CDR) amino acid sequences, and also includes variable region
XX amino acid sequences. Other variable region amino acid sequences are
XX given in AAB39517-B39560 and AAB40068-B40149. Sequences AAB39561-B39771
XX represent anti-IL-12 CDR3 related amino acid sequences, AAB39772-B40063
XX represent other CDR sequences. Light chain CDR3 consensus sequences are
XX given in AAB40064-B40067. Primers used in the identification and
XX construction of the antibodies of the invention are given in
XX AAB61062-C61071. The antibody of the invention is a neutralizing
XX antibody and has antirheumatic; antiarthritic; antisclerotic;
XX antiinflammatory; neutroprotective; antipsoaritic; antiaesthetic;
XX cardiant; antiparasitic; antibacterial and immunosuppressive activity.
XX The antibodies or antigen-binding fragments are useful in the treatment
XX of disorders associated with detrimental release of human IL-12,
XX especially Crohn's disease, multiple sclerosis and rheumatoid arthritis.
XX They can also be used in the manufacture of a pharmaceutical composition
XX to treat human IL-12 disorders.
XX
XX Sequence 98 AA;
XX
XX Query Match 100.0%; Score 512; DB 21; Length 98;
XX Best Local Similarity 100.0%; Pred. No. 1.9e-41;
XX Matches 98; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 1 OVQVBSGGGVVOPGRSLRLSCAAGFTFSSYAMHWVROAPGKGLIEWAVVVISYDGSNKYY 60
XX
XX 1 OVQVBSGGGVVOPGRSLRLSCAAGFTFSSYAMHWVROAPGKGLIEWAVVVISYDGSNKYY 60
XX
XX 61 ADSVKGRTTSPNSKNTLYLQWNSLRAEDTAYYYCAR 98
XX
XX 61 ADSVKGRTTSPNSKNTLYLQWNSLRAEDTAYYYCAR 98

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RESULT 8
AAB40110
XX ID AAB40110 standard; Protein; 98 AA.
XX
XX AAB40110;
XX
XX 05-FEB-2001 (first entry)
XX
XX Anti-IL12 antibody H chain V region amino acid sequence SEQ ID 636.
XX
XX Human, neutralizing antibody; interleukin-12; IL-12; antiinflammatory;
XX complementarity determining region; CDR; antirheumatic; antiarthritic;
XX antisclerotic; neutroprotective; antipsoaritic; antiaesthetic; cardiant;
XX antiparasitic; antibacterial; immunosuppressive; Crohn's disease;
XX multiple sclerosis; rheumatoid arthritis.
XX
XX Homo sapiens.
XX
XX WO200056772-A1.
XX
XX 28-SEP-2000.
XX
XX 24-MAR-2000; 2000MO-US07946.
XX
XX 25-MAR-1999; 99US-0126603.
XX
XX (BADI ) BASF AG.
XX (GEMV ) GENETICS INST INC.
XX
XX Salfeld JG, Roguska M, Paskind M, Banerjee S, Tracey DE, White M;
XX Kaymakcalan Z, Labkovsky B, Sakorafas P, Friedrich S, Myles A;
XX Veldman GM, Venturini A, Warne NW, Widom A, Elvin JG, Duncan AR;
XX Derbyshire EJ, Carmen S, Smith S, Holter TL, Du Fou SL;
XX WPI; 2000-638250/61.
XX
XX New human antibody specific for human interleukin-12 (IL-12) used to
XX treat disorders characterized by aberrant IL-12 expression e.g. Crohn's
XX disease and multiple sclerosis -
XX
XX Claim 75; Page 121; 377pp; English.
XX
XX This invention relates to a new human antibody specific for human
XX interleukin-12 (IL-12). The invention also includes antigen binding
XX portions that bind to IL-12. Sequences AAB39485-B39516 represent human
XX anti-IL-12 antibody heavy and light chain complementarity determining
XX region (CDR) amino acid sequences, and also includes variable region
XX amino acid sequences. Other variable region amino acid sequences are
XX given in AAB39517-B39560 and AAB40068-B40149. Sequences AAB39561-B39771
XX represent anti-IL-12 CDR3 related amino acid sequences, AAB39772-B40063
XX represent other CDR sequences. Light chain CDR3 consensus sequences are
XX given in AAB40064-B40067. Primers used in the identification and
XX construction of the antibodies of the invention are given in
XX AAB61062-C61071. The antibody of the invention is a neutralizing
XX antibody and has antirheumatic; antiarthritic; antisclerotic;
XX antiinflammatory; neutroprotective; antipsoaritic; antiaesthetic;
XX cardiant; antiparasitic; antibacterial and immunosuppressive activity.
XX The antibodies or antigen-binding fragments are useful in the treatment
XX of disorders associated with detrimental release of human IL-12,
XX especially Crohn's disease, multiple sclerosis and rheumatoid arthritis.
XX They can also be used in the manufacture of a pharmaceutical composition
XX to treat human IL-12 disorders.
XX
XX Sequence 98 AA;
XX
XX Query Match 100.0%; Score 512; DB 21; Length 98;
XX Best Local Similarity 100.0%; Pred. No. 1.9e-41;
XX Matches 98; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 1 OVQVBSGGGVVOPGRSLRLSCAAGFTFSSYAMHWVROAPGKGLIEWAVVVISYDGSNKYY 60
XX
XX 1 OVQVBSGGGVVOPGRSLRLSCAAGFTFSSYAMHWVROAPGKGLIEWAVVVISYDGSNKYY 60
XX
XX 61 ADSVKGRTTSPNSKNTLYLQWNSLRAEDTAYYYCAR 98
XX
XX 61 ADSVKGRTTSPNSKNTLYLQWNSLRAEDTAYYYCAR 98

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Db 1 QVQLVESGGGVQPGKSLRLSCAASGFTFSYAMHWVRQAPGKGLEWVAIVSYDGSNKYY 60
 QY 61 ADSVKGRFTISRDNKNTLYLQMSLRADPTAVYYCAR 98
 DB 61 ADSVKGRFTISRDNKNTLYLQMSLRADPTAVYYCAR 98

RESULT 9
 AAB67507.
 ID AAB67507 standard; peptide; 98 AA.
 AC AAB67507;
 DT 29-MAY-2001 (first entry)

Light chain variable region of anti-CTLA-4 antibody 3-30-3.

Complementarity determining region; CDR; immune response; antibody;
 cytotoxic T lymphocyte associated antigen-4; CTLA-4; B7 ligand; cancer;
 autoimmune disease; infectious disease; inflammation; allergy;
 rheumatoid arthritis; myasthenia gravis; lupus erythematosus;
 multiple sclerosis; insulin-dependent diabetes mellitus; inflammation;
 transplant rejection; graft versus host disease.

Homo sapiens.
 Key Location/Qualifiers
 Region 31..35 /note= "CDR1"
 Region 50..66 /note= "CDR2"

MO200114424-A2.
 01-MAR-2001.
 24-AUG-2000; 2000MO-US23356.
 24-AUG-1999; 99US-0150452.
 (MEDA-) MEDAREX INC.
 Korman AJ, Halk EL, Lonberg N;
 WPI; 2001-202933/20.

Novel human sequence antibody that binds to human cytotoxic T
 lymphocyte associated antigen-4, useful for inducing, augmenting or
 prolonging immune response to antigen or for suppressing immune
 response in patient

Example 3; Fig 7; 127bp; English.

The present sequence represents the light chain variable region of
 human antibody 10D1. This antibody specifically binds to human
 cytotoxic T lymphocyte associated antigen-4 (CTLA-4). Such antibodies
 are used in methods for inducing, augmenting or prolonging an immune
 response to an antigen in a patient, where the antibodies block
 binding of human CTLA-4 to human B7 ligands. The antibodies also
 also useful for treating autoimmune disease in a subject caused or
 exacerbated by increased activity of T cells and for treating prostate
 cancer, melanoma or epithelial cancer. A polyvalent or polyclonal
 antibody preparation comprising two antibodies of the invention are
 useful for suppressing a immune response in a patient. They are used for
 treating cancer, infectious diseases and promoting beneficial autoimmune
 components for the treatment of diseases with inflammatory or allergic
 reactions. The polyvalent or polyclonal preparations are useful for
 treating autoimmune diseases such as rheumatoid arthritis, myasthenia
 gravis and lupus erythematosus, multiple sclerosis, insulin-dependent
 diabetes mellitus, transplant rejection, and inflammation, graft versus
 host disease.

Sequence 98 AA;

Query Match 100.0%; Score 512; DB 22; Length 98;
 Best local Similarity 100.0%; Pred No. 1.9e-41;
 Matches 98; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QVQLVESGGGVQPGKSLRLSCAASGFTFSYAMHWVRQAPGKGLEWVAIVSYDGSNKYY 60
 DB 1 QVQLVESGGGVQPGKSLRLSCAASGFTFSYAMHWVRQAPGKGLEWVAIVSYDGSNKYY 60
 QY 61 ADSVKGRFTISRDNKNTLYLQMSLRADPTAVYYCAR 98
 DB 61 ADSVKGRFTISRDNKNTLYLQMSLRADPTAVYYCAR 98

RESULT 10
 AAB67512
 ID AAB67512 standard; peptide; 98 AA.
 AC AAB67512;
 DT 29-MAY-2001 (first entry)

Heavy chain variable region of anti-CTLA-4 antibody 3-30-3.

Complementarity determining region; CDR; immune response; antibody;
 cytotoxic T lymphocyte associated antigen-4; CTLA-4; B7 ligand; cancer;
 autoimmune disease; infectious disease; inflammation; allergy;
 rheumatoid arthritis; myasthenia gravis; lupus erythematosus;
 multiple sclerosis; insulin-dependent diabetes mellitus; inflammation;
 transplant rejection; graft versus host disease.

Homo sapiens.
 Key Location/Qualifiers
 Region 31..35 /note= "CDR1"
 Region 50..66 /note= "CDR2"

MO200114424-A2.
 01-MAR-2001.
 24-AUG-2000; 2000MO-US23356.
 24-AUG-1999; 99US-0150452.
 (MEDA-) MEDAREX INC.
 Korman AJ, Halk EL, Lonberg N;
 WPI; 2001-202933/20.

Novel human sequence antibody that binds to human cytotoxic T
 lymphocyte associated antigen-4, useful for inducing, augmenting or
 prolonging immune response to antigen or for suppressing immune
 response in patient

Example 3; Fig 8; 127bp; English.

The present sequence represents the heavy chain variable region of
 human antibody 3-30-3. This antibody specifically binds to human
 cytotoxic T lymphocyte associated antigen-4 (CTLA-4). Such antibodies
 are used in methods for inducing, augmenting or prolonging an immune
 response to an antigen in a patient, where the antibodies block
 binding of human CTLA-4 to human B7 ligands. The antibodies also
 also useful for treating autoimmune disease in a subject caused or
 exacerbated by increased activity of T cells and for treating prostate
 cancer, melanoma or epithelial cancer. A polyvalent or polyclonal
 antibody preparation comprising two antibodies of the invention are
 useful for suppressing a immune response in a patient. They are used for
 treating cancer, infectious diseases and promoting beneficial autoimmune
 reactions for the treatment of diseases with inflammatory or allergic

CC components. The polyvalent or polyclonal preparations are useful for
CC treating autoimmune diseases such as rheumatoid arthritis, myasthenia
CC gravis and lupus erythematosus, multiple sclerosis, insulin-dependent
CC diabetes mellitus, transplant rejection, and inflammation, graft versus
CC host disease.

50 Sequence 98 AA;

Query Match	100.0%	Score 512	DB 22	length 98
Best Local Similarity	100.0%	Pred. No. 1.9e-41		
Matches 98	Conservative 0	Mismatches 0	Indels 0	Gaps 0

Db

DQ
61 ADSVKGRFTISRDN SKNTLYLQMSLRADTAVYYCAR 98

DB
61 ADSVKGRFTISRDN SKNTLYLQMSLRADTAVYYCAR 98

RESULT 11
AAMS1164
ID AAMS1164 standard; Protein; 115 AA.
REV

DT 10-JUN-2002 (first entry)
xx

DE Anti-tumour necrosis factor antibody heavy chain variable region.

KW Tumour necrosis factor alpha; TNF; antihp; heavy chain; CDR;
KW Complementarity determining region; antirheumatic; antirheitic;
KW antitumor; antiaesthetic; antiallergic; antiinflammatory;
KW antiscaling; antidiabetic; antitubercleleptic;
KW antitubercleleptic; vasotropic; antanginal; cardiant;
KW antitubercleleptic; virucide; fungicide; antileptotic; protozoicide;
KW cytostatic; neuroprotective; antiparkinsonian; nootropic; human;
KW diagnostic; therapy.

OS Homo sapiens.

FH	Key	Location/Qualifiers
ET	Position	1 30

ET	Region	31	35	/Label= FRI
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FT	Region	/Label= CDR1
FT	36	49

ET	Region	/LADEN = FRZ
50	66	

FT	Region	67.198	/LADP=COR
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Region	99..107
FT	7.140612 E+0

FT	Region	108..115
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PR 29-SEP-2000; 2000US-236826P
DB 01-SEP-2001; 2001US-0000000

XX
PA (CENT) CENTOCOP INC.

Gil'ev-Komarov, I. I. knizhka DM

WP1: 2002-217194/27.

DR WPI; 2002-217194/27.

XX Novel isolated mammalian anti-tumor necrosis factor antibody, useful
PT for treating sickle cell anemia, diabetes, atherosclerosis, restenosis
PT angina pectoris, myocardial infarction, leprosy -
XX
XX
PS Claim 9; Page 129; 131pp; English.
IX

Claim 9; Page 129; 131pp; English.

The present sequence is that of the heavy chain variable region of an anti-tumour necrosis factor (TNF) antibody of the invention. The invention provides isolated human, primate, rodent, mammalian, chimeric, humanised and/or complementarily determining region (CDR)-grafted anti-TNF antibodies, immunoglobulins, cleavage products and other specified portions and variants, as well as anti-TNF antibody compositions, encoding or complementary nucleic acids, vectors, host cells, compositions, formulations, devices, transgenic animals, transgenic plants, and methods of making and using them. The anti-TNF antibody comprises at least a portion of an immunoglobulin molecule, especially the heavy chain and/or light chain variable regions given in the present sequence and in AAM51165, or either all of the CDRs of the heavy chain (see AAM51165-60) or all of the CDRs of the light chain (see AAM51161-63) AAM51165 may inhibit TNF-induced cell adhesion molecules, inhibit TNF binding to receptor, or provide Arthritis Index improvement in a mouse model. It is useful for diagnosing or treating a TNF related condition in a cell, tissue, organ or animal (claimed) such as rheumatoid arthritis, gastric ulcer, asthma, allergic rhinitis, Crohn's pathology, sickle cell anaemia, diabetes, a cardiovascular disease such as arteriosclerosis, atherosclerosis, restenosis, angina pectoris or myocardial infarction, an infectious disease in a cell such as bacterial, viral, and fungal infections, pneumonia, leprosy and malaria, a malignant disease such as leukemia, chronic myelocytic leukemia, Burkitt's lymphoma and multiple myeloma, or a neurological disease such as multiple sclerosis, Parkinson's disease, spinal ataxia, Alzheimer's disease and Creutzfeldt-Jakob disease.

SQ Sequence 115 AA;

Query March	100.0%	Score 512;	DB 23;	Length 115;
Best Local Similarity	100.0%	Pred. No. 2.2e-41;		
Matches 98;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0

Db 1 QVQLVESGGGVQPGKSLRLSCAASGTFSSYAMHWQAPGKGLEWVAISYDGSKYY 600
Dy 1 QVQLVESGGGVQPGKSLRLSCAASGTFSSYAMHWQAPGKGLEWVAISYDGSKYY 600

QY : 61 ADSVKGRFTISRDN SKNTLYLQMSLR AEDTAVYYCAR 98

RESULT 12
NAME1167

1D AAm5116 / standard; protein; 118 AA:
XX

AC AAAM5116 /
XX

DE Human DP-46 heavy chain variable region

KM Tumour necrosis factor alpha; TNF; antibody; heavy chain; CDR;
KM Complementarity determining region; antirheumatic; antiarthritic
KM anticler; antiaesthetic; antiallergic; antiinflammatoy;
KM anticlcking; antidiabetic; antituberculoctic;
KM antithrombotic; vasotropic; angiogenic; cadant;
KM antibacterial; vinucle; fungicide; antifibrotic; protozoide;
KM cytostatic; neuroprotective; antiparkinsonian; nootropic; human;
KM diagnosis; therapy; DP-66.

OS Homo sapiens

FH	Key	Location/Qualifiers
1	1	1
2	2	2
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100	100	100

FN Key

FT Region 1..30
 FT /label= FR1
 FT Region 31..35
 FT /label= CDR1
 FT Region 36..49
 FT /label= FR2
 FT Region 50..66
 FT /label= CDR2
 FT Region 67..98
 FT /label= FR3
 FT Region 99..107
 FT /label= CDR3
 FT Region 108..118
 FT /label= J6
 PN WO200212502-A2.
 XX 14-FEB-2002.
 PD 07-AUG-2001; 2001WO-US24785.
 XX 07-AUG-2001; 2001WO-US24785.
 XX 07-AUG-2000; 2000US-223360P.
 PR 29-SEP-2000; 2000US-236826P.
 PR 01-AUG-2001; 2001US-0920137.
 XX (CENZ) CENTOCOR INC.
 PA Giles-Komar J, Knight DM, Heavner G, Scallion B, Shealy D;
 PI WPI; 2002-217194/27.
 DR N-PSDB; ABL53507.
 DR Novel isolated mammalian anti-tumor necrosis factor antibody, useful
 PT for treating sickle cell anemia, diabetes, atherosclerosis, restenosis,
 PT angina pectoris, myocardial infarction, leprosy -
 XX Example 3; Fig 4; 13pp; English.
 PS The present sequence is that of a human DP-46 heavy chain variable
 XX region encoded by a human germline DP-46 gene in a transgenic mouse
 CC used in human monoclonal antibody (mab) construction. A GENTIV
 CC fusion was performed using spleen cells from a hybrid mouse
 CC containing human variable and constant region antibody transgenes
 CC (TNF) alpha. Human mabs were obtained that bound immobilised human
 CC TNF alpha with apparently high avidity. These mabs had a totally
 CC human IgG1, kappa isotype. Their heavy chain variable region
 CC deduced amino acid sequences (see AAM51168-72) showed high
 CC similarity to the DP-46 sequence. The invention provides isolated
 CC human, primate, rodent, mammalian, chimeric, humanised and/or
 CC complementarily determining region (CDR)-grafted anti-TNF antibodies,
 CC immunoglobulins, and cleavage products and variants, as well as
 CC anti-TNF antibody compositions, encoding or complementary nucleic
 CC acids, vectors, host cells, compositions, formulations, devices,
 CC transgenic animals, transgenic plants, and methods of making and
 CC using them. The anti-TNF antibody comprises at least a portion of
 CC an immunoglobulin molecule, especially the heavy chain and/or light
 CC chain variable regions given in the present sequence and in
 CC AAM51165, or either all of the CDRs of the heavy chain (see
 CC AAM51158-60) or all of the CDRs of the light chain (see AAM51161-63).
 CC The antibodies may inhibit TNF-induced cell adhesion molecules,
 CC inhibit TNF binding to receptor, or provide Arthritis Index
 CC improvement in a mouse model. They are useful for diagnosing or
 CC treating a TNF related condition in a cell, tissue, organ or animal
 CC (claimed) such as rheumatoid arthritis, gastric ulcer, asthma,
 CC allergic rhinitis, Crohn's pathology, sickle cell anaemia, diabetes,
 CC a cardiovascular disease such as arteriosclerosis, atherosclerosis,
 CC restenosis, angina pectoris or myocardial infarction, an infectious
 CC disease in a cell such as bacterial, viral, and fungal infections,
 CC pneumonia, chronic myelocytic leukaemia, Burkitt's lymphoma and
 CC leukemia, chronic myelocytic leukaemia, a malignant disease such as
 CC multiple myeloma, or a neurological disease such as multiple
 CC sclerosis, Parkinson's disease, spinal ataxia, Alzheimer's disease

CC and Creutzfeldt-Jakob disease.
 XX SQ Sequence 118 AA,
 Query Match 100.0%; Score 512; DB 23; Length 118;
 Best Local Similarity 100.0%; Pred. No. 2,3e-41;
 Matches 98; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 QVQLVDSGGGVQPGSRSLRLSCASGFTFSYAMHWYRQAPGKLEWYAVISYDGSNRY 60
 DB 1 QVQLVDSGGGVQPGSRSLRLSCASGFTFSYAMHWYRQAPGKLEWYAVISYDGSNRY 60
 QY ADSYKGRFTISRDNSKNTLYLQNMNSLAEDPAVYYCAR 98
 DB ADSYKGRFTISRDNSKNTLYLQNMNSLAEDPAVYYCAR 98
 RESULT 13
 AAR52064
 ID AAR52064 standard; Protein; 120 AA.
 AC AAR52064;
 DT 11-OCT-1996 (first entry)
 XX Heavy chain variable region of human G36005 antibody.
 DE antibody; humanised; murine; human; heavy chain; light; variable;
 KW framework region; complementarity determining region; reshaping;
 KM modelling; surface residue; modify.
 XX Homo sapiens.
 OS
 XX Key Location/Qualifiers
 FH 1..30
 FT Region /label= framework_region_1
 FT /note= "FR 1"
 FT Region 31..35
 FT /label= complementarity_determining_region_1
 FT /note= "CDR 1"
 FT Region 36..49
 FT /note= "FR 2"
 FT Region 50..59
 FT /note= "CDR 2"
 FT Region 60..98
 FT /note= "FR 3"
 FT Region 99..110
 FT /note= "CDR 3"
 XX EP592106-A1.
 XX 13-APR-1994.
 PD 07-SEP-1993; 93EP-0307051.
 PF 09-SEP-1992; 92US-0942245.
 PR (PEDE/) PEDERSEN J T.
 PA (IMMU-) IMMUNOGEN INC.
 XX Guild BC, Pedersen JT, Rees AR, Roguska MA, Searle SM;
 DR WPI, 1994-120230/15.
 XX Method of resurfacing of rodent antibodies to produce humanised
 PT antibody forms - for producing non-human antibodies with improved
 PT therapeutic efficiency by presenting human surface on V-region
 PS Example 1; Fig 4B; 230pp; English.
 XX Modification of a rodent antibody (Ab) or fragment by resurfacing in
 CC order to produce a humanised rodent Ab can be determined by calculating
 CC homology between murine and human Ab antibody surfaces. In order to test

PT Forty four human secreted proteins (referred to as SECP-1 to SECP-44),
 useful in the diagnosis, treatment and prevention of cardiovascular
 (e.g. atherosclerosis), autoimmune/inflammatory (e.g. allergies) and
 cell proliferative disorders -

PS Claim 1, Page 142-143, 195pp; English.

XX The invention relates to forty four human secreted proteins (referred to
 CC as SECP-1 to SECP-44) and the nucleic acids encoding them. Also
 CC included are a host cell transformed with the nucleic acid, a
 CC transgenic animal comprising the nucleic acid, an anti-SECP
 CC antibody, use of the SECP proteins in isolating agonists and antagonists
 CC of SECP activity and a method of isolating compounds which alter the
 CC expression of the SECP nucleic acid. The SECP polynucleotides and
 CC polypeptides are useful in the diagnosis, treatment and prevention of
 CC cardiovascular (e.g. atherosclerosis), hypertension, myocardial
 CC infarction), autoimmune/inflammatory (e.g. acquired immunodeficiency
 CC syndrome (AIDS), allergies, rheumatoid arthritis), cell proliferative
 CC (e.g. cancer), developmental (e.g. Duchenne and Becker muscular
 CC dystrophy), and neurological (e.g. epilepsy, Alzheimer's disease)
 CC disorders. Numerous other examples of each disorder are given in the
 CC specification. The present sequence represents a SECP protein.

XX Sequence 519 AA;

Query Match

Best Local Similarity 100.0%; Score 512; DB 23; Length 519;

Matches 98; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
QY 1 QVQVIESGGGVOPGRSLRLSCAAGFTFSSYAMHWVROAPGKLEWAVIYSYDGSNKYY 60
    |||
DB 20 QVQVIESGGGVOPGRSLRLSCAAGFTFSSYAMHWVROAPGKLEWAVIYSYDGSNKYY 79
    |||
QY 61 ADSYKGRFTISRNSKNTLYLQWNSLRAEDTAVYYCAR 98
    |||
DB 80 ADSYKGRFTISRNSKNTLYLQWNSLRAEDTAVYYCAR 117
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Search completed: June 3, 2003, 08:14:46
 Job time : 45.1502 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: June 3, 2003, 08:21:07 ; Search time 23.2457 Seconds

(without alignments)
426.742 Million cell updates/sec.

Title: US-09-644-668a-15

Perfect score: 512

Sequence: 1 QVQLVESGGGVQPGKSLRLT...LYQMNSLRADTAVYTCAR 98

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 383519 seqs, 101223694 residues

Total number of hits satisfying chosen parameters: 383519

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	512	100.0	98	US-10-194-975-24	Sequence 24, Appl
2	512	100.0	247	US-09-880-748-924	Sequence 924, App
3	508	99.2	252	US-09-880-748-1731	Sequence 1731, Ap
4	506	98.8	254	US-09-880-748-983	Sequence 983, App
5	505	98.6	98	US-10-194-975-23	Sequence 23, Appl
6	505	98.6	98	US-10-194-975-25	Sequence 25, Appl
7	505	98.6	122	US-09-144-886-69	Sequence 1627, Ap
8	505	98.6	252	US-09-880-748-1627	Sequence 1627, Ap
9	504	98.4	249	US-09-880-748-1109	Sequence 1109, Ap
10	503	98.2	122	US-09-144-886-68	Sequence 68, Appl
11	501	97.9	98	US-10-194-975-26	Sequence 26, Appl
12	501	97.9	249	US-09-880-748-512	Sequence 512, Appl
13	501	97.9	451	US-10-153-362-17	Sequence 17, Appl
14	499	97.5	241	US-09-880-748-2055	Sequence 1305, Ap
15	499	97.5	247	US-09-880-748-1330	Sequence 1330, Ap
16	499	97.5	248	US-09-880-748-1421	Sequence 1421, Ap
17	499	97.5	252	US-09-880-748-1394	Sequence 1394, Ap
18	499	97.5	252	US-09-880-748-1519	Sequence 1519, Ap
19	498	97.3	254	US-09-880-748-981	Sequence 981, App

20	496	96.9	123	US-10-243-265-2	Sequence 2, Appl1
21	496	96.9	238	US-09-880-748-1931	Sequence 1931, Ap
22	496	96.9	240	US-09-880-748-1912	Sequence 1912, Ap
23	496	96.9	252	US-09-880-748-1201	Sequence 1201, Ap
24	495	96.7	254	US-09-880-748-881	Sequence 881, App
25	494	96.5	254	US-09-880-748-877	Sequence 877, App
26	493	96.3	248	US-09-880-748-1890	Sequence 1890, Ap
27	493	96.3	249	US-09-880-748-1724	Sequence 1724, Ap
28	493	96.3	249	US-09-880-748-1725	Sequence 1725, Ap
29	493	96.3	254	US-09-880-748-1759	Sequence 1759, Ap
30	493	96.3	256	US-09-880-748-839	Sequence 839, App
31	492	96.1	119	US-10-073-644C-6	Sequence 6, Appl1
32	492	96.1	253	US-09-880-748-1200	Sequence 1200, Ap
33	491	95.9	123	US-10-243-265-10	Sequence 10, Appl1
34	491	95.9	240	US-09-880-748-1898	Sequence 1898, Ap
35	491	95.9	252	US-09-880-748-956	Sequence 956, App
36	490	95.7	249	US-09-880-748-1397	Sequence 1397, App
37	490	95.7	249	US-09-880-748-1102	Sequence 1102, App
38	490	95.7	249	US-09-880-748-1115	Sequence 1115, Ap
39	488	95.3	123	US-10-243-265-4	Sequence 4, Appl1
40	488	95.3	225	US-09-453-234-60	Sequence 60, Appl1
41	488	95.3	225	US-09-453-234-92	Sequence 92, Appl1
42	488	95.3	249	US-09-880-748-911	Sequence 911, App
43	488	95.3	249	US-09-880-748-1113	Sequence 1113, App
44	488	95.3	251	US-09-880-748-955	Sequence 955, App
45	488	95.3	252	US-09-880-748-988	Sequence 988, App

ALIGNMENTS

```
RESULT 1
US-10-194-975-24
; Sequence 24, Application US/10194975
; Publication No US2003003649A1
; GENERAL INFORMATION:
; APPLICANT: Foote, Jefferson
; TITLE OF INVENTION: Super Humanized Antibodies
; FILE REFERENCE: 501231.01
; CURRENT APPLICATION NUMBER: US/10/194,975
; CURRENT FILING DATE: 2002-10-10
; PRIOR APPLICATION NUMBER: US 60/305,111
; PRIOR FILING DATE: 2001-07-12
; NUMBER OF SEQ ID NOS: 122
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 24
; LENGTH: 98
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-194-975-24

Query Match      100.0%; Score 512; DB 9; Length 98;
Best Local Similarity 100.0%; Pred. No. 2.6e-33;
Matches 98; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 QVQLVESGGGVQPGKSLRLTCAASGFTFSYAMHWYRQAPGKLEWVAIVSYDGNKYY 60
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DB      1 QVQLVESGGGVQPGKSLRLTCAASGFTFSYAMHWYRQAPGKLEWVAIVSYDGNKYY 60
      |||

QY      61 ADSVKGFTISRDNKNTLYIQMNSLRADTAVYTCAR 98
      |||
DB      61 ADSVKGFTISRDNKNTLYIQMNSLRADTAVYTCAR 98
      |||

RESULT 2
US-09-880-748-924
; Sequence 924, Application US/09880748
; Publication No. US2003005937A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: P5523
; CURRENT APPLICATION NUMBER: US/09/880,748
```


;; CURRENT FILING DATE: 2001-06-15
;; PRIOR APPLICATION NUMBER: 60/212,210
;; PRIOR FILING DATE: 2000-06-15
;; PRIOR APPLICATION NUMBER: 60/240,816
;; PRIOR FILING DATE: 2000-10-17
;; PRIOR APPLICATION NUMBER: 60/276,248
;; PRIOR FILING DATE: 2001-03-16
;; PRIOR APPLICATION NUMBER: 60/277,379
;; PRIOR FILING DATE: 2001-03-21
;; PRIOR APPLICATION NUMBER: 60/293,499
;; PRIOR FILING DATE: 2001-05-25
;; NUMBER OF SEQ ID NOS: 3239
;; SOFTWARE: PatentIn Ver. 2.0
;; SEQ ID NO 924
;; LENGTH: 247
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-09-880-748-924

Query Match 100.0%; Score 512; DB 9; Length 247;
Best Local Similarity 100.0%; Pred. No. 6,2e-33;
Matches 98; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QVOLVESGGGVOPGSRSLRLSCAASGFTFSYAMHWVROAPGKGLEWVAVISYDGSNKYY 60
DB 1 QVOLVESGGGVOPGSRSLRLSCAASGFTFSYAMHWVROAPGKGLEWVAVISYDGSNKYY 60
QY 61 ADVKGRFTISRDNKNTLYLQNNSLRAEDTAVYYCAR 98
DB 61 ADVKGRFTISRDNKNTLYLQNNSLRAEDTAVYYCAR 98

RESULT 3

US-09-880-748-1731
;; Sequence 1731, Application US/09880748
;; Publication No. US2003005937A1
;; GENERAL INFORMATION:
;; APPLICANT: Ruben et al.
;; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
;; FILE REFERENCE: PP523
;; CURRENT APPLICATION NUMBER: US/09/880,748
;; CURRENT FILING DATE: 2001-06-15
;; PRIOR APPLICATION NUMBER: 60/212,210
;; PRIOR FILING DATE: 2000-06-15
;; PRIOR APPLICATION NUMBER: 60/240,816
;; PRIOR FILING DATE: 2000-10-17
;; PRIOR APPLICATION NUMBER: 60/276,248
;; PRIOR FILING DATE: 2001-03-16
;; PRIOR APPLICATION NUMBER: 60/277,379
;; PRIOR FILING DATE: 2001-03-21
;; PRIOR APPLICATION NUMBER: 60/293,499
;; PRIOR FILING DATE: 2001-05-25
;; NUMBER OF SEQ ID NOS: 3239
;; SOFTWARE: PatentIn Ver. 2.0
;; SEQ ID NO 1731
;; LENGTH: 252
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-09-880-748-1731

Query Match 99.2%; Score 508; DB 9; Length 252;
Best Local Similarity 99.0%; Pred. No. 1,3e-32;
Matches 97; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QVOLVESGGGVOPGSRSLRLSCAASGFTFSYAMHWVROAPGKGLEWVAVISYDGSNKYY 60
DB 1 QVOLVESGGGVOPGSRSLRLSCAASGFTFSYAMHWVROAPGKGLEWVAVISYDGSNKYY 60
QY 61 ADVKGRFTISRDNKNTLYLQNNSLRAEDTAVYYCAR 98
DB 61 ADVKGRFTISRDNKNTLYLQNNSLRAEDTAVYYCAR 98

RESULT 4
US-09-880-748-983
;; Sequence 983, Application US/09880748
;; Publication No. US2003005937A1
;; GENERAL INFORMATION:
;; APPLICANT: Ruben et al.
;; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
;; FILE REFERENCE: PP523
;; CURRENT APPLICATION NUMBER: US/09/880,748
;; CURRENT FILING DATE: 2001-06-15
;; PRIOR APPLICATION NUMBER: 60/212,210
;; PRIOR FILING DATE: 2000-06-15
;; PRIOR APPLICATION NUMBER: 60/240,816
;; PRIOR FILING DATE: 2000-10-17
;; PRIOR APPLICATION NUMBER: 60/276,248
;; PRIOR FILING DATE: 2001-03-16
;; PRIOR APPLICATION NUMBER: 60/277,379
;; PRIOR FILING DATE: 2001-03-21
;; PRIOR APPLICATION NUMBER: 60/293,499
;; PRIOR FILING DATE: 2001-05-25
;; NUMBER OF SEQ ID NOS: 3239
;; SOFTWARE: PatentIn Ver. 2.0
;; SEQ ID NO 983
;; LENGTH: 254
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-09-880-748-983

Query Match 98.8%; Score 506; DB 9; Length 254;
Best Local Similarity 99.0%; Pred. No. 1,9e-32;
Matches 97; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QVOLVESGGGVOPGSRSLRLSCAASGFTFSYAMHWVROAPGKGLEWVAVISYDGSNKYY 60
DB 1 QVOLVESGGGVOPGSRSLRLSCAASGFTFSYAMHWVROAPGKGLEWVAVISYDGSNKYY 60
QY 61 ADVKGRFTISRDNKNTLYLQNNSLRAEDTAVYYCAR 98
DB 61 ADVKGRFTISRDNKNTLYLQNNSLRAEDTAVYYCAR 98

RESULT 5

US-10-194-975-23
;; Sequence 23, Application US/10194975
;; Publication No. US20030039649A1
;; GENERAL INFORMATION:
;; APPLICANT: Foote, Jefferson
;; TITLE OF INVENTION: Super Humanized Antibodies
;; FILE REFERENCE: 501231.01
;; CURRENT APPLICATION NUMBER: US/10/194,975
;; CURRENT FILING DATE: 2002-10-10
;; PRIOR APPLICATION NUMBER: US 60/305,111
;; PRIOR FILING DATE: 2001-07-12
;; NUMBER OF SEQ ID NOS: 122
;; SOFTWARE: PatentIn version 3.1
;; SEQ ID NO 23
;; LENGTH: 98
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-10-194-975-23

Query Match 98.6%; Score 505; DB 9; Length 98;
Best Local Similarity 98.0%; Pred. No. 9,1e-33;
Matches 96; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 QVOLVESGGGVOPGSRSLRLSCAASGFTFSYAMHWVROAPGKGLEWVAVISYDGSNKYY 60
DB 1 QVOLVESGGGVOPGSRSLRLSCAASGFTFSYAMHWVROAPGKGLEWVAVISYDGSNKYY 60
QY 61 ADVKGRFTISRDNKNTLYLQNNSLRAEDTAVYYCAR 98
DB 61 ADVKGRFTISRDNKNTLYLQNNSLRAEDTAVYYCAR 98

Query Match	98.6%;	Score 505;	DB 9;	Length 98;
Best Local Similarity	98.0%;	Pred No. 9.1e-33;		
Matches	96;	Conservative	1;	Mismatches 1; Indels 0; Gaps 0;
QY	1	QVQLVESGGGVQVQPGSRSLRLSCAASGFFSSYAMHWMOAPGKGEWYAVISYDGSNKYY	60	
Db	1	QVQLVESGGGVQVQPGSRSLRLSCAASGFFSSYAMHWMOAPGKGEWYAVISYDGSNKYY	60	
QY	61	ADSVKGRFTISRDNSKNTLYIQOMSLRAEDPAVYYCAR	98	
Db	61	ADSVKGRFTISRDNSKNTLYIQOMSLRAEDPAVYYCAR	98	

	Query Match	Best Local Similarity	Score 505;	DB 9;	Length 122;
	Matches	Conservative	96.9%;	Pred. No. 1,16-32;	
	95;	3;	Mismatches	0;	Gaps 0;
QY	1	QVQLVGGGSGGVVQGRSLRSLSCAASGPFSSSYAMHWMAQABGKLEWYAVISYDQSNKTY	60		
Db	1	QIQILQSGGSGGVQGRSLRSLSCAASGPFSSSYAMHWMAQABGKLEWYAVISYDQSNKTY	60		
QY	61	ADSVYKGRFTISRDNSSKNTLYIQNNMSLRADTAIVYICAR	98		
Db	61	ADSVYKGRFTISRDNSSKNTLYIQNNMSLRADTAIVYICAR	98		

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US-09-880-748-1109
Publication No. US20030059937A1
GENERAL INFORMATION:
APPLICANT: Ruben et al.
TITLE OF INVENTION: Antibodies that immunospecifically bind BlyS
FILE REFERENCE: PF523
CURRENT APPLICATION NUMBER: US/09/880,748
PRIOR FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: 60/212,210
PRIOR FILING DATE: 2000-06-15
PRIOR APPLICATION NUMBER: 60/240,816
PRIOR FILING DATE: 2000-10-17
PRIOR APPLICATION NUMBER: 60/276,248
PRIOR FILING DATE: 2001-03-16
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/293,499
NUMBER OF SEQ ID NOS: 3239
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1109
LENGTH: 249
TYPE: PRT
ORGANISM: Homo sapiens
US-09-880-748-1109
Query Match
Best Local Similarity 98.4%; Score 504; DB 9; Length 249;
Matches 96; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Db
1 QVQLVSGGAVVQPGKSLRLISCAASGTFSSYAMHWYRAQPGKLEWYAVISYDGSKNTY 60
QVQLVSGGAVVQPGKSLRLISCAASGTFSSYAMHWYRAQPGKLEWYAVISYDGSKNTY 60
Db
61 ADSVKGRFTISRDNKNTLYLQNMSLRAEDTAVYYCAR 98
ADSVKGRFTISRDNKNTLYLQNMSLRAEDTAVYYCAR 98
Db
RESULT 9
US-09-880-748-1109
Publication No. US20030059937A1
GENERAL INFORMATION:
APPLICANT: Ruben et al.
TITLE OF INVENTION: Antibodies that immunospecifically bind BlyS
FILE REFERENCE: PF523
CURRENT APPLICATION NUMBER: US/09/880,748
PRIOR FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: 60/212,210
PRIOR FILING DATE: 2000-06-15
PRIOR APPLICATION NUMBER: 60/240,816
PRIOR FILING DATE: 2000-10-17
PRIOR APPLICATION NUMBER: 60/276,248
PRIOR FILING DATE: 2001-03-16
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/293,499
NUMBER OF SEQ ID NOS: 3239
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1109
LENGTH: 249
TYPE: PRT
ORGANISM: Homo sapiens
US-09-880-748-1627
Query Match
Best Local Similarity 98.6%; Score 505; DB 9; Length 252;
Matches 96; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
Db
1 QVQLVSGGAVVQPGKSLRLISCAASGTFSSYAMHWYRAQPGKLEWYAVISYDGSKNTY 60
QVQLVSGGAVVQPGKSLRLISCAASGTFSSYAMHWYRAQPGKLEWYAVISYDGSKNTY 60
Db
61 ADSVKGRFTISRDNKNTLYLQNMSLRAEDTAVYYCAR 98
ADSVKGRFTISRDNKNTLYLQNMSLRAEDTAVYYCAR 98

```

QY 61 ADVKGRFTISRDNKNTLYLQWNSLRADTAIVYCAR 98
DB 61 VDSVKGRTISRDNKNTLYLQWNSLRADTAIVYCAR 98

RESULT 10
US-09-144-886-68
Sequence 68, Application US/09144886
Patent No. US20020155114A1
GENERAL INFORMATION:
APPLICANT: Marks, James D
TITLE OF INVENTION: Therapeutic Monoclonal Antibodies That Neutralize Botulinum Neurotoxins
FILE REFERENCE: 2500.117USO
CURRENT FILING DATE: 1998-08-31
CURRENT APPLICATION NUMBER: US/09/144,886
NUMBER OF SEQ ID NOS: 98
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 68
LENGTH: 122
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: BONT/A clone
US-09-144-886-68

Query Match 98.2%; Score 503; DB 9; Length 122;
Best Local Similarity 98.0%; Pred. No. 1.6e-32;
Matches 96; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 QVOLVESGGGVQPGRSRLSCASGFTSSYAMHWROAPGKLEWVAIVSYDGSNKYY 60
DB 1 EVOLQESGGGVQPGRSRLSCASGFTSSYAMHWROAPGKLEWVAIVSYDGSNKYY 60
QY 61 ADVKGRFTISRDNKNTLYLQWNSLRADTAIVYCAR 98
DB 61 ADVKGRFTISRDNKNTLYLQWNSLRADTAIVYCAR 98

RESULT 11
US-10-194-975-26
Sequence 26, Application US/10194975
Publication No. US20030039649A1
GENERAL INFORMATION:
APPLICANT: Foote, Jefferson
TITLE OF INVENTION: Super Humanized Antibodies
FILE REFERENCE: 501231.01
CURRENT APPLICATION NUMBER: US/10/194,975
CURRENT FILING DATE: 2002-10-10
PRIOR APPLICATION NUMBER: US 60/305,111
PRIOR FILING DATE: 2001-07-12
NUMBER OF SEQ ID NOS: 122
SOFTWARE: PatentIn version 3.1
SEQ ID NO 26
LENGTH: 98
TYPE: PRT
ORGANISM: Homo sapiens
US-10-194-975-26

Query Match 97.9%; Score 501; DB 9; Length 98;
Best Local Similarity 98.0%; Pred. No. 1.9e-32;
Matches 96; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 QVOLVESGGGVQPGRSRLSCASGFTSSYAMHWROAPGKLEWVAIVSYDGSNKYY 60
DB 1 QVOLVESGGGVQPGRSRLSCASGFTSSYAMHWROAPGKLEWVAIVSYDGSNKYY 60
QY 61 ADVKGRFTISRDNKNTLYLQWNSLRADTAIVYCAR 98
DB 61 ADVKGRFTISRDNKNTLYLQWNSLRADTAIVYCAR 98

RESULT 12
US-09-880-748-512
Sequence 512, Application US/09880748
Publication No. US20030059937A1
GENERAL INFORMATION:
APPLICANT: Ruben et al.
TITLE OF INVENTION: Antibodies that Immunospecifically Bind BlyS
FILE REFERENCE: PF523
CURRENT APPLICATION NUMBER: US/09/880,748
CURRENT FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: 60/212,210
PRIOR FILING DATE: 2000-06-15
PRIOR APPLICATION NUMBER: 60/240,816
PRIOR FILING DATE: 2000-10-17
PRIOR APPLICATION NUMBER: 60/276,248
PRIOR FILING DATE: 2001-03-16
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/293,499
PRIOR FILING DATE: 2001-05-25
NUMBER OF SEQ ID NOS: 3239
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 512
LENGTH: 249
TYPE: PRT
ORGANISM: Homo sapiens
US-09-880-748-512

Query Match 97.9%; Score 501; DB 9; Length 249;
Best Local Similarity 96.9%; Pred. No. 4.5e-32;
Matches 95; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 QVOLVESGGGVQPGRSRLSCASGFTSSYAMHWROAPGKLEWVAIVSYDGSNKYY 60
DB 1 QVOLVESGGGVQPGRSRLSCASGFTSSYAMHWROAPGKLEWVAIVSYDGSNKYY 60
QY 61 ADVKGRFTISRDNKNTLYLQWNSLRADTAIVYCAR 98
DB 61 ADVKGRFTISRDNKNTLYLQWNSLRADTAIVYCAR 98

RESULT 13
US-10-153-382-17
Sequence 17, Application US/10153382
Publication No. US20030086930A1
GENERAL INFORMATION:
APPLICANT: Pfizer Products Inc.
TITLE OF INVENTION: USES OF ANTI-CTLA-4 ANTIBODIES
FILE REFERENCE: PC23019A
CURRENT APPLICATION NUMBER: US/10/153,382
CURRENT FILING DATE: 2002-05-22
PRIOR APPLICATION NUMBER: 60/293042
PRIOR FILING DATE: 2001-05-23
NUMBER OF SEQ ID NOS: 39
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 17
LENGTH: 451
TYPE: PRT
ORGANISM: Homo sapiens
US-10-153-382-17

Query Match 97.9%; Score 501; DB 9; Length 451;
Best Local Similarity 98.0%; Pred. No. 7.8e-32;
Matches 96; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 QVOLVESGGGVQPGRSRLSCASGFTSSYAMHWROAPGKLEWVAIVSYDGSNKYY 60
DB 1 QVOLVESGGGVQPGRSRLSCASGFTSSYAMHWROAPGKLEWVAIVSYDGSNKYY 60
QY 61 ADVKGRFTISRDNKNTLYLQWNSLRADTAIVYCAR 98
DB 61 ADVKGRFTISRDNKNTLYLQWNSLRADTAIVYCAR 98

Db 61 ADVKGRFTISRDNKNTLYLQMSLRADPTAVYYCAR 98

RESULT 14
US-09-880-748-2055

Sequence 2055, Application US/09880748
Publication No. US20030059937A1

GENERAL INFORMATION:

APPLICANT: Ruben et al.

TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys

FILE REFERENCE: PF523

CURRENT APPLICATION NUMBER: US/09/880,748

PRIOR FILING DATE: 2001-06-15

PRIOR APPLICATION NUMBER: 60/212,210

PRIOR FILING DATE: 2000-06-15

PRIOR APPLICATION NUMBER: 60/240,816

PRIOR FILING DATE: 2000-10-17

PRIOR APPLICATION NUMBER: 60/276,248

PRIOR FILING DATE: 2001-03-16

PRIOR APPLICATION NUMBER: 60/277,379

PRIOR FILING DATE: 2001-03-21

PRIOR APPLICATION NUMBER: 60/293,499

PRIOR FILING DATE: 2001-05-25

NUMBER OF SEQ ID NOS: 3239

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 2055

LENGTH: 241

TYPE: PRT

ORGANISM: Homo sapiens

US-09-880-748-2055

Query Match 97.5%; Score 499; DB 9; Length 241;

Best Local Similarity 96.9%; Pred. No. 6.2e-32; Mismatches 1; Indels 0; Gaps 0;

Matches 95; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

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Db 1 QVQLVESGGGVVQPGKSLRLSCAASGFTSSYAMHWVRQAPGKLEWVAVISYDSNKYY 60

OY 61 ADVKGRFTISRDNKNTLYLQMSLRADPTAVYYCAR 98

Db 61 ADVKGRFTISRDNKNTLYLQMSLRADPTAVYYCAR 98

RESULT 15

US-09-880-748-1330

Sequence 1330, Application US/09880748

Publication No. US20030059937A1

GENERAL INFORMATION:

APPLICANT: Ruben et al.

TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys

FILE REFERENCE: PF523

CURRENT APPLICATION NUMBER: US/09/880,748

PRIOR FILING DATE: 2001-06-15

PRIOR APPLICATION NUMBER: 60/212,210

PRIOR FILING DATE: 2000-06-15

PRIOR APPLICATION NUMBER: 60/240,816

PRIOR FILING DATE: 2000-10-17

PRIOR APPLICATION NUMBER: 60/276,248

PRIOR FILING DATE: 2001-03-16

PRIOR APPLICATION NUMBER: 60/277,379

PRIOR FILING DATE: 2001-03-21

PRIOR APPLICATION NUMBER: 60/293,499

PRIOR FILING DATE: 2001-05-25

NUMBER OF SEQ ID NOS: 3239

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 1330

LENGTH: 247

TYPE: PRT

ORGANISM: Homo sapiens

US-09-880-748-1330

Query Match 97.5%; Score 499; DB 9; Length 241;

Best Local Similarity 96.9%; Pred. No. 6.3e-32; Mismatches 1; Indels 0; Gaps 0;

Matches 95; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 QVQLVESGGGVVQPGKSLRLSCAASGFTSSYAMHWVRQAPGKLEWVAVISYDSNKYY 60

Db 1 QVQLVESGGGVVQPGKSLRLSCAASGFTSSYAMHWVRQAPGKLEWVAVISYDSNKYY 60

OY 61 ADVKGRFTISRDNKNTLYLQMSLRADPTAVYYCAR 98

Db 61 ADVKGRFTISRDNKNTLYLQMSLRADPTAVYYCAR 98

Search completed: June 3, 2003, 08:52:53
Job time: 24.2457 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: June 3, 2003, 08:10:19 ; Search time 14.884 Seconds
(without alignments)
193.728 Million cell updates/sec

Title: US-09-644-668A-15

Perfect score: 512 1 QVQLVESGGGVQPGKSLRL.....LYLQNNSLRAEDTAVYYCAR 98

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-Processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents AA:*

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- 2: /cgn2_6/prodata/1/iaa/5B-COMB.pep:*
- 3: /cgn2_6/prodata/1/iaa/5A-COMB.pep:*
- 4: /cgn2_6/prodata/1/iaa/5B-COMB.pep:*
- 5: /cgn2_6/prodata/1/iaa/5A-COMB.pep:*
- 6: /cgn2_6/prodata/1/iaa/5B-COMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	512	100.0	98	1	US-08-211-202-118
2	512	100.0	120	1	US-07-942-245-35
3	509	99.4	119	1	US-08-331-398A-46
4	509	99.4	119	2	US-08-331-397B-46
5	509	99.4	119	2	US-08-759-804A-46
6	509	99.4	119	4	US-09-227-693-46
7	508	99.2	117	3	US-08-545-809A-115
8	507	99.0	116	1	US-08-211-202-141
9	501.5	97.9	123	4	US-08-983-607-38
10	489	95.5	120	1	US-08-211-202-135
11	487	95.1	117	3	US-08-545-809A-117
12	486	94.9	117	4	US-09-025-765B-24
13	482	94.1	126	4	US-09-240-274-26
14	482	94.1	310	4	US-09-079-029-11
15	481	93.9	128	1	US-08-476-039-96
16	481	93.9	128	1	US-08-476-349A-96
17	479	93.6	125	4	US-09-240-274-24
18	478	93.4	125	4	US-09-240-274-9
19	477	93.2	123	1	US-08-478-039-94
20	477	93.2	123	1	US-08-476-349A-94
21	477	93.2	125	4	US-09-240-274-8
22	477	93.2	125	4	US-09-240-274-20
23	477	93.2	125	4	US-09-240-274-21
24	477	93.2	125	4	US-09-240-274-22
25	477	93.2	125	4	US-09-240-274-1
26	476	93.0	125	2	US-08-428-197-5
27	476	93.0	125	2	US-08-428-197-6

28	476	93.0	125	5	PCT-US93-10555-5	Sequence 5, Appl1
29	476	93.0	125	5	PCT-US93-10555-6	Sequence 5, Appl1
30	476	93.0	126	4	US-09-240-274-153	Sequence 153, Appl
31	476	93.0	141	1	US-08-259-372A-2	Sequence 2, Appl1
32	476	93.0	141	1	US-08-468-671-2	Sequence 2, Appl1
33	474	92.6	126	4	US-09-240-274-25	Sequence 25, Appl1
34	471.5	92.1	126	4	US-09-240-274-149	Sequence 149, Appl
35	471	92.0	128	4	US-09-240-274-142	Sequence 142, Appl
36	469	91.6	125	4	US-09-240-274-152	Sequence 152, Appl
37	469	91.6	126	4	US-09-240-274-152	Sequence 152, Appl
38	465	90.8	124	4	US-09-240-274-5	Sequence 5, Appl1
39	465	90.8	124	4	US-09-240-274-6	Sequence 6, Appl1
40	465	90.8	125	4	US-09-240-274-140	Sequence 140, Appl
41	465	90.8	125	4	US-09-240-274-151	Sequence 151, Appl
42	464	90.6	287	4	US-08-862-124-17	Sequence 17, Appl
43	464	90.6	304	4	US-08-862-124-14	Sequence 14, Appl
44	462	90.2	113	3	US-08-974-899-6	Sequence 6, Appl1
45	462	90.2	122	2	US-07-934-373C-21	Sequence 21, Appl

ALIGNMENTS

RESULT 1
US-08-211-202-118
Sequence 118, Application US/08211202
Patent No. 5565332
GENERAL INFORMATION:
APPLICANT: HOOGENBOOM, Hendricus Renerus Jacobus Matreus
APPLICANT: BATER, Michael
APPLICANT: JESPEERS, Laurent Stephane Anne Therese
APPLICANT: WINTER, Gregory Paul
TITLE OF INVENTION: Production of chimeric antibodies - a
TITLE OF INVENTION: Combinatorial approach
NUMBER OF SEQUENCES: 144
CORRESPONDENCE ADDRESS:
ADDRESSEE: David W. Clough, Marshall O'Toole Gerstein Murray &
ADDRESSEE: Borlun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/211,202
FILING DATE: 23-SEP-1992
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9120252.3
FILING DATE: 23-SEP-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9120377.8
FILING DATE: 25-SEP-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9206316.9
FILING DATE: 24-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9206372.6
FILING DATE: 24-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB92/00883
FILING DATE: 15-MAY-1992
ATTORNEY/AGENT INFORMATION:
NAME: David W. Clough
REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 28111/31960
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300

APPLICANT: PADLAN, Eduardo A.
APPLICANT: JUNG, Sun-Hee
APPLICANT: LEE, Byungkook
TITLE OF INVENTION: HUMANIZED TUMOR-SPECIFIC ANTIBODY
TITLE OF INVENTION: FRAGMENTS, FUSION PROTEINS, AND USES THEREOF
NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Kourile and Crew
STREET: Stewart Street Tower, One Market Plaza
CITY: San Francisco
STATE: California
COUNTRY: US
ZIP: 94105-1493
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/227,693
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/331,396
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/767,331
FILING DATE: 30-SEP-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/596,289
FILING DATE: 12-OCT-1990
ATTORNEY/AGENT INFORMATION:
NAME: Weber, Ellen Lauver
REGISTRATION NUMBER: 32,762
REFERENCE/DOCKET NUMBER: 15280-126-1-3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 543-9600
TELEFAX: (415) 543-5043
INFORMATION FOR SEQ ID NO: 46:
SEQUENCE CHARACTERISTICS:
LENGTH: 119 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Protein
LOCATION: 1..119
OTHER INFORMATION:
OTHER INFORMATION: 56P1/CL VH region"
US-09-227-693-46
Query Match 99.4%; Score 509, DB 4, Length 119,
Best Local Similarity 99.0%; Pred. No. 2e-47;
Matches 97, Conservative 1, Mismatches 0, Indels 0, Gaps 0;
QY 1 QVQLVESGGGVGVQGRSLRLSCAASGFTFSYAMHWYRQAPGKLEWYAVISYGSNKYY 60
DB 1 QVQLVESGGGVGVQGRSLRLSCAASGFTFSYAMHWYRQAPGKLEWYAVISYGSNKYY 60
QY 61 ADSVKGRTISRDNKNTLYLQWNSLAEDTAVYYCAR 98
DB 61 ADSVKGRTISRDNKNTLYLQWNSLAEDTAVYYCAR 98
RESULT 7
US-08-545-809A-115
Sequence 115, Application US/08545809A
Patent No. 6096878
GENERAL INFORMATION:
APPLICANT: Honjo, Tadaaki
APPLICANT: Matsuda, Fumihiko
TITLE OF INVENTION: HUMAN IMMUNOGLOBULIN VH GENE
TITLE OF INVENTION: SEGMENTS AND DNA FRAGMENTS CONTAINING THE SAME

NUMBER OF SEQUENCES: 145
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson, P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: US
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/545,809A
FILING DATE: 27-MAR-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/JP93/00603
FILING DATE: 10-MAY-1993
ATTORNEY/AGENT INFORMATION:
NAME: Freeman, John W.
REGISTRATION NUMBER: 29,066
REFERENCE/DOCKET NUMBER: 06501/004001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-542-5070
TELEFAX: 617-542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 115:
SEQUENCE CHARACTERISTICS:
LENGTH: 117 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-545-809A-115
Query Match 99.2%; Score 508, DB 3, Length 117,
Best Local Similarity 99.0%; Pred. No. 2.5e-47;
Matches 97, Conservative 0, Mismatches 1, Indels 0, Gaps 0;
QY 1 QVQLVESGGGVGVQGRSLRLSCAASGFTFSYAMHWYRQAPGKLEWYAVISYGSNKYY 60
DB 20 QVQLVESGGGVGVQGRSLRLSCAASGFTFSYAMHWYRQAPGKLEWYAVISYGSNKYY 79
QY 61 ADSVKGRTISRDNKNTLYLQWNSLAEDTAVYYCAR 98
DB 80 ADSVKGRTISRDNKNTLYLQWNSLAEDTAVYYCAR 117
RESULT 8
US-08-211-202-141
Sequence 141, Application US/08211202
Patent No. 5565332
GENERAL INFORMATION:
APPLICANT: HOOGENBOOM, Hendricus Renetus Jacobus Matheus
APPLICANT: BAYER, Michael
APPLICANT: JESPER, Laurent Stephane Anne Therese
APPLICANT: WINTER, Gregory Paul
TITLE OF INVENTION: Production of chimeric antibodies - a
TITLE OF INVENTION: combinatorial approach
NUMBER OF SEQUENCES: 144
CORRESPONDENCE ADDRESS:
ADDRESSEE: David W. Clough, Marshall O'Toole Gerstein Murray &
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/211,202
FILING DATE: 23-SEP-1992
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9120252.3
FILING DATE: 23-SEP-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9120377.8
FILING DATE: 25-SEP-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9206318.9
FILING DATE: 24-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9206372.6
FILING DATE: 24-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB92/00883
FILING DATE: 15-MAY-1992
ATTORNEY/AGENT INFORMATION:
NAME: David W. Clough
REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 28111/31960
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
TELEFAX: 312-474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 141:
SEQUENCE CHARACTERISTICS:
LENGTH: 116 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-211-202-141

Query Match 99.0%; Score 507; DB 1; Length 116;
Best Local Similarity 100.0%; Pred. No. 3,2e-47;
Matches 97; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QVQLVESGGGVQPGKSLRLSCAASGTPSSYAMHWVRQAPGKLEWVAIVSYDGSNKYY 60
DB 1 QVQLVESGGGVQPGKSLRLSCAASGTPSSYAMHWVRQAPGKLEWVAIVSYDGSNKYY 60
QY 61 ADSVKGRTISRDNKNTLYLQNSLRADDTAVYYCA 97
DB 61 ADSVKGRTISRDNKNTLYLQNSLRADDTAVYYCA 97

RESULT 9
US-08-983-607-38
Sequence 38, Application US/08983607.
Patent No. 6140470
GENERAL INFORMATION:
APPLICANT: Alan Garen
APPLICANT: Xiaohong Cai
TITLE OF INVENTION: Human Anti-Tumor Monoclonal Anti-
TITLE OF INVENTION: bodies
NUMBER OF SEQUENCES: 51
CORRESPONDENCE ADDRESS:
ADDRESSER: Department of Molecular Biophysics
AND Biochemistry, Yale University
STREET: 266 Whitney Avenue
CITY: New Haven
STATE: Connecticut
COUNTRY: United States of America
ZIP: 06520-8114
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" 1.44 MB diskette
COMPUTER: IBM PC
OPERATING SYSTEM: MS DOS
SOFTWARE: Word Processing
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/983,607

FILING DATE: April 27, 1998
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/IB96/01032
FILING DATE: June 28, 1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Mary M. Klineky
REGISTRATION NUMBER: 32423
REFERENCE/DOCKET NUMBER: OCR-679
TELECOMMUNICATION INFORMATION:
TELEPHONE: 203-773-9544
TELEFAX: 203-773-1183
INFORMATION FOR SEQ ID NO: 38:
SEQUENCE CHARACTERISTICS:
LENGTH: 123 residues
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE:
DESCRIPTION: polypeptide
ORIGINAL SOURCE:
ORGANISM: Homo sapiens (melanoma patient
ORGANISM: immunized with autologous tumor cells)
INDIVIDUAL ISOLATE: peripheral blood lympho-
INDIVIDUAL ISOLATE: cyles
IMMEDIATE SOURCE:
LIBRARY: DM414 scFv antibodies obtained from
LIBRARY: fuses fusion phage construct
CLONE: V575
FEATURE:
NAME/KEY: heavy chain
US-08-983-607-38

Query Match 97.9%; Score 501.5; DB 4; Length 123;
Best Local Similarity 99.0%; Pred. No. 1.3e-46;
Matches 98; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 QVQLVESGGGVQPGKSLRLSCAASGTPSSYAMHWVRQAPGKLEWVAIVSYDGSNKYY 60
DB 1 QVQLVESGGGVQPGKSLRLSCAASGTPSSYAMHWVRQAPGKLEWVAIVSYDGSNKYY 60
QY 61 ADSVKGRTISRDNKNTLYLQNSLRADDTAVYYCAR 98
DB 61 ADSVKGRTISRDNKNTLYLQNSLRADDTAVYYCAR 99

RESULT 10
US-08-211-202-135
Sequence 135, Application US/08211202
Patent No. 5565332
GENERAL INFORMATION:
APPLICANT: HOOGERBOOM, Hendricus Remerus Jacobus Mattheus
APPLICANT: BATER, Michael
APPLICANT: JESPEERS, Laurent Stephane Anne Therese
APPLICANT: WINTER, Gregory Paul
TITLE OF INVENTION: Production of chimeric antibodies - a
TITLE OF INVENTION: combinatorial approach
NUMBER OF SEQUENCES: 144
CORRESPONDENCE ADDRESS:
ADDRESSER: David W. Clough, Marshall O'Toole Gerstein Murray &
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/211,202
FILING DATE: 23-SEP-1992
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9120252.3
FILING DATE: 23-SEP-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9120377.8
FILING DATE: 25-SEP-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9206318.9
FILING DATE: 24-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9206372.6
FILING DATE: 24-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB92/00883
FILING DATE: 15-MAY-1992
ATTORNEY/AGENT INFORMATION:
NAME: David W. Clough
REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 28111/31960
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
TELEFAX: 312-474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 135:
SEQUENCE CHARACTERISTICS:
LENGTH: 120 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-211-202-135

Query Match 95.5%; Score 489; DB 1; Length 120;
Best Local Similarity 94.9%; Pred. No. 2.8e-45;
Matches 93; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
QY 1 QVQLVESGGGVVQPGKSLRLSCAASGFTFSYAMHWVQAPKGLIEWAVISYDGSNKTY 60
DB 1 QVQLVESGGGVVQPGKSLRLSCAASGFTFSYAMHWVQAPKGLIEWAVISYDGSNKTY 60
QY 61 ADSVKGRTISRDNKNTLYLQMSLRADETAVYYCAR 98
DB 61 ADSVKGRTISRDNKNTLYLQMSLRADETAVYYCAR 98

RESULT 11
US-08-545-809A-117
Sequence 117, Application US/08545809A
Patent No. 6096878
GENERAL INFORMATION:
APPLICANT: Honjo, Tasuku
APPLICANT: Matsuda, Fumihiko
TITLE OF INVENTION: HUMAN IMMUNOGLOBULIN VH GENE
NUMBER OF SEQUENCES: 145
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson, P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: US
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/545,809A
FILING DATE: 27-MAR-1996
PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/JP93/00603
FILING DATE: 10-MAY-1993
ATTORNEY/AGENT INFORMATION:
NAME: Freeman, John W.
REGISTRATION NUMBER: 29,066
REFERENCE/DOCKET NUMBER: 06501/004001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-542-5070
TELEFAX: 617-542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 117:
SEQUENCE CHARACTERISTICS:
LENGTH: 117 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-545-809A-117

Query Match 95.1%; Score 487; DB 3; Length 117;
Best Local Similarity 94.9%; Pred. No. 4.5e-45;
Matches 93; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
QY 1 QVQLVESGGGVVQPGKSLRLSCAASGFTFSYAMHWVQAPKGLIEWAVISYDGSNKTY 60
DB 20 QVQLVESGGGVVQPGKSLRLSCAASGFTFSYAMHWVQAPKGLIEWAVISYDGSNKTY 79
QY 61 ADSVKGRTISRDNKNTLYLQMSLRADETAVYYCAR 98
DB 80 ADSVKGRTISRDNKNTLYLQMSLRADETAVYYCAR 117

RESULT 12
US-09-025-769B-24
Sequence 24, Application US/09025769B
Patent No. 6300064
GENERAL INFORMATION:
APPLICANT: Knappik, Achim
APPLICANT: Pack, Peter
APPLICANT: Illeg, Vic
APPLICANT: Ge, Liming
APPLICANT: Moroney, Simon
APPLICANT: Plueckhuhn, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
NUMBER OF SEQUENCES: 373
CORRESPONDENCE ADDRESS:
ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
STREET: 1251 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10021
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30. (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/025,769B
FILING DATE: 18-FEB-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: James F. Haley, Jr., Esq.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: MORPHO/5
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)596-9000
TELEFAX: (212)596-9090
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 117 amino acids
TYPE: amino acid

STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-025-769B-24

Query Match 94.9%; Score 486; DB 4; Length 117;
Best Local Similarity 93.9%; Pred. No. 5.7e-45;
Matches 92; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 QVQLVSGGAVQPGKSLRLSCAASGFTSSVAMHWROAPGKLEWVAIVISYDGSNKYY 60
DB 1 EVQLVSGGAVQPGKSLRLSCAASGFTSSVAMHWROAPGKLEWVAIVISYDGSNKYY 60

QY 61 ADSVKGRTISRDNKNTLYLQMSLRADPTAVYYCAR 98
DB 61 ADSVKGRTISRDNKNTLYLQMSLRADPTAVYYCAR 98

RESULT 13

US-09-240-274-26
Sequence 26, Application US/09240274
Patent No. 6255455

GENERAL INFORMATION:
APPLICANT: Siegel, Donald L.
TITLE OF INVENTION: RH(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
FILE REFERENCE: 09596-4202
CURRENT APPLICATION NUMBER: US/09/240,274
CURRENT FILING DATE: 1999-01-29
EARLIER APPLICATION NUMBER: 60/081,380
EARLIER FILING DATE: 1998-04-10
EARLIER APPLICATION NUMBER: 60/028,550
NUMBER OF SEQ ID NOS: 224
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 26
LENGTH: 126
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: anti-Rh(D) chain D31
US-09-240-274-26

Query Match 94.1%; Score 482; DB 4; Length 126;
Best Local Similarity 91.8%; Pred. No. 1.7e-44;
Matches 90; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

QY 1 QVQLVSGGAVQPGKSLRLSCAASGFTSSVAMHWROAPGKLEWVAIVISYDGSNKYY 60
DB 1 EVQLVSGGAVQPGKSLRLSCAASGFTSSVAMHWROAPGKLEWVAIVISYDGSNKYY 60

QY 61 ADSVKGRTISRDNKNTLYLQMSLRADPTAVYYCAR 98
DB 61 ADSVKGRTISRDNKNTLYLQMSLRADPTAVYYCAR 98

RESULT 14

US-09-079-029-11
Sequence 11, Application US/09079029
Patent No. 6342369

GENERAL INFORMATION:
APPLICANT: Adams, Camilla W.
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Chunchatrapal, Anan
APPLICANT: Kim, Kyung J.
TITLE OF INVENTION: Apo-2 Receptor
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA

ZIP: 94080

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/079,029
FILING DATE:

CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Maerschang, Diane L.

REGISTRATION NUMBER: 35,600

REFERENCE/DOCKET NUMBER: P1101R2

TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/425-5416

TELEFAX: 650/952-9881

INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 310 amino acids
TYPE: Amino Acid
TOPOLOGY: linear
US-09-079-029-11

Query Match 94.1%; Score 482; DB 4; Length 310;
Best Local Similarity 93.9%; Pred. No. 4.7e-44;
Matches 92; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 1 QVQLVSGGAVQPGKSLRLSCAASGFTSSVAMHWROAPGKLEWVAIVISYDGSNKYY 60
DB 40 QVQLVSGGAVQPGKSLRLSCAASGFTSSVAMHWROAPGKLEWVAIVISYDGSNKYY 99

QY 61 ADSVKGRTISRDNKNTLYLQMSLRADPTAVYYCAR 98
DB 100 ADSVKGRTISRDNKNTLYLQMSLRADPTAVYYCAR 137

RESULT 15

US-08-478-039-96
Sequence 96, Application US/08478039
Patent No. 5681722

GENERAL INFORMATION:
APPLICANT: Newman, Roland A.
APPLICANT: Hanna, Nabil
APPLICANT: Raab, Ronald W.
TITLE OF INVENTION: Recombinant Antibodies for Human Therapy
NUMBER OF SEQUENCES: 114
CORRESPONDENCE ADDRESS:
ADDRESSEE: BURNS, DOANE, SWICKER & MATHIS
STREET: 699 Prince St.
CITY: Alexandria
STATE: VA
COUNTRY: USA
ZIP: 22313-1404

COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/478,039
FILING DATE: 07-JUN-1995

CLASSIFICATION: 435

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/379,072
FILING DATE: 25-JAN-1995

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/912,292
FILING DATE: 10-JUL-1992

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/856,281
FILING DATE: 23-MAR-1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/735,064
FILING DATE: 25-JUL-1991
ATTORNEY/AGENT INFORMATION:
NAME: Teskin Esq., Robin L.
REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 012712-160
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-836-6620
TELEFAX: 703-836-2021
INFORMATION FOR SEQ ID NO: 96:
SEQUENCE CHARACTERISTICS:
LENGTH: 128 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
MOLECULE TYPE: peptide
POSITION IN GENOME:
CHROMOSOME/SEGMENT: RF SJ2
US-08-478-039-96

Query Match 93.9%; Score 481; DB 1; Length 128;
Best Local Similarity 94.9%; Pred. No. 2.2e-44;
Matches 93; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY	1	QVQLVSGGCVVQPGKSLRLSCAASGFTSSVAMHWVQAPGKGLIEWVAIVSYDGSNKYY	60
DB	1	QVQLVSGGCVVQPGKSLRLSCAASGFTSSVAMHWVQAPGKGLIEWVXIVSYDGSNKYY	60
QY	61	ADSVKGRFTISRDNKNTLYLQMNSLRADDTAVYYCAR	98
DB	61	ADSVKGRFTISRDNKNTLYLQMNSLRADDTAVYYCAR	98

Search completed: June 3, 2003, 08:24:17
Job time: 15.884 secs